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Genotex version 9.1.4
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:15:05 : Search time 29.0579 Seconds
(without alignments)
350.688 Million cell updates/sec

Title: US-09-893-615-89

Sequence: 1 QIVLSQSPAILSLASPEKVT.....COOWSSNPPTFGCGTMLR 106

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR_73
2: PIR_73
3: PIR_73
4: PIR_73

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	523	94.1	106	2	PL0082
2	492	88.5	107	2	A42848
3	480	86.3	107	2	PC4405
4	474	85.3	107	2	A30562
5	473	85.1	105	2	S26338
6	469	84.4	107	2	B30562
7	465.5	83.9	108	2	G30560
8	465.5	83.7	108	2	S38720
9	462	83.1	140	2	PL0013
10	459	82.6	106	2	PS0071
11	458	82.4	107	2	B49049
12	458	82.4	104	2	HP0011
13	458	82.4	130	1	JL0079
14	457	82.2	103	2	S29591
15	454	81.7	100	2	S29590
16	454	81.7	107	2	PF0406
17	452	81.3	97	2	S26341
18	446	80.2	106	2	B54378
19	445	80.0	235	2	S35058
20	444	79.9	107	2	S11118
21	442.5	79.6	104	2	JC6076
22	442	79.5	107	2	S11119
23	440	79.1	130	2	A32513
24	437	78.6	97	2	PH1084
25	434	78.1	107	2	S11121
26	433	77.9	107	2	S11117
27	433	77.9	130	2	B32456
28	433	77.9	130	2	S04573
29	430	77.3	99	2	S29585

30	429	77.2	106	2	G27887	ig kappa chain v r
31	427	76.8	97	2	PH1084	ig light chain v r
32	426	76.6	94	2	S26440	ig kappa chain v r
33	426	76.6	99	2	D38601	ig kappa chain v r
34	425	76.4	109	2	PRO405	ig light chain v r
35	423	76.1	95	2	D33730	ig kappa chain v r
36	423	76.1	107	2	S11112	ig kappa chain v r
37	423	76.1	107	2	S11113	ig kappa chain v r
38	423	76.1	108	2	S29581	ig kappa chain v r
39	421	75.7	108	2	PL0278	ig kappa chain v r
40	420	75.5	109	2	PRO404	ig kappa chain v r
41	420	75.5	132	2	S05268	ig kappa chain v r
42	419	75.4	106	2	PS0070	ig kappa chain v r
43	418	75.2	107	1	KVMSX4	ig kappa chain v r
44	417	75.0	108	2	PL0276	ig kappa chain v r
45	417	75.0	108	2	PL0277	ig kappa chain v r

ALIGNMENTS

RESULT 1
PL0082
ig kappa chain v region (2D3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0082
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brail, M.; Slanov, M.; Urbain, J. Exp. Med. 169, 519-533, 1989
J. Title: Structural characterization of antidiabetic antibodies: evidence that Ab A:Reference number: PL0080; MUID:89094246; PMID:2452056
A:Accession: PL0082
A:Molecule type: mRNA
A:Residues: 1-106 <MEM>
A:Experimental source: strain BALB/c
A:Note: the sequence shown here is from the V kappa region of an antidiabetic monoclonal antibody
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:16-89/Domain: Immunoglobulin homology <IMW>

Query Match 94.1% Score 523; DB 2; Length 106;
Best Local Similarity 94.3% Pred. No. 9.2e-38;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps

OY 1 QIVLSQSPAILSLASPEKVTTCRASSSVNMYOQKPPSSPRKWTASINLASGVAR 60
DB 1 QIVLSQSPAILSLASPEKVTTCRASSSVNMYOQKPPSSPRKWTASINLASGVAR 60
OY 61 FSGSGSTSYSLTISRVEAEDATYYCOOWSSNPPTFGCGTMLR 106
DB 61 FSGSGSTSYSLTISRVEAEDATYYCOOWSSNPPTFGCGTMLR 106

RESULT 2

A42848
ig light chain v region - mouse (fragment)
N:Alternate names: L6 anti-tumor antibody
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A42848; S33902
R:Feil, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schlawen, G.L.; Marken, J. Biol. Chem. 267, 15552-15558, 1992
J. Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and characterization of the antibody
A:Reference number: A42848; MUID:92348410; PMID:1635794
A:Accession: A42848
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <FEU>
A:Cross-references: EMBL:M90690
A:Note: sequence extracted from NCBI database (NCBI:109958, NCBI:109959)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:16-89/Domain: Immunoglobulin homology <IMW>

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DR	N-PSDB: AAT79900.
XX	Inhibiting thrombosis with self-limiting antibody to coagulation
PT	factor - avoids uncontrolled bleeding by providing only partial
PT	inhibition
XX	
PS	Example 7: Page 128; 150pp; English.
XX	
CC	This polypeptide comprises a mouse-human chimeric antibody
CC	light chain in which the variable region is derived from mouse
CC	anti-human factor IX monoclonal antibody BC2 (see AA24531) and
CC	human sequences from the immunoglobulin RF-TS3'CL framework.
CC	It can be expressed in transfected mammalian cells utilizing a
CC	cDNA construct (see AAT79900) obtained by PCR amplification (see
CC	AAT79997-98) of BC2 cDNA and insertion of the PCR product into
CC	pFgZHC 1-3 cDNA (see AAT7374). Claimed anti-factor IX chimeric
CC	antibodies are useful in the treatment of thrombosis.
XX	
SO	Sequence 106 AA:
Query Match	94.6%; Score 526; DB 18; Length 106;
Best Local Similarity	95.3%; Pred. No. 1.8e-30;
Matches 101; Conservative	1; Mismatches 4; Indels 0; Gaps 0.
OY	1 OYLVSOSPAILIASAGGEKVTMTCRASSSYNYMHVYQOKPGSPKPMISATSNLASGVPAR 60
Dd	1 OLVLSSOPAILLSASPEKEKVTMTCRASSSYNYMHVYQOKPGSPKPMIVATSNLASGVPAR 60
OY	61 FSGSGSGTYSYSLTISRFEADAATYYCQOWSSNPFTFGGTMLEIR 106
Dd	61 FSGSGSGTYSYSLTISRFEADAATYYCQOWSSINPRTFGGCTKLEIK 106
RESULT 2	
AAU81002	
ID	AAU81002 standard; Protein: 106 AA.
XX	
AC	AMU81002:
DT	
XX	09-APR-2002 (first entry)
DE	
XX	Mouse-human light chain polypeptide.
KW	Human; mouse: BC2; animal post-thromboembolic induced ischaemia;
KM	thrombolytic agent; anti-factor IX antibody; plasminogen activator;
KM	thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KM	vasotrophic; cardiac; anti-respiratory syncytial virus;
XX	heavy chain variable region; light chain variable region.
OS	Chimeric - Mus sp.
OS	Chimeric - Homo sapiens.
XX	
PN	WO200187339-A1.
XX	
PD	22-NOV-2001.
PF	05-OCT-2000; 2000WO-US27438.
PR	15-MAY-2000; 2000US-0571434.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PI	Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
XX	
XX	WPI: 2002-082944/11.
DR	N-PSDB: ABK24005.
PT	Treating post-thromboembolic induced ischaemia in an animal by
PT	administering anti-factor IX antibody in combination with a plasminogen
XX	activator
XX	
PS	Example 7: Page 155-156; 163pp; English.
XX	

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CC The invention relates to a method for treating an animal
CC post-thrombotic induced ischemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thrombotic induced
CC ischemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating
CC post-thrombotic-induced ischemia, for preventing thrombotic
CC stroke in an animal, and for reducing a required dose of a thrombotic
CC agent. Sequences AA08972-AA09104 represent antibodies and vector
CC polypeptides used in the method of the invention.
CC
SO Sequence 106 AA:
SO
Query Match 94.6% Score 526 DB 33 Length 106:
Best Local Similarity 95.3% Pred. No. 1.8e-35
Matches 101: Conservative 1; Mismatches 4; Indels 0; Gaps 0.
OY 1 OIVISOSPALTSPEKVTMTGRASSSVNWMWVQOKPGSS-SKWTLSATSNLASGVPAR 60
DB 1 OIVISOSPALTSPEKVTMTGRASSSVNWMWVQOKPGSS-SKWTLSATSNLASGVPAR 60
OY 61 FSGSGSGTSTLTISRVEAEDAATYYCOQWSSNPRTFGCGTNIILK 104
DB 61 FSGSGSGTSTLTISRVEAEDAATYYCOQWSSNPRTFGCGTNIILK 105
RESULT 3
AAW24520
AAW24520 standard; Protein: 107 AA.
XX
XX AAW24520:
XX
XX 26-DEC-1997 (first entry)
XX
DE Mouse anti-human factor IX antibody BC2 light chain variable region.
XX
XX Thrombosis: therapy: factor IX: anticoagulant: monoclonal antibody:
XX humanised antibody: antibody engineering: light chain: CDR:
XX complementarity determining region: myocardial infarction:
XX angina: atrial fibrillation: stroke: kidney damage:
XX pulmonary embolism: deep vein thrombosis: coronary angioplasty:
XX disseminated intravascular coagulation: artificial organ: sepsis:
XX shunt: prosthesis.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 24..33
XX /label= CDR1
XX /note= "(Claim 23)"
XX Region 49..55
XX /label= CDR2
XX /note= "(Claim 23)"
XX Region 88..96
XX /label= CDR3
XX /note= "(Claim 23)"
XX
XX WO9726010-A1.
XX
XX 24-JUL-1997.
XX
XX 17-JAN-1997: 97WO-US00759.
XX
XX 24-OCT-1996: 96US-0029119.
XX
XX 17-JAN-1996: 96US-0010108.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
XX Nichols AJ, Padian EA, Patel AH, Sylvester DR;
XX
XX WPI: 1997-385117/35.

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:25:20 ; Search time 2.25869 Seconds
(without alignments)
638.431 Million cell updates/sec

Title: US-09-893-615-1
Perfect score: 15

Sequence: 1 WRMYFSHRHAHLRSP 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries


Database :

1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	296	2	A40996 phenylalanine 4-mo
2	6	40.0	352	2	A71447 hypothetical prote
3	6	40.0	556	2	T19824 hypothetical prote
4	6	40.0	910	2	E89918 2-oxoglutarate deh
5	6	40.0	942	2	C81139 probable oxoglutar
6	6	40.0	943	1	S07776 oxoglutarate deh
7	6	40.0	943	2	G83448 2-oxoglutarate deh
8	6	40.0	1037	2	T27345 hypothetical prote
9	5	33.3	98	2	S39402 hupf protein - Bra
10	5	33.3	101	2	F72515 hypothetical prote
11	5	33.3	142	2	T22156 hypothetical prote
12	5	33.3	147	2	D83261 probable transcrip
13	5	33.3	148	2	AB0200 conserved hypotet
14	5	33.3	151	2	AC2084 phosphate metabo
15	5	33.3	176	2	T08254 probable transpo
16	5	33.3	190	2	D70828 hypothetical prote
17	5	33.3	195	2	S34993 nitrite reductase
18	5	33.3	196	2	S81553 conserved hypotet
19	5	33.3	198	2	S25656 T-cell surface gly
20	5	33.3	200	2	G83032 hypothetical prote
21	5	33.3	210	2	T28824 hypothetical prote
22	5	33.3	214	2	AB3589 protocatechuate 3,
23	5	33.3	216	2	A99333 hypothetical prote
24	5	33.3	216	2	D70554 hypothetical prote
25	5	33.3	216	2	T38520 conserved hypotet
26	5	33.3	217	2	G69547 conserved hypotet
27	5	33.3	225	2	T15228 probable histone B
28	5	33.3	226	2	A11168 transcription regu
29	5	33.3	234	2	A53367 phosphatase codb -



30	5	33.3	234	2	T34600 hypothetical prote
31	5	33.3	235	1	RWHU8 T-cell surface gly
32	5	33.3	243	2	C95266 probable ABC trans
33	5	33.3	244	2	T29079 hypothetical prote
34	5	33.3	246	2	T31956 hypothetical prote
35	5	33.3	248	2	B95334 probable transcrip
36	5	33.3	249	2	T37609 hypothetical zinc
37	5	33.3	252	2	A84866 probable glyoxalas
38	5	33.3	252	2	AC1181 hypothetical prote
39	5	33.3	252	2	AD1538 hypothetical prote
40	5	33.3	253	2	D75301 hypothetical prote
41	5	33.3	254	2	H83334 probable transcrip
42	5	33.3	257	2	T48058 RING-H2 zinc flnge
43	5	33.3	261	2	S51935 probable MADS-box
44	5	33.3	270	2	B84813 probable RING zinc
45	5	33.3	273	2	G83968 hypothetical prote

ALIGNMENTS

RESULT 1
A40996 phenylalanine 4-monooxygenase (EC 1.14.16.1) - Chromobacterium violaceum
N:Alternate names: phenylalaninase, phenylalanine 4-hydroxylase
C:Species: Chromobacterium violaceum
C>Date: 03-Aug-1992 #sequence, revision 03-Aug-1992 #text, change 31-Mar-2000
C:Accession: A40996; #40996
R:Onishi, A.; Liotta, L.J.; Benkovic, S.J.
J. Biol. Chem. 266, 18454-18459, 1991
A:Title: Cloning and expression of Chromobacterium violaceum phenylalanine hydroxylase
A:Reference number: A40996; MUID:92011593; PMID:1655752
A:Accession: A40996
A:Molecule type: DNA
A:Residues: 1-296 <ONS>
A:Cross-references: GB:M55915; NID:g144481; PIDN:AAA23115.1; PID:g144482
A:Accession: B40996
A:Molecule type: protein
A:Residues: 1-20 <ONS>
A:Experimental source: strain ATCC 12540
C:Keywords: bioplerin; oxidoreductase

Query Match 40.0% Score 6: DB 2: Length 296:
Best Local Similarity 100.0% Pred. No. 12:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 RHHLR 13
|||||
Db 192 RHHLR 197

RESULT 2
A71447 hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C>Date: 03-Aug-1998 #sequence, revision 03-Aug-1998 #text, change 05-Dec-1998
C:Accession: A71447
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D.
P.; Weiler, H.; Weiler, E.; Wamboldt, R.; Weltzenegger, T.; Pohl, T.M.; Terry, N.; G.
avanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puidomen
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Reichman, S.;
C.; Chalmatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t.
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: A71447
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-352 <BEV>
A:Cross-references: GB:297344; NID:g2245126; PID:e327078; PID:g2245129
C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 40.0%; Score 6; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AMLRSP 15
DB 179 AMLRSP 184

RESULT 3

hypothetical protein C38D4.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19824

R:Colles, L.
submitted to the EMBL Data Library, October 1994

A:Reference number: Z19183

A:Accession: T19824

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-556 <M1>

A:Cross-references: EMBL:Z46241; PIDN:CAA86317.1; GSPDB:GN00021; CESP:C38D4.4

A:Experimental source: clone C38D4

C:Genetics:

A:Gene: CESP:C38D4.4

A:Map position: 3

A:introns: 40/2; 80/2; 148/3; 257/3; 370/1; 405/1; 488/3

Query Match 40.0%; Score 6; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AMLRSP 15
DB 126 AMLRSP 131

RESULT 4

E89918 2-oxoglutarate dehydrogenase E1 [Imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: E89918

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, M.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1223-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: E89918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-910 <KUR>

A:Cross-references: GB:BA000018; PID:q13701210; PIDN:BA842505.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: ocha

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom

Query Match 40.0%; Score 6; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
DB 599 FSHRHA 604

RESULT 5

C81139

probable oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) E1 component NMA1149 [lm

C:Species: *Neisseria meningitidis*

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001

C:Accession: C81139; H81881

R:Retelink, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

rl, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignan, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: C81139

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-942 <RET>

A:Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAFA1361.1; PID:g722

A:Experimental source: serogroup B, strain MC58

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: H81881

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-942 <PAR>

A:Cross-references: GB:AL62755; GB:AL157959; NID:g7379742; PIDN:CAB84411.1; PID:g737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: suca; NMB0955; NMA1149

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding

C:Keywords: oxidoreductase

Query Match 40.0%; Score 6; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
DB 626 FSHRHA 631

RESULT 6

S07776 oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - *Azotobacter vinelandii*

N:Alternate names: 2-oxoglutarate dehydrogenase complex chain E1

C:Species: *Azotobacter vinelandii*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999

C:Accession: S07776

R:Schulze, E.; Westphal, A.H.; Hanemaaijer, R.; de Kok, A.

Eur. J. Biochem. 187, 229-234, 1990

A:Title: The 2-oxoglutarate dehydrogenase complex from *Azotobacter vinelandii*. 1. Mol

A:Reference number: S07776; MUID:90126823; PMID:2404759

A:Accession: S07776

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-943 <SCH>

A:Cross-references: GB:X52433; NID:g39231; PIDN:CAA36680.1; PID:g39232

C:Genetics:

A:Gene: suca

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding

C:Keywords: oxidoreductase; thiamin pyrophosphate; tricarboxylic acid cycle

F:359-405/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 40.0%; Score 6; DB 1; Length 943;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
DB 631 FSHRHA 636

RESULT 7
683448
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: 683448
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,
L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen
A:Reference number: A82950; MUID:2043737; PMID:10984043
A:Accession: 683448
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-943 <STO>
A:Cross-references: GB:AE004586; GB:AE004091; NID:99947536; PIDN:AG04974.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: suCA; PA1585
C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom
ain

Query Match 40.0%; Score 6; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRA 10
|||||
Db 631 FSHRA 636

RESULT 8
T27345
hypothetical protein Y70C5A.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27345
R:Steward, C.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z20349
A:Accession: T27345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1037 <WIL>
A:Cross-references: EMBL:Z99282; PIDN:CA16532.1; CESP:Y70C5A.2
A:Experimental source: clone Y70C5A
C:Genetics:
A:Gene: CESP:Y70C5A.2
A:Introns: 21/2; 71/1; 144/3; 246/1; 283/1; 319/2; 559/3; 636/3; 671/2; 950/3

Query Match 40.0%; Score 6; DB 2; Length 1037;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRSP 15
|||||
Db 983 AHLRSP 988

RESULT 9
S39402
hupF protein - Bradyrhizobium japonicum
C:Species: Bradyrhizobium japonicum
C:Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
C:Accession: S39402
R:van Soom, C.; Browne, J.; Verreth, C.; Vandertuyden, J.
J. Mol. Biol. 234, 508-512, 1993
A:Title: Nucleotide sequence analysis of four genes, hupC, hupD, hupE and hupG, downstre
am
A:Reference number: S39400; MUID:94047099; PMID:8230232
A:Accession: S39402
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <VAN>

A:Cross-references: EMBL:Z21948; NID:9311536; PIDN:CA79945.1; PID:9311539
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
C:Superfamily: hydrogenase expression/formaton protein hupC

Query Match 33.3%; Score 5; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRSP 14
|||||
Db 93 AHLRSP 97

RESULT 10
F72515
hypothetical protein APE2099 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: F72515
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
pyrum pernix
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: F72515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KAW>
A:Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BA81110.1; PID:95105798
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2099
C:Superfamily: Aeropyrum pernix hypothetical protein APE2099

Query Match 33.3%; Score 5; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRSP 14
|||||
Db 2 AHLRSP 6

RESULT 11
T22156
hypothetical protein F44A6.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22156
R:Stinson, J.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19524
A:Accession: T22156
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-142 <WIL>
A:Cross-references: EMBL:Z50858; PIDN:CAA90724.1; GSPDB:GN00028; CESP:F44A6.4
A:Experimental source: clone F44A6
C:Genetics:
A:Gene: CESP:F44A6.4
A:Map position: X
A:Introns: 17/1; 41/1; 97/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F44A6.4

Query Match 33.3%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 HRHAH 11
|||||
Db 4 HRHAH 8

RESULT 12
D83261
probable transcription regulator PA3067 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83261
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lardig, K.; Lam,
.. Lory, S.; Olson, M.V.
Nucleotide 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; M01D:20437337; PMID:10984043
A:Accession: D83261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <STO>
A:Cross-references: GB:AE004731; GB:AE004091; NID:g9949171; PIDN:AAG06455.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Superfamily: Mycobacterium leprae hypothetical protein MLCB57.31

Query Match 33.3%; Score 5; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRS 14
DB 11 AHLRS 15

RESULT 13
AB0200
conserved hypothetical protein YPO1639 [Imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0200
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Harraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nucleotide 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; M01D:21470413; PMID:11586360
A:Accession: AB0200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC90461.1; PID:g15979677; GSPDB:GN00175
C:Genetics:
A:Gene: YPO1639
C:Superfamily: unassigned mutr domain proteins; mutr domain homology

Query Match 33.3%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 HLRSR 15
DB 117 HLRSR 121

RESULT 14
AC2084
phosphonate metabolism protein [Imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp.
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AC2084
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; M01D:21595285; PMID:11759840

A:Accession: AC2084
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073924.1; PID:g17131316; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: phnG
C:Superfamily: *Escherichia coli* phnG protein

Query Match 33.3%; Score 5; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 SHRNA 10
DB 91 SHRNA 95

RESULT 15
T08254
probable transposase H0455 - *Halobacterium* sp. (strain NRC-1) insertion sequence ISH5
N:Alternate names: hypothetical protein H1903
C:Species: *Halobacterium* sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
C:Accession: T08254; T08389
R:Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid o
A:Reference number: Z16408; M01D:99063795; PMID:9847077
A:Accession: T08254
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176 <NGM>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822315; HALOSP:H0455
A:Experimental source: strain NRC-1
A:Genetics: COP1
A:Accession: T08389
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176 <DAS>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822450; HALOSP:H1903
A:Experimental source: strain NRC-1
A:Genetics: COP2
C:Genetics: <COP1>
A:Gene: HALOSP:H0455
A:Genome: plasmid pNRC100
C:Genetics: <COP2>
A:Gene: HALOSP:H1903
A:Genome: plasmid pNRC100
A:Mobile element: insertion sequence ISH5

Query Match 33.3%; Score 5; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 RHANL 12
DB 124 RHANL 128

Search completed: November 27, 2002, 07:31:16
Job time : 8.25869 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:23:05 ; Search time 1.44788 Seconds
(without alignments) 429.695 Million cell updates/sec

Title: US-09-893-615-1
Perfect score: 15
Sequence: 1 WRMYFSHRHRLRSP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	6	40.0	943	1	ODOL_AZOVI
2	5	33.3	98	1	HUPF_BRAJA
3	5	33.3	162	1	YAJG_RHISN
4	5	33.3	189	1	UREF_STAXY
5	5	33.3	198	1	CD8A_PONPY
6	5	33.3	207	1	FRDA_MOUSE
7	5	33.3	235	1	CD8A_HUMAN
8	5	33.3	309	1	VAGE_ECOLI
9	5	33.3	312	1	V531_METTH
10	5	33.3	331	1	GL2M_ARATH
11	5	33.3	349	1	AMBP_RAT
12	5	33.3	372	1	Y906_MYCTU
13	5	33.3	377	1	RAPB_BACSU
14	5	33.3	384	1	Y823_MYCLE
15	5	33.3	388	1	GSPE_ABRHY
16	5	33.3	394	1	UXPA_HAEIN
17	5	33.3	395	1	STF8_MOUSE
18	5	33.3	397	1	O22A_DROME
19	5	33.3	397	1	O22B_DROME
20	5	33.3	410	1	APKA_ARATH
21	5	33.3	411	1	VGLG_HSVBR
22	5	33.3	411	1	VGLX_HSVBR
23	5	33.3	416	1	PIRC_DEIRA
24	5	33.3	426	1	YEV2_YEAST
25	5	33.3	443	1	GLMU_BUCAT
26	5	33.3	459	1	SYN_BUCAT
27	5	33.3	466	1	TRP2_ARATH
28	5	33.3	475	1	TRP2_ARATH
29	5	33.3	483	1	KG3A_HUMAN
30	5	33.3	483	1	KG3A_RAT
31	5	33.3	490	1	DNMA_CACR
32	5	33.3	494	1	VGA_BPAL3
33	5	33.3	494	1	VGA_BPPKH

34	5	33.3	505	1	FIXL_RHIME	P10955 rhizobium m
35	5	33.3	508	1	GALT_BACD	09Kdv2 bacillus ha
36	5	33.3	523	1	SYN_TREPA	083618 treponema p
37	5	33.3	545	1	CIP4_HUMAN	015642 homo sapien
38	5	33.3	571	1	PUR6_YEAST	P1264 saccharomyc
39	5	33.3	628	1	V7OK_TYMW	P10357 turnip yell
40	5	33.3	628	1	V7OK_TYMW	P20131 turnip yell
41	5	33.3	642	1	NOGL_SCHRO	094659 schizosacch
42	5	33.3	647	1	NOGL_YEAST	002892 saccharomyc
43	5	33.3	699	1	YOOA_CAEEL	009299 caenorhabdi
44	5	33.3	701	1	TBX2_MOUSE	060707 mus musculi
45	5	33.3	702	1	TBX2_HUMAN	013207 homo sapien

ALIGNMENTS

```

RESULT 1
ID      ODOL_AZOVI      STANDARD:      PRT:      943 AA.
AC      P20707
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) (Alpha-
DE      ketoglutarate dehydrogenase).
GN      SUCR OR ODBA.
OS      Azotobacter vinelandii.
OC      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC      Azotobacter.
OX      NCBI_TaxID=354;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90126823; PubMed=2404759;
RA      Schulze E., Westphal A.H., Hanemaaijer R., de Kok A.;
RT      "The 2-oxoglutarate dehydrogenase complex from Azotobacter
RT      vinelandii. 1. Molecular cloning and sequence analysis of the gene
RT      encoding the 2-oxoglutarate dehydrogenase component."
RN      Eur. J. Biochem. 187:229-234(1990).
RN      [2]
RN      SEQUENCE OF 909-943 FROM N.A.
RX      MEDLINE=90126825; PubMed=2404760;
RA      Westphal A.H., de Kok A.;
RT      "The 2-oxoglutarate dehydrogenase complex from Azotobacter
RT      vinelandii. 2. Molecular cloning and sequence analysis of the gene
RT      encoding the succinyltransferase component."
RN      Eur. J. Biochem. 187:235-239(1990).
CC      -!- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
CC      OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT
CC      CONTAINS MULTIPLE COPIES OF 3 ENZYMIC COMPONENTS: 2-OXOGLUTARATE
CC      DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND
CC      LIPOAMIDE DEHYDROGENASE (E3).
CC      -!- CATALYTIC ACTIVITY: 2-oxoglutarate + lipoamide = S-
CC      succinylidihydrolipoamide + CO(2).
CC      -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC      -!- SUBUNIT: HOMODIMER.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X52433; CA36680.1; -.
DR      EMBL: X52432; CA36677.1; -.
DR      PIR: S07776; S07776.
DR      InterPro: IPR001017; Dehydrogenase_E1.
DR      InterPro: IPR000360; Transketolase.
DR      Pfam: PF00676; E1-dehydrog. 1.
DR      Pfam: PF02779; transket.pyr. 1.
DR      TIGRfams: TIGR00239; 2oxo_ch_E1; 1.

```

KM Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate.
SQ SEQUENCE 943 AA; 105687 MW; D3F35356D454E2A1 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 943;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
|||||
Db 631 FSHRHA 636

RESULT 2

HUPE_BRAJA STANDARD; PRT; 98 AA.

AC 045352;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Hydrogenase expression/formation protein hupf.
GN HUPE

OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94047099; PubMed=8230232;
RA van Soom C., Browaes J., Verreth C., Vanderleyden J.,
RT "Nucleotide sequence analysis of four genes, hupC, hupD, hupF and
hupG, downstream of the hydrogenase structural genes in
Bradyrhizobium japonicum."
RL J. Mol. Biol. 234:508-512(1993).

CC -1 SIMILARITY: BELONGS TO THE HUPE/HYPC FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: 221948; CAA79945.1;
DR InterPro: IPR001109; HupF_HYPC.
DR Pfam: PF01455; HupF_HYPC.1.
DR ProDom: PD003112; HupF_HYPC.1.
DR TIGRFAMs: TIGR00074; hupC_hupF.1.
DR PROSITE: PS01097; HupF_HYPC; FALSE_NEG.
SQ SEQUENCE 98 AA; 10633 MW; A9BD353F9DA240F7 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRS 14
|||||
Db 93 AHLRS 97

RESULT 3
Y4JG_RHISN STANDARD; PRT; 162 AA.

AC P55507;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE Hypothetical 17.9 kDa protein Y4JG.

GN Y4JG.

OS Rhizobium sp. (strain NGR234).

OC Plasmid sym pNCR234a.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=394;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97305956; PubMed=9163424;

RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,

RA Perret X.;

RT "Molecular basis of symbiosis between Rhizobium and legumes."

RL Nature 387:394-401(1997).

CC -1 SIMILARITY: NONE OBVIOUS.

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CC or send an email to license@isb-sib.ch).

DR EMBL: AE000079; AAB91719.1;

DR Hypothetical protein; Plasmid; Transmembrane.

KM TRANSMEM 108 126 POTENTIAL.

FT SEQUENCE 162 AA; 17910 MW; B32FA1D10F64950C CRC64;

Query Match 33.3%; Score 5; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRS 14
|||||
Db 22 AHLRS 26

RESULT 4

UREF_STAXY STANDARD; PRT; 189 AA.

AC P42876;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Urease accessory protein uref.

GN UREF.

OS Staphylococcus xylosum.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1288;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DSM 20267 / Isolate C2A;

RA Jose J.;

RL Thesis (1994), University of Saarlandes, Germany.

CC -1 FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.

CC -1 SIMILARITY: BELONGS TO THE UREF FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: Z35136; CAA84508.1;

DR InterPro: IPR002639; Uref.

DR Pfam: PF01730; Uref.1.

DR ProDom: PD004961; Uref.1.

KM NICKEL.

SQ SEQUENCE 189 AA; 21987 MW; 6E6965557014FA6F CRC64;

Query Match 33.3%; Score 5; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AHLRS 13
|||||

Db 4 HAHLR 8

RESULT 5

CD8A_PONPY STANDARD; PRT; 198 AA.

AC P30433;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/LEU-2).
 GN CD8A.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
 NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate Jarl;
 RX MEDLINE=92307742; PubMed=1612644;
 RA Lawlor D.A., Parham P.;
 RT "Structure of CD8 alpha and beta chains of the orangutan: novel patterns of mRNA splicing encoding hingeless polypeptides.";
 RL Immunogenetics 36:121-125(1992).
 CC -1- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO CLASS I MHC MOLECULES ALPHA-3 DOMAINS.
 CC -1- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X60223; CAA42784.1; -;
 DR HSSP: P01732; LCD8.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell; Immune response; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 198
 FT -----
 FT BY SIMILARITY.
 FT T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN.
 FT -----
 FT DOMAIN 22 145
 FT TRANSMEM 146 166
 FT DOMAIN 167 198
 FT DOMAIN 22 135
 FT DISULFID 43 115
 FT SEQUENCE 198 AA; 22099 MW; F3EC093EAD805561 CRC64;
 SQ

Query Match 33.3%; Score 5; DB 1; Length 198;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MYFSH 7

Db 123 MYFSH 127

RESULT 6
 FRDA_MOUSE STANDARD; PRT; 207 AA.
 ID FRDA_MOUSE

AC O35943;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fratxin, mitochondrial precursor (Fxn).
 GN FRDA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=97385237; PubMed=9241270;
 RA Koutnikova H., Campuzano V., Fourny F., Dolle P., Cazzalini O., Koenig M.;
 RT "Studies of human, mouse and yeast homologues indicate a mitochondrial function for fratxin.";
 RL Nat. Genet. 16:345-351(1997).
 CC -1- FUNCTION: PROBABLY INVOLVED IN IRON HOMEOSTASIS.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- PTM: PROCESSED BY MITOCHONDRIAL PROCESSING PEPTIDASE (MPP).
 CC -1- SIMILARITY: BELONGS TO THE FRATAXIN FAMILY.
 CC -----

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 CC -----
 DR EMBL: U95736; AAB67778.1; -;
 DR HSSP: Q16595; IDLX.
 DR MGD: MGI:1096879; Frda.
 DR InterPro: IPR001794; Fratxin.
 DR InterPro: IPR002908; Fratxin_1like.
 DR Pfam: PF01491; Fratxin_Cyay; 1.
 DR PRINTS: PR00904; FRATAXIN.
 DR PRODOM: PD006646; Fratxin_1like; 1.
 DR PROSITE: PS01344; FRATAXIN_1; 1.
 DR PROSITE: PS50810; FRATAXIN_2; 1.
 KW Mitochondrion; Transit peptide.
 FT TRANSIT 1 40
 FT CHAIN 41 207
 FT SEQUENCE 207 AA; 22924 MW; C46FD1B44FB26A2 CRC64;
 SQ

Query Match 33.3%; Score 5; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RHAHL 12
 Db 51 RHAHL 55

RESULT 7

CD8A_HUMAN STANDARD; PRT; 235 AA.

AC P01732;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/Leu-2).
 GN CD8A OR MAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85099337; PubMed=3871356;
 RL Titman D.R., Thomas Y., Madden P.J., Chess L., Axel R.;

RT "The isolation and sequence of the gene encoding T8: a molecule
RT defining functional classes of T lymphocytes.";
RL Cell 40:237-246(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86103103; PubMed=3936473;
RA Parnes J.R., Sizer K.C., Sukhatme V.P., Hunkapiller T.;
RT "Structure of Leu-2/T8 as deduced from the sequence of a cDNA clone";
RN Behring Inst. Mitt. 77:48-55(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85124610; PubMed=3918796;
RA Sukhatme V.P., Sizer K.C., Vollmer A.C., Hunkapiller T.,
RA Parnes J.R.;
RT "The T cell differentiation antigen Leu-2/T8 is homologous to
RT immunoglobulin and T cell receptor variable regions";
RL Cell 40:591-597(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90035142; PubMed=2509342;
RA Nakayama K.-I., Tokito S., Okumura K., Nakauchi H.;
RT "Structure and expression of the gene encoding CD8 alpha chain (Leu-
RT 2/T8).";
RL Immunogenetics 30:393-397(1989).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=89215302; PubMed=2496167;
RA Norment A.M., Lonberg N., Lacey E., Littman D.R.;
RT "Alternatively spliced mRNA encodes a secreted form of human CD8
RT alpha. Characterization of the human CD8 alpha gene.";
RL J. Immunol. 142:3312-3319(1989).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 22-135.
RX MEDLINE=92191292; PubMed=1547508;
RA Leahy D.J., Axel R., Hendrickson W.A.;
RT "Crystal structure of a soluble form of the human T cell coreceptor
RT CD8 at 2.6-A resolution.";
RL Cell 68:1145-1162(1992).
RN [7]
RP FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT
CC WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN
CC THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO
CC CLASS I MHC MOLECULES ALPHA-3 DOMAINS.
CC -1- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN
CC LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS PATTERNS OF DIFFERENTIAL SPLICING
CC OF CD8 ALPHA TRANSCRIPTS INVOLVE EXCISION OF THE TRANSMEMBRANE OR
CC CYTOPLASMIC DOMAINS.
CC -1- PTM: ALL OF THE FIVE MOST CARBOXYL-TERMINAL CYSTEINES ARE USED TO
CC FORM INTER-CHAIN DISULFIDE BONDS IN DIMERS AND HIGHER MULTIMERS,
CC WHILE THE FOUR AMINO-TERMINAL CYSTEINES ARE NOT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD8a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd8alpha.htm".
CC -----
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CC -----
DR EMBL: M26315; AAA79217.1; -
DR EMBL: M26313; AAA79217.1; JOINED.
DR EMBL: M26314; AAA79217.1; JOINED.
DR EMBL: M12824; AAA61133.1; -
DR EMBL: M12828; AAB04637.1; -
DR EMBL: M27161; AAA59674.1; -
DR PIR: A01999; RWHUT8.
DR PIR: A22824; A22824.
DR PIR: JP0105; JP0105.

DR PIR: A30604; A30604.
DR PIR: A45888; A45888.
DR PDB: 1CD8; 31-JAN-94.
DR Genew; HGNC:1706; CD8A.
DR MIM; 186910; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin domain; Transmembrane; Glycoprotein; Phosphorylation;
KW T-cell; Immune response; Signal; 3d-structure; Alternative splicing.
FT SIGNAL 1 21
FT CHAIN 22 235
FT DOMAIN 22 182
FT TRANSMEM 183 203
FT DOMAIN 204 235
FT DOMAIN 22 135
FT DISULFID 43 115
FT STRAND 24 27
FT TURN 35 36
FT STRAND 39 45
FT STRAND 54 59
FT STRAND 68 73
FT STRAND 79 80
FT TURN 82 83
FT TURN 86 88
FT STRAND 89 94
FT TURN 95 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 119
FT TURN 120 121
FT STRAND 122 125
FT STRAND 129 131
SQ SEQUENCE 235 AA; 25729 MW; FCCA29BA73726BB CRC64;
Query Match 33.3%; Score 5; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MYFSH 7
Db 123 MYFSH 127
YAGE_ECOLI
ID YAGE_ECOLI STANDARD; PRT; 309 AA.
AC P75682; Q9R2D5;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yage.
GN YAGE OR B0268.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 1-128 FROM N.A.
RX STRAIN-K12 / WJ110;
RA Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,

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RA Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
RA Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.,
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 4.0 - 6.0 mln (189,987 - 281,416bp) region."
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE DHPS FAMILY. STRONG, TO E.COLI YJHH.
CC -----
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CC -----
DR EMBL; AE000134; AAC73371.1; -
DR EMBL; D83536; BAA77934.1; -
DR EcGene; EG13344; Yage.
DR InterPro: IPR002220; DHPS.
DR Pfam: PF00701; DHPS.1.
DR PRINTS; PR00146; DHPS1NTHASE.
DR ProDom; PD001859; DHPS.1.
DR PROSITE; PS00665; DHPS.1.1.
DR PROSITE; PS00666; DHPS.2.1.
KM Hypothetical protein; Lyase; Complete proteome.
FT ACT_SITE 174 174
FT CONFLICT 105 106 QQ -> HE (IN REF. 2).
SQ SEQUENCE 309 AA; 3316 MW; 94FC34AD08C52BE CRC64;

Query Match 33.3%; Score 5; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHRSS 14
|1111
Db 181 AHRSS 185

RESULT 9
Y31_METH STANDARD; PRT; 312 AA.
ID Y31_METH
AC 026631;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MTH531.
GN MTH531.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanobacter.
OX NCBI_Taxid=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Delta H;
RX MEDLINE-98037514; Pubmed-9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pochler B., Qiu D.,
RA Spadatore R., Viccare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Pirbhakar S.,
RA Douganall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7153(1997).
CC -1- SIMILARITY: BELONGS TO THE MURDEF FAMILY.
CC -----
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CC -----
DR EMBL; AE000836; AAB85037.1; -
DR InterPro: IPR000713; Mur_ligase.
DR InterPro: IPR000205; NAD_binding.
DR Pfam: PF01225; Mur_ligase.1.
KM Hypothetical protein; Ligase; ATP-binding; Complete proteome.
FT NP_BIND 112 118
SQ SEQUENCE 312 AA; 34742 MW; 4AA7AFEF0A793002 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 HLRSF 15
|1111
Db 303 HLRSF 307

RESULT 10
GL2M_ARATH STANDARD; PRT; 331 AA.
ID GL2M_ARATH
AC 024495; 024494; 022857;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hydroxyacylglytathione hydrolase, mitochondrial precursor (EC 3.1.2.6)
DE (Glyoxalase II) (GLX II).
GN GLX2-1 OR AT2G43430 OR T1024.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eusteroideae; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Massilewskij;
RX MEDLINE-98009983; Pubmed-9349270;
RA Malt M.K., Krishnasamy S., Owen H.A., Makaroff C.A.;
RT "Molecular characterization of glyoxalase II from Arabidopsis
RT thaliana.";
RL Plant Mol. Biol. 35:471-481(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Columbia;
RX MEDLINE-20083487; Pubmed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shree T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rouning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umeyam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Greasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGSC).";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIOLESTERASE THAT CATALYZES THE HYDROLYSIS OF S-D-
CC LACTOYL-GLUTATHIONE TO FORM GLUTATHIONE AND D-LACTIC ACID.
CC -1- CATALYTIC ACTIVITY: (S)-(2-hydroxyacetyl)glutathione + H(2)O -
CC -1- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -1- PATHWAY: Glyoxal pathway.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
CC -----

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DR EMBL; U90927; AAC49865.1; -
 DR EMBL; U90928; AAC49866.1; -
 DR EMBL; AC002335; AAB64315.2; -
 DR EMBL; AY091278; AAM44217.1; -
 DR EMBL; AY063806; AAL36162.1; -
 DR HSSP; Q16775; 1QHS.
 DR InterPro: IPR001279; Bactemase-like.
 DR Pfam: PF00753; Lactamase_B.1.
 DR Hydrolase; Zinc; Mitochondrion; Transit peptide.
 FT TRANSIT 1 76 MITOCHONDRION (POTENTIAL).
 FT CHAIN 77 331 HYDROXYACETYLGLUTATHIONE HYDROLASE.
 FT METAL 131 131 ZINC 1 (BY SIMILARITY).
 FT METAL 133 133 ZINC 1 (BY SIMILARITY).
 FT METAL 135 135 ZINC 2 (BY SIMILARITY).
 FT METAL 136 136 ZINC 2 (BY SIMILARITY).
 FT METAL 189 189 ZINC 1 (BY SIMILARITY).
 FT METAL 208 208 ZINC 1 AND 2 (BY SIMILARITY).
 FT CONFLICT 159 159 D -> H (IN REF. 1; AAC49866).
 FT SEQUENCE 331 AA; 36499 MW; 2EDC21B4902419C5 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 331;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 AHLRS 14
 11111
 Db 274 AHLRS 278

RESULT 11
 AMBP_RAT STANDARD: PRT: 349 AA.
 ID 064240; O63336; P19603;
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
 DE trypsin inhibitor light chain (ITR-LC) (Bikunin) (HI-30); Trypsatin].
 GN AMBP OR ITRL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=92182014; PubMed=1371936;
 RA Lindqvist A., Bratt T., Altieri M., Kasterstroem B.;
 RT "Rat alpha 1-microglobulin: co-expression in liver with the light
 RT chain of inter-alpha-trypsin inhibitor";
 RL Biochim. Biophys. Acta 1130:63-67(1992).
 RN [2]
 RN SEQUENCE OF 141-195 FROM N.A.
 RX MEDLINE=87033744; PubMed=2429963;
 RA Kasterstroem M., Bjorck L., Akerstroem B.;
 RT "Developmental and tissue-specific expression of alpha 1-microglobulin
 RT mRNA in the rat";
 RL J. Biol. Chem. 261:15070-15074(1986).
 RN [3]
 RP SEQUENCE OF 283-343, AND CHARACTERIZATION.
 RC STRAIN=Mistar;
 RX MEDLINE=89053978; PubMed=3263966;
 RA Kido H., Yokogoshi Y., Katunuma N.;
 RT "Kunitz-type protease inhibitor found in rat mast cells. Purification,
 RT properties, and amino acid sequence";

RL J. Biol. Chem. 263:18104-18107(1988).
 RN [4]
 RP PROCESSING.
 RX MEDLINE=9414892; PubMed=7508921;
 RA Itoh H., Ide H., Ishikawa N., Nawa Y.;
 RT "Mast cell protease inhibitor, trypstatin, is a fragment of
 RT inter-alpha-trypsin inhibitor light chain";
 RL J. Biol. Chem. 269:3818-3822(1994).
 CC -1- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
 CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
 CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
 CC AND ALBUMIN (BY SIMILARITY).
 CC -1- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR. PRESENT IN PLASMA AND
 CC URINE. INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTTIC
 CC ELASTASE (BY SIMILARITY).
 CC -1- FUNCTION: Trypsatin is a trypsin inhibitor. It inhibits blood
 CC coagulation factor Xa and trypsin about 100-fold more rapidly
 CC than porcine pancreatic trypsin and chymase. It is a monomer but
 CC is also found in mast cells as a complex with trypase.
 CC -1- SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from
 CC one or two heavy chains (H1, H2 or H3) and one light chain,
 CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2
 CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and
 CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized in the liver and secreted in
 CC plasma. Trypsatin is present in mast cell granules.
 CC -1- PTM: The precursor is proteolytically processed into two
 CC separately functioning proteins.
 CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-
 CC yellow chromophores (by similarity).
 CC -1- PTM: Heavy chains are interlinked with bikunin via a chondroitin
 CC 4-sulfate bridge to the their C-terminal aspartate (by
 CC similarity).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
 CC FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).

DR EMBL; S87544; AAB21782.1; -
 DR EMBL; J02600; AAA1596.1; -
 DR PIR; A31890; A31890.
 DR HSSP; P02760; 1BIK.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocalin_cytfabp.
 DR Pfam; PF00061; Lipocalin_1.
 DR Pfam; PF00014; Kunitz_BPTI_2.
 DR PRINTS; PR00179; BASICPASE.
 DR PRINTS; PR00179; LIPOCALIN.
 DR ProDom; PD000222; Kunitz_BPTI_2.
 DR SMART; SM00131; KU; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
 DR PROSITE; PS00213; LIPOCALIN_1.
 KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
 KW Lipocalin.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 202 ALPHA-1-MICROGLOBULIN
 FT CHAIN 205 349 INTER-ALPHA-TRYPsin INHIBITOR LIGHT
 FT CHAIN 283 343 TRYPSATIN.
 FT DOMAIN 230 280 BPTI/KUNITZ INHIBITOR 1.
 FT DOMAIN 286 336 BPTI/KUNITZ INHIBITOR 2.
 FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).

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FT BINDING 110 110 CHROMOPHORE (BY SIMILARITY).
FT BINDING 136 136 CHROMOPHORE (BY SIMILARITY).
FT BINDING 148 148 CHROMOPHORE (BY SIMILARITY).
FT DISULFID 90 187 BY SIMILARITY.
FT DISULFID 230 280 BY SIMILARITY.
FT DISULFID 239 263 BY SIMILARITY.
FT DISULFID 255 276 BY SIMILARITY.
FT DISULFID 286 336 BY SIMILARITY.
FT DISULFID 295 319 BY SIMILARITY.
FT DISULFID 311 332 BY SIMILARITY.
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 240 241 INHIBITORY SITE (P1) (CHYMOTRYPSIN, ELASTASE) (BY SIMILARITY).
FT ACT_SITE 296 297 INHIBITORY SITE (P1) (TRYPSIN) (BY SIMILARITY).
FT CONFLICT 142 142 G->A (IN REF. 2).
FT CONFLICT 302 302 W->L (IN REF. 3).
FT CONFLICT 323 323 G->N (IN REF. 3).
FT CONFLICT 330 331 KE->PK (IN REF. 3).
FT CONFLICT 334 334 E->W (IN REF. 3).
SQ SEQUENCE 349 AA: 38851 MW: 18787DCB0824E01 CRC64:

Query Match 33.3%; Score 5; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHR 9
Db 137 FSHR 141

RESULT 12
Y906_MYCTU STANDARD: PRT: 372 AA.
ID Y906_MYCTU
AC Q10562;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV0906 precursor.
GN RV0906 OR MT0929 OR MTCY31.34.
OS Mycobacterium tuberculosis.
OC Bacteria: Actinobacteria: Actinobacteria (class): Actinobacteridae: Actinomycetales: Corynebacteriaceae: Mycobacteriaceae: Mycobacterium.
NCBI_TaxID=1773;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigemeier K., Gass S., Barry C.E. III, Tekela F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S., Hovansky T., Jagsels K., Krogsh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Ruter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RC FLEISCHMAN R.D., ALLAND D., EISEN J.A., CARPENTER L., WHITE O., KOLEJONY J., DEBOY R., DODSON R., GWYN M.L., HAFT D., HICKEY E., KOJANOV J.F., NELSON W.C., UMEYAN L.A., ERMOLEVA M.D., SALZBERG S.L., DELCHER A., UTERBACK T., WEIDMAN J., KHOURI H., GILL J., MIKULA A., BISHAI W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO K.PNEUMONIAE ROMA.

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CC -----
DR EMBL: Z73101; CAA97381.1; -
DR EMBL: AE006979; AAK45176.1; -
DR TIGR: MT0929; -
KW Hypothetical protein: Signal: Complete proteome.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 372 HYPOTHETICAL PROTEIN RV0906.
SQ SEQUENCE 372 AA: 40641 MW: 0A85549D2429D335 CRC64:

Query Match 33.3%; Score 5; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRS 14
Db 195 AHLRS 199

RESULT 13
RAPB_BACSU STANDARD: PRT: 377 AA.
ID RAPB_BACSU
AC P70962;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Response regulator aspartate phosphatase B (EC 3.1.-.-) (Stage 0 sporulation protein P).
GN RAPB OR SPOOP.
OS Bacillus subtilis.
OC Bacteria: Firmicutes: Bacillales: Bacillaceae: Bacillus.
NCBI_TaxID=1423;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=95094268; PubMed=8001132;
RA Perego M., Hanstein C., Welsh K., Djavahishvili T., Glaser P., Hoch J.;
RA "Multiple protein-aspartate phosphatases provide a mechanism for the integration of diverse signals in the control of development in B. subtilis."
RL Cell 79:1047-1055(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertaino M.G., Bessieres P., Bilotin A., Borchert S., Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerthon I.F., Cummings N.J., Daniel R.A., Denlioz F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hujilo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koelter P., Koningsstein G., Krogsh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Melledo R.P., Mizuno M., Moesti D., Nakai S., Nockack M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porrolik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,

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RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccoti E., Takagi T., Takahashi H., Takemaru K.,
 RA Takenchi M., Tamakoshi A., Tanaka T., Terpstra P., Togroni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambolt R., Wedler E., Wedler H., Welterngger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: Prevents sporulation by dephosphorylating SpoOF.
 CC -1- SIMILARITY: BELONGS TO THE RAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 6 TPR REPEATS.
 CC -----
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 CC -----
 DR EMBL: 281356; CAB03684.1; -;
 DR EMBL: 291122; CAB15686.1; -;
 DR Subtilist; BG11965; rapB.
 DR InterPro: IPR001440; TPR.
 DR Pfam: PF00515; TPR: 4.
 KM Hydrolyase; Repeat; TPR repeat; Sporulation; Complete proteome.
 FT REPEAT 100 133 TPR 1.
 FT REPEAT 147 180 TPR 2.
 FT REPEAT 181 214 TPR 3.
 FT REPEAT 221 254 TPR 4.
 FT REPEAT 260 293 TPR 5.
 FT REPEAT 335 368 TPR 6.
 SQ SEQUENCE 377 AA; 45037 MW; 617B29614B483971 CRC64;
 Query Match 33.3%; Score 5; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 YESHR 8
 Db 344 YESHR 348
 RESULT 14
 Y823_MYCLE STANDARD; PRT; 384 AA.
 ID Y823_MYCLE
 AC 050049;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein ML2186 (NCRB).
 GN ML2186.
 OS Mycobacterium leprae.
 OC Bacteria: Actinobacteria: Actinobacteria (class): Actinobacteridae;
 OC Actinomycetales: Corynebacterineae: Mycobacteriaceae: Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R., Rodison K.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Whangul K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Davis K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holtroyd S., Horsley T., Jagsels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

RA Rutter S., Seeger K., Simon S., Simmonds M., Skellon J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrall B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- SIMILARITY: BELONGS TO THE UPF0034 (NIFR3/SNM1) FAMILY.
 CC -----
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 CC -----
 DR EMBL: U15182; AAA62994.1; -;
 DR EMBL: AL583824; CAC31141.1; -;
 DR Lepioma; ML2186; -;
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR004652; NIFR3_YhdG.
 DR InterPro: IPR001269; UPF0034.
 DR Pfam: PF01207; UPF0034: 1.
 DR TIGRfam: TIGR00737; nifR3_YhdG: 1.
 DR PROSITE: PS01136; UPF0034: 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 384 AA; 41100 MW; 44B6D0B1D678E43C CRC64;
 Query Match 33.3%; Score 5; DB 1; Length 384;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 11 HLRSF 15
 Db 34 HLRSF 38
 RESULT 15
 GSPF_AERHY STANDARD; PRT; 388 AA.
 ID GSPF_AERHY
 AC P11743;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE General secretion pathway protein F.
 GN EXEF.
 OS Aeromonas hydrophila.
 OC Bacteria: Proteobacteria: gamma subdivision: Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_TaxID=644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Ah65;
 RX MEDLINE=92349663; PubMed=1640836;
 RA Jiang B., Howard S.P.;
 RL "The *Aeromonas hydrophila* exef gene, required both for protein
 RT secretion and normal outer membrane biogenesis, is a member of a
 RT general secretion pathway.";
 RL Mol. Microbiol. 6:1351-1361(1992).
 CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
 CC EXPORT OF PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Probable).
 CC -1- SIMILARITY: BELONGS TO THE PULF/OUTF/EXEF/XPSF/XCPS FAMILY.
 CC -----
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 CC -----
 DR EMBL: X65504; CAA47127.1; -;

DR PIR: S22670; S22670.
DR InterPro: IPR003004; Bac_GSPF.
DR InterPro: IPR001992; Bac_sec_systII.
DR Pfam: PF00462; GSPIL_F; 1.
DR PRINTS: PR00812; BCTERIALGSPF.
DR PROSITE: PS00874; T2SP_F; 1.
KW Transport; Transmembrane; Inner membrane.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 351 371 POTENTIAL.
SQ SEQUENCE 388 AA; 43463 MW; D47B1628F977ED50 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRS 14
|||||
Db 81 AHLRS 85

Search completed: November 27, 2002, 07:28:42
Job time : 6.44788 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:24:25 : Search time 4.2278 Seconds
(Without alignments) 731.044 Million cell updates/sec

Title: US-09-893-615-1
Perfect score: 15
Sequence: 1 WRMYFSHRAHLRSP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0.

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	6	40.0	212	16	Q98A19 rhizobium 1
2	6	40.0	254	17	Q8TRU4 Q8TRU4 methanocarc
3	6	40.0	306	5	Q9BK13 Q9BK13 parametium
4	6	40.0	352	10	Q23610 Q23610 arabidops
5	6	40.0	354	11	Q9CYT9 Q9CYT9 mus musculu
6	6	40.0	390	4	Q9H6C3 Q9H6C3 homo sapien
7	6	40.0	390	4	Q96ET4 Q96ET4 homo sapien
8	6	40.0	449	16	Q53668 Q53668 mycobacteri
9	6	40.0	468	17	Q8TUC6 Q8TUC6 methanocarc
10	6	40.0	511	2	Q9KH39 Q9KH39 mycobacteri
11	6	40.0	556	5	Q18509 Q18509 caenorhabdi
12	6	40.0	582	2	Q50992 Q50992 neisseria 9
13	6	40.0	633	5	Q9VZK2 Q9VZK2 drosophila
14	6	40.0	664	5	Q24140 Q24140 drosophila
15	6	40.0	901	5	Q9VA02 Q9VA02 drosophila
16	6	40.0	910	16	Q99U74 Q99U74 staphylococ

17	6	40.0	916	2	Q8VUQ0 Q8VUQ0 pseudomonas
18	6	40.0	924	16	Q931R8 Q931R8 staphylococ
19	6	40.0	942	16	Q9J5R8 Q9J5R8 neisseria m
20	6	40.0	943	2	Q85487 Q85487 pseudomonas
21	6	40.0	943	16	Q913D3 Q913D3 pseudomonas
22	6	40.0	1037	5	Q62495 Q62495 caenorhabdi
23	6	33.3	72	4	Q9UH63 Q9UH63 homo sapien
24	5	33.3	82	12	Q8Q017 Q8Q017 camelpox vl
25	5	33.3	84	11	Q9R295 Q9R295 mus musculu
26	5	33.3	98	2	Q45250 Q45250 bradyrhizob
27	5	33.3	101	17	Q9VA40 Q9VA40 aeropyrum p
28	5	33.3	119	2	Q9RCE0 Q9RCE0 xanthomonas
29	5	33.3	125	5	Q95T72 Q95T72 drosophila
30	5	33.3	127	4	Q96MT4 Q96MT4 homo sapien
31	5	33.3	142	5	Q20386 Q20386 caenorhabdi
32	5	33.3	142	5	Q95WE4 Q95WE4 phlebotomus
33	5	33.3	142	11	Q9D7M7 Q9D7M7 mus musculu
34	5	33.3	142	11	Q9D1E4 Q9D1E4 mus musculu
35	5	33.3	147	16	Q9HZE1 Q9HZE1 pseudomonas
36	5	33.3	148	16	Q8ZFO4 Q8ZFO4 yersinia pe
37	5	33.3	149	11	Q60874 Q60874 mus musculu
38	5	33.3	151	16	Q8YUV6 Q8YUV6 anabena sp
39	5	33.3	152	2	Q9AE56 Q9AE56 aeromonas h
40	5	33.3	168	16	Q9S4X5 Q9S4X5 escherichia
41	5	33.3	169	5	Q9VR7 Q9VR7 drosophila
42	5	33.3	170	5	Q9NBE8 Q9NBE8 philodina r
43	5	33.3	176	17	Q54600 Q54600 halobacteri
44	5	33.3	186	5	Q9V69 Q9V69 drosophila
45	5	33.3	190	16	Q53749 Q53749 mycobacteri

ALIGNMENTS

RESULT 1

Q98A19 PRELIMINARY: PRT: 212 AA.
AC Q98A19: 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein ml16193.
GN ML16193.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti".
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003008; BAB52525.1; -
KW Hypothetical protein: Complete proteome.
SO SEQUENCE 212 AA; 23199 MW; 9C52FE82191E38A3 CMC54;

Query Match 40.0%; Score 6; DB 16; Length 212;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HAHLS 14
Db 71 HAHLS 76

RESULT 2

08TTU4
ID 08TTU4 PRELIMINARY: PRT: 254 AA.
AC 08TTU4:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
FT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein MA0331.
GN MA0331.
OS Methanosarcina acetivorans.
OC Archaea: Euryarchaeota: Methanococci: Methanosarcinales:
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_Taxid=2214;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atwood D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
RA Linton L., McSwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer R., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:537-542(2002).
DR EMBL: AE010691; AM03784.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 254 AA; 28615 MW; 627C0A84EA185BF0 CRC64;

Query Match 40.0%; Score 6; DB 17; Length 254;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FSHRHA 10
111111
Db 110 FSHRHA 115

RESULT 3
09BK13
ID 09BK13 PRELIMINARY: PRT: 306 AA.
AC 09BK13:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN GAPC.
OS Parametium tetraurelia.
OC Eukaryota: Alveolata: Ciliophora: Oligohymenophorea: Peniculiida:
OC Parametium.
OX NCBI_Taxid=5888;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=21143069; PubMed=11230543;
RX Fast N.M., Kissinger J.C., Roos D.S., Keeling P.J.;
RT "Nuclear-Encoded, Plastid-Targeted Genes Suggest a Single Common
RT Origin for Apicomplexan and Dinoflagellate Plastids."
RL Mol. Biol. Evol. 18:418-426(2001).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + PHOSPHATE +
CC NAD(+) -> 3-PHOSPHO-D-GLYCEROYL PHOSPHATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
CC EMBL: AF319452; AK20731.1;
DR HSSP: P56649; IDS.
DR InterPro: IPR000173; GAP_dhndrogenase.
DR Pfam: PF00044; gpoh; 1.
DR Pfam: PF02800; gpoh_C; 1.
DR PRINTS: PR00078; G3PDHDSGNASE.

DR PROSITE: PS00071; GAPDH; 1.
KW Glycolysis; NAD; Oxidoreductase.
FT NON_TER 1
FT NON_TER 306
SQ SEQUENCE 306 AA; 32657 MW; 680D7EC6EDA527C CRC64;

Query Match 40.0%; Score 6; DB 5; Length 306;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 AHLRSP 15
111111
Db 41 AHLRSP 46

RESULT 4
023610
ID 023610 PRELIMINARY: PRT: 352 AA.
AC 023610:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Hypothetical 40.0 kDa protein.
GN ATG17700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=98121113; PubMed=9461215;
RX Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Medler H.,
RA Medler E., Wamburt R., Weitzengruber T., Pohl T.M., Terryn N.,
RA Giesen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Eutian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Pulgomech P., Douka A.,
RA Vouklatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermayer B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palmer K., Benes V., Reckman S., Ansoorge V., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klotzerman S.,
RA Schueller C., Chalmatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT Arabidopsis thaliana."
RL Nature 391:485-488(1998).
RN [2]
RC SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: 297344; CAB10550.1;
DR EMBL: AL161547; CAB78773.1;
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 39986 MW; EF85363502BBE161 CRC64;

Query Match 40.0%; Score 6; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 AHLRSP 15
111111
Db 179 AHLRSP 184

RESULT 5
09CYT9
ID 09CYT9 PRELIMINARY: PRT: 354 AA.
AC 09CYT9:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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DE 2810450N13R1k protein.
GN 2810450N13R1k
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Arizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK013322; BAB28790.1;
DR MGD: MGI:1920024; 2810450N13R1k.
DR InterPro: IPR000191; Fapy_DNA_glyco.
DR Pfam: PF01149; Fapy_DNA_glyco; 1.
DR ProDom: PD003680; Fapy_DNA_glyco; 1.
SQ SEQUENCE 354 AA; 39604 MW; 86378B9E94A55CD CRC64;

Query Match 40.0%; Score 6; DB 11; Length 354;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RHAHLR 13
DB 95 RHAHLR 100

RESULT 6
ID 09H6C3 PRELIMINARY; PRT; 390 AA.
AC 09H6C3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CDNA: FLJ22402 fls, clone HRC08117.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isono S., Sugano S.;
RT "NEO human cDNA sequencing project.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AA026055; BAB1537.1;
DR InterPro: IPR000191; Fapy_DNA_glyco.
DR Pfam: PF01149; Fapy_DNA_glyco; 1.
DR ProDom: PD003680; Fapy_DNA_glyco; 1.
SQ SEQUENCE 390 AA; 43685 MW; 8BB040DC8D21B719 CRC64;

Query Match 40.0%; Score 6; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RHAHLR 13
DB 95 RHAHLR 100

RESULT 7
ID 096F14 PRELIMINARY; PRT; 390 AA.
AC 096F14;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 43.7 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010876; AAH10876.1;
DR InterPro: IPR000191; Fapy_DNA_glyco.
DR Pfam: PF01149; Fapy_DNA_glyco; 1.
DR ProDom: PD003680; Fapy_DNA_glyco; 1.
SQ SEQUENCE 390 AA; 43712 MW; 2BB040D9EF689382 CRC64;

Query Match 40.0%; Score 6; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RHAHLR 13
DB 95 RHAHLR 100

RESULT 8
ID 053668 PRELIMINARY; PRT; 449 AA.
AC 053668;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative membrane protein.
GN RV0246 OR MT0260 OR MT034.12.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLaren J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

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RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA DeCher A., Uterback T., Weldman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021929; CAAL738.1; ALT_INIT.
DR EMBL; AE006934; AA44478.1; -.
DR TIGR; MT0260; -.
DR Tuberculist; RV0246; -.
KW Complete proteome.
SO SEQUENCE 449 AA; 46926 MW; FCE6EF930F03D1E6 CRC64;

Query Match 40.0%; Score 6; DB 16; Length 449;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 HAHRS 14
Db 2 HAHRS 7
|||||

RESULT 9
Q8TUC6 PRELIMINARY; PRT; 468 AA.
AC Q8TUC6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ethanolamine permease.
GN MTPP OR MA0143.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smitrov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearlano K., Johnson R.,
RA Linton L., McGowan P., McKernan K., Talamas J., Threlk A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010671; AA003596.1; -.
KW Complete proteome.
SO SEQUENCE 468 AA; 51099 MW; 3B1D465FE13F77DC CRC64;

Query Match 40.0%; Score 6; DB 17; Length 468;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YFSHRH 9
Db 428 YFSHRH 433
|||||

RESULT 10
Q9KH39 PRELIMINARY; PRT; 511 AA.
AC Q9KH39;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE Hypothetical 55.5 kDa protein.
OS Mycobacterium smegmatis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RA Sikder D., Gupta S., Nagaraia V.;
RT "A hypothetical protein.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272032; AAF76209.1; -.
KW Hypothetical protein.
SO SEQUENCE 511 AA; 55543 MW; 735256A6DE3A035B CRC64;

Query Match 40.0%; Score 6; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRSP 15
Db 246 AHLRSP 251
|||||

RESULT 11
Q18509 PRELIMINARY; PRT; 556 AA.
AC Q18509;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C38D4.4 protein.
GN C38D4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Coles L.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z46241; CAA86317.1; -.
SO SEQUENCE 556 AA; 60548 MW; 79D13559EADBDIAE CRC64;

Query Match 40.0%; Score 6; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRSP 15
Db 126 AHLRSP 131
|||||

RESULT 12
Q50992 PRELIMINARY; PRT; 582 AA.
AC Q50992;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SuCA protein (Fragment).
GN SUCA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-MS11;
 RA Porcella S.F., Belland R.J., Judd R.C.;
 RT "The sucAB-1pd operon of *Neisseria gonorrhoeae*."
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L36381; AAA96485.1; -
 DR InterPro: IPR001017; Dehydrogenase_E1.
 DR InterPro: IPR004360; Gly_dleo_diox.
 DR InterPro: IPR000360; Transketolase.
 DR Pfam: PF00676; ELdehydrg; 1.
 DR Pfam: PF00903; G1yoxalase; 1.
 DR Pfam: PF02779; transket_pyr; 1.
 DR NON_TR 1
 FT SEQUENCE 582 AA; 65653 MW; 32470A34CF254DEB CRC64;
 Query Match 40.0%; Score 6; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 FSHRHA 10
 Db 266 FSHRHA 271
 RESULT 13
 09VZK2 PRELIMINARY; PRT; 653 AA.
 ID 09VZK2
 AC 09VZK2: 09Y144;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE SCRT protein (SCRATCH).
 GN SCRT OR CG1130.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe C.R., Miklos G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,
 RA Adell J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman J.J., Hernandez J.R., Honck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jostali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE OF 1-567 FROM N.A.
 RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
 RA Agbayani A., Arcalata T.T., Baxter E., Blazer J.G., Butenoff C.,
 RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
 RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
 RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Paclob J.M.,
 RA Park S., Sequeira A., Sethi H., Shtl E., Svirskas R.R., Weinburg T.,
 RA Celniker S.E.;
 RT "Full length *Drosophila melanogaster* cDNA sequence."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003479; AAF47819.1; -
 DR EMBL: AF145627; AAD38602.1; -
 DR HSSP: P08048; 7ZNF.
 DR FLYBase: FBgn0004880; scrt.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00096; Zf-C2H2; 5.
 DR ProDom: PD000003; Znf_C2H2; 1.
 DR SMART: SM00355; Znf_C2H2; 5.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 3.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SO SEQUENCE 653 AA; 70774 MW; 15C27EE93F3FF45D CRC64;
 Query Match 40.0%; Score 6; DB 5; Length 653;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 HAHURS 14
 Db 343 HAHURS 348
 RESULT 14
 024140 PRELIMINARY; PRT; 664 AA.
 ID 024140
 AC 024140;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Neuron specific zinc finger transcription factor.
 GN SCRT OR SCRATCH OR CG1130.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96010286; PubMed=7557390;
 RA Roark M., Sturtevant M.A., Emery J., Veassin H., Grell E., Bter E.;
 RT "scratch, a pan-neural gene encoding a zinc finger protein related to
 RT snail, promotes neuronal development."
 RL Genes Dev. 9:2384-2398(1995).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: U36477; AAA91035.1; -
 DR HSSP: P08048; 7ZNF.
 DR FLYBase: FBgn0004880; scrt.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00096; Zf-C2H2; 5.
 DR PRINTS: PR00048; ZINCFINGER.
 DR ProDom: PD000003; Znf_C2H2; 1.
 DR SMART: SM00355; Znf_C2H2; 5.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 6.
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
 SO SEQUENCE 664 AA; 72569 MW; 687F2DABFE8968F CRC64;

Query Match 40.0%; Score 6; DB 5; Length 664;
 Best Local Similarity 100.0%; Pred No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 HAHRS 14
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 Db 343 HAHRS 348

RESULT 15

O9VA02 PRELIMINARY; PRT; 901 AA.
 ID O9VA02
 AC O9VA02
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CG1544 protein.
 GN CG1544.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 OX [1]
 RN RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003777; AAF57126.1; -;
 DR FLYBase; FBgn0039827; CG1544.
 DR InterPro; IPR001017; Dehydrogenase_E1.
 DR InterPro; IPR000360; Transketolase.
 DR Pfam; PF00676; El.dehydrog; 1.
 DR Pfam; PF02779; transket_dyr; 1.
 DR TrnFRAMS; TIGR00239; zoxo_dh_E1; 1.

SQ SEQUENCE 901 AA; 101506 MM; 656BFCF752E65F83 CRC64;
 Query Match 40.0%; Score 6; DB 5; Length 901;
 Best Local Similarity 100.0%; Pred No. 59;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
 |||||
 Db 584 FSHRHA 589

Search completed: November 27, 2002, 07:30:18
 Job time: 11.4778 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:19:05 : Search time 5.32819 Seconds
(Without alignments)
375.129 Million cell updates/sec

Title: US-09-893-615-1

Perfect score: 15

Sequence: 1 WRMYFSHRHRLSP 15

Scoring table: OLIGO
Gapop-60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002.*

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	20	AAW94701
2	15	100.0	19	20	AAW94733
3	15	100.0	19	20	AAW94714
4	15	100.0	19	20	AAW94715
5	15	100.0	19	20	AAW94717
6	15	100.0	19	20	AAW94718
7	15	100.0	19	20	AAW94719
8	6	40.0	76	23	ABP38325
9	6	40.0	129	22	AAU48733
10	6	40.0	132	23	ABP06906

11	6	40.0	238	22	AAU66845
12	6	40.0	252	20	AAV35921
13	6	40.0	350	20	AAV35922
14	6	40.0	365	22	AAW25386
15	6	40.0	390	20	AAV35923
16	6	40.0	413	20	AAV34811
17	6	40.0	653	22	ABW57870
18	6	40.0	899	22	AAU33860
19	6	40.0	901	22	ABW58224
20	6	40.0	912	22	ABW52560
21	6	40.0	932	22	AAW97701
22	6	40.0	943	22	AAU36221
23	6	40.0	943	22	AAU36241
24	5	33.3	14	22	AAW8006
25	5	33.3	14	22	AAW8007
26	5	33.3	14	22	AAW8008
27	5	33.3	18	22	ABW33959
28	5	33.3	18	22	ABW19398
29	5	33.3	18	22	AAW54723
30	5	33.3	18	22	AAW14984
31	5	33.3	18	22	AAW27417
32	5	33.3	18	22	AAW02709
33	5	33.3	18	23	ABG36782
34	5	33.3	21	23	AAU88558
35	5	33.3	26	21	AAW3840
36	5	33.3	36	20	AAV49674
37	5	33.3	41	23	ABW94072
38	5	33.3	46	22	ABW07585
39	5	33.3	48	22	AAW64327
40	5	33.3	48	22	AAW77154
41	5	33.3	48	22	AAW37285
42	5	33.3	48	23	ABG46166
43	5	33.3	50	22	AAU55721
44	5	33.3	51	22	AAU59920
45	5	33.3	51	22	AAU65435

ALIGNMENTS

RESULT 1
AAW94701
AAW94701 standard; peptide: 15 AA.
AC AAW94701;
DT 22-APR-1999 (first entry)
XX
XX Lipoteichoic acid epitope peptide mimic for Mab 9C-110.
DE
XX
XX Monoclonal antibody: Mab; lipoteichoic acid; gram positive; bacteria;
KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 9C-110.
XX
XX Staphylococcus sp.
OS
XX
XX W09857994-AZ.
PN
XX
XX 23-DEC-1998.
PD
XX
XX 16-JUN-1998; 98WO-US12402.
PF
XX
XX 16-JUN-1997; 97US-0049871.
PR
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PA Fischer GW, Schuman RF, Stinson JL, Wong H;
XX
XX WPI: 1999-095329/08.
DR
XX
XX New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria

XX Claim 16; Page 120; 150pp; English.
 PS
 CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic acid
 CC of gram positive bacteria, where the Mab is a chimeric immunoglobulin
 CC comprising at least part of a human immunoglobulin constant region and
 CC at least part of a non-human immunoglobulin variable region having
 CC specificity to lipoteichoic acid of gram positive bacteria. The
 CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
 CC the bacteria and enhance protection from lethal infection. The antibodies
 CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
 CC acid antibody or characterised by amino acids corresponding to one or
 CC more of the complementarily determining regions (CDRs) of the variable
 CC region of the antibody) can be used for treating or preventing infections
 CC caused by gram positive bacteria. They can also be used for the diagnosis
 CC of gram positive bacterial infections. The present sequence represents a
 CC specifically claimed lipoteichoic acid epitope peptide mimic that can be
 CC bound by the antibody of the invention (Mab 96-110).
 CC
 SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
 DB 1 WRMYFSHRHAHLRSP 15

RESULT 2
 AAW94733
 ID AAW94733 standard; Protein; 19 AA.
 XX

AC AAW94733;

DT 22-APR-1999 (first entry)

XX Sequence 15mer 2nd.12 resulting from library panning experiments.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KM immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KM Mab 96-110; panning.

XX Staphylococcus sp.

OS WO9857994-A2.

PN 23-DEC-1998.

PD 16-JUN-1998; 98WO-US12402.

PF 16-JUN-1997; 97US-0049871.

PR (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PA Fischer GW, Schuman RF, Stinson JL, Wong H;

PI MPI: 1999-095329/08.

PT N-PSDB; AAX05559.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX

PS Example 5; Fig 8; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and

CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarily determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94726-34 represent common-peptide sequences resulting from
 CC all library panning experiments. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 CC
 SQ Sequence 19 AA;

Query Match 100.0%; Score 15; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
 DB 3 WRMYFSHRHAHLRSP 17

RESULT 3
 AAW94714
 ID AAW94714 standard; Protein; 19 AA.
 XX

AC AAW94714;

DT 22-APR-1999 (first entry)

XX Sequence 15mer 2-12/0 resulting from library panning experiment.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KM immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KM Mab 96-110; panning.

XX Staphylococcus sp.

OS WO9857994-A2.

PN 23-DEC-1998.

PD 16-JUN-1998; 98WO-US12402.

PF 16-JUN-1997; 97US-0049871.

PR (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PA Fischer GW, Schuman RF, Stinson JL, Wong H;

PI MPI: 1999-095329/08.

PT N-PSDB; AAX05540.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX

PS Example 5; Fig 6A-B; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarily determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also

CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
CC panning second experiment. Three series of panning experiments were
CC conducted to identify peptide sequences to which antibody of the
CC invention (Mab 96-110) bound strongly. The translated sequences provide
CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
XX
SQ Sequence 19 AA:
Query Match 100.0%; Score 15; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 2,2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WRMYFSHRHAHLRSP 15
Db 3 WRMYFSHRHAHLRSP 17
RESULT 4
AAW94715 standard; Protein: 19 AA.
XX
AC AAW94715:
XX 22-APR-1999 (first entry)
XX
DE Sequence 15mer2-13/0 resulting from 15mer library panning experiment.
XX
KW Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110; panning.
XX
OS Staphylococcus sp.
XX
PN MO9857994-A2.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX WPI: 1999-095329/08.
DR N-PSDB: AAX05541.
XX
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Example 5; Fig 6A-B; 150pp; English.
XX
CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic
CC acid of gram positive bacteria, where the Mab is a chimeric
CC immunoglobulin comprising at least part of a human immunoglobulin
CC constant region and at least part of a non-human immunoglobulin variable
CC region having specificity to lipoteichoic acid of gram positive bacteria.
CC The antibodies bind to whole bacteria and enhance phagocytosis and
CC killing of the bacteria and enhance protection from lethal infection. The
CC antibodies or peptides (encoded by a DNA of the variable region of
CC anti-lipoteichoic acid antibody or characterised by amino acids
CC corresponding to one or more of the complementarity determining regions
CC (CDRs) of the variable region of the antibody) can be used for treating
CC or preventing infections caused by gram positive bacteria. They can also
CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
CC panning second experiment. Three series of panning experiments were
CC conducted to identify peptide sequences to which antibody of the
CC invention (Mab 96-110) bound strongly. The translated sequences provide
CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

XX
SQ Sequence 19 AA:
Query Match 100.0%; Score 15; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 2,2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WRMYFSHRHAHLRSP 15
Db 3 WRMYFSHRHAHLRSP 17
RESULT 5
AAW94717 standard; Protein: 19 AA.
XX
AC AAW94717:
XX 22-APR-1999 (first entry)
XX
DE Sequence 15mer2-10/0 resulting from 15mer library panning experiment.
XX
KW Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110; panning.
XX
OS Staphylococcus sp.
XX
PN MO9857994-A2.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX WPI: 1999-095329/08.
DR N-PSDB: AAX05543.
XX
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Example 5; Fig 6A-B; 150pp; English.
XX
CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic
CC acid of gram positive bacteria, where the Mab is a chimeric
CC immunoglobulin comprising at least part of a human immunoglobulin
CC constant region and at least part of a non-human immunoglobulin variable
CC region having specificity to lipoteichoic acid of gram positive bacteria.
CC The antibodies bind to whole bacteria and enhance phagocytosis and
CC killing of the bacteria and enhance protection from lethal infection. The
CC antibodies or peptides (encoded by a DNA of the variable region of
CC anti-lipoteichoic acid antibody or characterised by amino acids
CC corresponding to one or more of the complementarity determining regions
CC (CDRs) of the variable region of the antibody) can be used for treating
CC or preventing infections caused by gram positive bacteria. They can also
CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
CC panning second experiment. Three series of panning experiments were
CC conducted to identify peptide sequences to which antibody of the
CC invention (Mab 96-110) bound strongly. The translated sequences provide
CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
XX
SQ Sequence 19 AA:
Query Match 100.0%; Score 15; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 2,2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRAHLRSP 15
 DB 3 WRMYFSHRAHLRSP 17

RESULT 6
 AAW94718
 ID AAW94718 standard; Protein; 19 AA.

AC AAW94718;
 DT 22-APR-1999 (first entry)

DE Sequence 15mer2-16/0 resulting from 15mer library panning experiment.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KM Mab 96-110; panning.

OS Staphylococcus sp.

PN WO9857994-A2.

PD 23-DEC-1998.

PF 16-JUN-1998; 98WO-US12402.

PR 16-JUN-1997; 97US-0049871.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Fischer GW, Schuman RF, Stinson JL, Wong H;

XX WPI; 1999-095329/08.

DR N-PSDB; AAX05344.

PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria

XX Example 5; Fig 6A-B; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope mimics to which Mab96-110 bound.

XX Sequence 19 AA;

Query Match 100.0%; Score 15; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred No. 2.2e-10;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRAHLRSP 15
 DB 3 WRMYFSHRAHLRSP 17

RESULT 7
 AAW94719
 ID AAW94719 standard; Protein; 19 AA.

AC AAW94719;

DT 22-APR-1999 (first entry)

DE Sequence 15mer2-17/0 resulting from 15mer library panning experiment.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KM Mab 96-110; panning.

OS Staphylococcus sp.

PN WO9857994-A2.

PD 23-DEC-1998.

PF 16-JUN-1998; 98WO-US12402.

PR 16-JUN-1997; 97US-0049871.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Fischer GW, Schuman RF, Stinson JL, Wong H;

XX WPI; 1999-095329/08.

DR N-PSDB; AAX05345.

PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria

XX Example 5; Fig 6A-B; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope mimics to which Mab96-110 bound.

XX Sequence 19 AA;

Query Match 100.0%; Score 15; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred No. 2.2e-10;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRAHLRSP 15
 DB 3 WRMYFSHRAHLRSP 17

RESULT 8
 ABP38325
 ID ABP38325 standard; Protein; 76 AA.
 AC ABP38325;

DT	24-JUL-2002	(first entry)
XX	Staphylococcus epidermidis	ORF amino acid sequence SEQ ID NO:3170.
DE	Staphylococcus epidermidis	: open reading frame; ORF; bacterial infection;
XX	antibacterial; gene therapy.	
KW	Staphylococcus epidermidis.	
XX	Staphylococcus epidermidis.	
OS	US6380370-B1.	
XX	US6380370-B1.	
PN	30-APR-2002.	
PD	13-AUG-1998;	98US-0134001.
XX	14-AUG-1997;	97US-055779P.
XX	08-NOV-1997;	97US-064964P.
PR	(GENO-)	GENOME THERAPEUTICS CORP.
XX	Doucette-Stamm LA,	Bush D;
PI	WPI: 2002-381255/41.	
DR	N-PSDB: ABN90870.	
XX	Novel isolated nucleic acid encoding a Staphylococcus epidermidis	
PT	polypeptide, useful for diagnosing and treating bacterial infections -	
PS	Disclosure; SEQ ID 3170; 267pp; English.	
XX	ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading	
CC	frame (ORF) nucleic acid sequences which encode the amino acid sequences	
CC	given in ABP35124 to ABP37960. The S. epidermidis sequences have	
CC	antibacterial activity and can be used in gene therapy. The sequences	
CC	can also be used in the diagnosis and treatment of bacterial infections,	
CC	particularly S. epidermidis infections. The sequences can be used to	
CC	screen for compounds able to interfere with the S. epidermidis life	
CC	cycle or inhibit S. epidermidis infection.	
CC	N.B. The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from the	
CC	USPTO web site.	
XX	Sequence	76 AA;
XX	Query Match	40.0%; Score 6; DB 23; Length 76;
XX	Best Local Similarity	100.0%; Pred. No. 9.8;
XX	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	5 FSHRHA 10	
DB		
DB	10 FSHRHA 15	
XX	RESULT 9	
XX	AAU48733	
XX	AAU48733 standard; Protein: 129 AA.	
XX	AAU48733;	
DT	27-FEB-2002	(first entry)
XX	Propionibacterium acnes immunogenic protein #9629.	
DE	SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;	
KW	uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;	
KW	Inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;	
XX	dermatological; osteopathic; neuroprotectant.	
XX	Propionibacterium acnes.	
OS	WO200181581-A2.	
XX	01-NOV-2001.	

```

XX 20-APR-2001; 2001WO-US12865.
PF
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhalla A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI: 2001-616774/71.
DR N-PSDB; AAS39543.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Example 1: SEQ ID NO 9928; 1069pp; English.
PS
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 129 AA;
XX
XX Query Match 40.0%; Score 6; DB 22; Length 129;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 10 AHLRSP 15
XX |||||
DB 78 AHLRSP 83
XX
RESULT 10
ID ABP06906 standard: Protein; 132 AA.
XX
XX ABP06906;
XX
XX 24-JUN-2002 (first entry)
DT
XX
XX Human ORFX protein sequence SEQ ID NO:13794.
DE
XX
XX Human: open reading frame; ORFX: gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumor; hemorrhage;
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX hyperparathyroidism; hypothyroidism; cholesterol ester storage disease;
XX immune deficiency; immune disorder; infectious disease;
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX myasthenia gravis.
XX
XX Homo sapiens
XX

```

XX WO200192523-A2.
 PN
 XX
 PD 06-DEC-2001.
 XX
 XX
 PF 29-MAY-2001; 2001WO-US10836.
 PR
 XX 30-MAY-2000; 2000US-206132P.
 PR 29-AUG-2000; 2000US-228716P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach MD;
 XX
 DR WPI; 2002-106308/14.
 DR N-PSDB; ABN22658.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders
 PS
 PS Disclosure; SEQ ID 13794; 1037pp; English.

XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification), ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 132 AA;

Query Match 40.0%; Score 6; DB 23; Length 132;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
 |||||
 Db 49 FSHRHA 54

RESULT 11
 AAU66845
 ID AAU66845 standard; Protein; 238 AA.
 XX
 AC AAU66845;

DE 13-FEB-2002 (first entry)
 XX
 XX Propionibacterium acnes immunogenic protein #27741.

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.
 XX
 XX Propionibacterium acnes.
 OS
 XX
 PN WO200181581-A2.
 XX
 XX
 PD 01-NOV-2001.
 XX
 XX
 PF 20-APR-2001; 2001WO-US12865.
 PR
 XX 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhalla A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59760.
 XX

PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 PS
 PS Example 1; SEQ ID NO 28040; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 238 AA;

Query Match 40.0%; Score 6; DB 22; Length 238;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHLRSP 15
 |||||
 Db 187 AHLRSP 192

RESULT 12
 AAY35921
 ID AAY35921 standard; Protein; 252 AA.
 XX
 AC AAY35921;

DE 13-SEP-1999 (first entry)
 XX
 XX Extended human secreted protein sequence, SEQ ID NO. 170.

KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
 KM cellular differentiation; immune system regulator; anti-inflammatory;
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;

KM reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 KW genetic disease.
 XX
 OS Homo sapiens.
 XX
 PN MO9931236-A2.
 XX
 PD 24-JUN-1999.
 XX
 XX 17-DEC-1998; 98WO-IB02122.
 XX
 PR 10-AUG-1998; 98US-0096116.
 PR 17-DEC-1997; 97US-0069957.
 PR 09-FEB-1998; 98US-0074121.
 PR 13-APR-1998; 98US-0081563.
 XX
 PA (GEST) GENSET.
 XX
 PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
 XX
 DR WPI; 1999-385906/32.
 DR N-PSDB; AAX97605.
 XX
 PT New isolated human secreted proteins
 PS
 XX Claim 9; Page 201-202; 516pp; English.
 CC This sequence is encoded by an extended human secreted protein coding
 CC sequence of the invention. The secreted proteins can be used in treating
 CC or controlling a variety of human conditions. The secreted proteins may
 CC act as cytokines or may affect cellular proliferation or differentiation
 CC or may act as immune system regulators, haematopoiesis regulators, tissue
 CC growth regulators, regulators of reproductive hormones or cell movement
 CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 CC tumour inhibition activity. The DNAs can be used in forensic procedures
 CC to identify individuals or in diagnostic procedures to identify
 CC individuals having genetic diseases resulting from abnormal expression of
 CC the genes corresponding to the extended cDNAs. They are also useful for
 CC constructing a high resolution map of the human chromosomes. They can
 CC also be used for gene therapy to control or treat genetic diseases.
 CC
 XX
 SQ Sequence 252 AA;
 Query Match 40.0%; Score 6; DB 20; Length 252;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 RHAHLR 13
 |||||
 Db 95 RHAHLR 100
 RESULT 13
 AAY35922
 ID AAY35922 standard; Protein: 350 AA.
 XX
 AC AAY35922;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Extended human secreted protein sequence, SEQ ID NO. 171.
 XX
 KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
 KW cellular differentiation; immune system regulator; anti-inflammatory;
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 KW genetic disease.
 XX
 OS Homo sapiens.
 XX
 PN MO9931236-A2.
 XX
 PD 24-JUN-1999.

XX
 PF 17-DEC-1998; 98WO-IB02122.
 XX
 PR 10-AUG-1998; 98US-0096116.
 PR 17-DEC-1997; 97US-0069957.
 PR 09-FEB-1998; 98US-0074121.
 PR 13-APR-1998; 98US-0081563.
 XX
 PA (GEST) GENSET.
 XX
 PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
 XX
 DR WPI; 1999-385906/32.
 DR N-PSDB; AAX97606.
 XX
 PT New isolated human secreted proteins
 PS
 XX Claim 9; Page 203-204; 516pp; English.
 CC This sequence is encoded by an extended human secreted protein coding
 CC sequence of the invention. The secreted proteins can be used in treating
 CC or controlling a variety of human conditions. The secreted proteins may
 CC act as cytokines or may affect cellular proliferation or differentiation
 CC or may act as immune system regulators, haematopoiesis regulators, tissue
 CC growth regulators, regulators of reproductive hormones or cell movement
 CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 CC tumour inhibition activity. The DNAs can be used in forensic procedures
 CC to identify individuals or in diagnostic procedures to identify
 CC individuals having genetic diseases resulting from abnormal expression of
 CC the genes corresponding to the extended cDNAs. They are also useful for
 CC constructing a high resolution map of the human chromosomes. They can
 CC also be used for gene therapy to control or treat genetic diseases.
 CC
 XX
 SQ Sequence 350 AA;
 Query Match 40.0%; Score 6; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 RHAHLR 13
 |||||
 Db 95 RHAHLR 100
 RESULT 14
 AAM25386
 ID AAM25386 standard; Protein: 365 AA.
 XX
 AC AAM25386;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO: 901.
 XX
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antitumour; cardiovascular; antihaemic; anaemia;
 KW antiaggregant; haemostatic; vulnerary; antitumor; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antiinflammatory; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO200153455-A2.

PX		PD		26-JUL-2001.	
PF		PE			
XX		22-DEC-2000;	2000OWO-US35017.		
PR		23-DEC-1999;	99US-0471275.		
PR		21-JAN-2000;	2000OUS-0488725.		
XX		25-APR-2000;	2000OUS-0552317.		
PA	(HYSF-) HNSQ INC.				
XX		Tang YT,	Liu C, Drmanac RT;		
XX		WPI:	2001-457603/49.		
DR	N-PDB; AAH99327.				
PT		Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -			
PS	Claim 20; Page 197; 121pp; English.				
XX		AAH99166 to AAH99904 encode the human proteins given in AAM25225 to			
CC		AAM25963. The proteins can have activities based on the tissues and			
CC		cells they are expressed in, such as: antineoplastic; anti-infective;			
CC		antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;			
CC		central nervous system; virucide; anti-HIV; fungicide; antimutagen;			
CC		cardiovascular; antianemic; antilipidic; haemostatic; vulnerary;			
CC		antidiabetic; osteopathic; dermatological; antiallergic; antiasthmatic;			
CC		antiparkinsonian; and immunostimulant. The proteins and polynucleotides			
CC		encoding them can be used in gene therapy, antisense therapy and vaccine			
CC		production. The proteins and polynucleotides are useful for screening for			
CC		agonists or antagonists of a protein and for the treatment and diagnosis			
CC		of disorders associated with the activity of a protein e.g. inflammation,			
CC		rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,			
CC		neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal			
CC		infections, autoimmunity, genetic diseases, haematopoietic disorders,			
CC		anemia, platelet disorders, thrombocytopoenia, wounds, burns, ulcers,			
CC		osteoporosis, severe combined immunodeficiency, eczema, allergic			
CC		rinitis, asthma, diabetes, cancer, multiple sclerosis, depression,			
CC		Alzheimer's disease, Parkinson's disease, neurodegenerative and			
CC		neurological disorders.			
SQ	Sequence	365 AA;			
Query Match		40.0%; Score 6; DB 22; Length 365;			
Best Local Similarity		100.0%; Pred. No. 44;			
Matches	6; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
OY	8 RHAHR 13 				
Dd	141 RHAHR 146				
RESULT 15					
ID	AAV35923 standard; Protein; 390 AA.				
XX	AAV35923;				
DT	13-SEP-1999 (first entry)				
DE	Extended human secreted protein sequence, SEQ ID NO. 172.				
KM	Secreted protein: human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy; genetic disease. Homo sapiens. WO9931236-A2				

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XX 24-JUN-1999.
PD
XX
XX PF 17-DEC-1998; 98WO-IB02122.
XX
XX PR 10-AUG-1998; 98US-0096116.
XX PR 17-DEC-1997; 97US-0069957.
XX PR 09-FEB-1998; 98US-0074121.
XX PR 13-APR-1998; 98US-0081563.
XX
XX (GEST ) GENSET.
XX
XX Bougueleret L, Duclert A, Dumas Milne Edwards J:
XX
XX WPI: 1999-385906/32.
XX DR N-PSDB; AAX97607.
XX
XX
XX New isolated human secreted proteins
XX
XX PS
XX PT
XX PS Claim 9; Page 204-205; 516pp; English.
XX
XX This sequence is encoded by an extended human secreted protein coding
XX sequence of the invention. The secreted proteins can be used in treating
XX or controlling a variety of human conditions. The secreted proteins may
XX act as cytokines or may affect cellular proliferation or differentiation
XX or may act as immune system regulators, haematopoiesis regulators, tissue
XX growth regulators, regulators of reproductive hormones or cell movement
XX or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
XX tumour inhibition activity. The DNAs can be used in forensic procedures
XX to identify individuals or in diagnostic procedures to identify
XX individuals having genetic diseases resulting from abnormal expression of
XX the genes corresponding to the extended CDNAs. They are also useful for
XX constructing a high resolution map of the human chromosomes. They can
XX also be used for gene therapy to control or treat genetic diseases.
XX
XX Sequence 390 AA;
XX
XX Query Match 40.0%; Score 6; DB 20; Length 390;
XX Best Local Similarity 100.0%; Pred. No. 47;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 RHAHLR 13
XX |||||
XX Db 95 RHAHLR 100

```


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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:26:06 ; Search time 2.08494 Seconds

(without alignments)
211.682 Million cell updates/sec

Title: US-09-893-615-1

Sequence: 1 WRMYFSHRHAHLRSP 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2_6/p10data/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/p10data/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/p10data/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/p10data/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/p10data/1/1aa/PCtus_COMB.pep.*
- 6: /cgn2_6/p10data/1/1aa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	76	4 US-09-134-001C-3170	Sequence 3170, Ap
2	6	40.0	932	4 US-08-887-534A-45	Sequence 45, Appl
3	5	33.3	36	4 US-09-183-706-41	Sequence 41, Appl
4	5	33.3	36	4 US-09-567-995-41	Sequence 41, Appl
5	5	33.3	63	2 US-08-338-530A-6	Sequence 6, Appli
6	5	33.3	63	4 US-09-267-384-6	Sequence 6, Appli
7	5	33.3	70	4 US-09-134-001C-3950	Sequence 3950, Ap
8	5	33.3	114	1 US-08-372-952-1	Sequence 1, Appli
9	5	33.3	114	4 US-08-875-309-1	Sequence 1, Appli
10	5	33.3	114	5 PCT-US96-00310-1	Sequence 1, Appli
11	5	33.3	149	2 US-08-815-175-3	Sequence 3, Appli
12	5	33.3	179	3 US-08-665-259-1	Sequence 1, Appli
13	5	33.3	179	3 US-08-762-500-1	Sequence 1, Appli
14	5	33.3	200	4 US-09-562-737-110	Sequence 12, Appl
15	5	33.3	235	1 US-07-940-605A-12	Sequence 12, Appl
16	5	33.3	235	2 US-08-690-096-12	Sequence 12, Appl
17	5	33.3	273	2 US-08-403-853-12	Sequence 12, Appl
18	5	33.3	355	3 US-08-872-979-7	Sequence 7, Appli
19	5	33.3	376	3 US-08-751-512-8	Sequence 8, Appli
20	5	33.3	379	2 US-08-576-626A-50	Sequence 50, Appl
21	5	33.3	385	4 US-09-323-872A-19	Sequence 19, Appl
22	5	33.3	387	4 US-09-916-109-6	Sequence 6, Appli
23	5	33.3	411	2 US-08-338-530A-3	Sequence 3, Appli
24	5	33.3	411	4 US-09-267-384-3	Sequence 3, Appli
25	5	33.3	483	4 US-09-916-109-4	Sequence 4, Appli
26	5	33.3	524	4 US-09-134-001C-4315	Sequence 4315, Ap
27	5	33.3	678	1 US-08-282-141-2	Sequence 2, Appli

28	5	33.3	678	1 US-08-435-434-2	Sequence 2, Appli
29	5	33.3	678	1 US-08-435-436-2	Sequence 2, Appli
30	5	33.3	678	2 US-08-438-863-2	Sequence 2, Appli
31	5	33.3	678	2 US-08-438-864-2	Sequence 2, Appli
32	5	33.3	678	3 US-08-438-862-2	Sequence 2, Appli
33	5	33.3	678	4 US-08-628-747-2	Sequence 2, Appli
34	5	33.3	678	4 US-08-402-253-2	Sequence 2, Appli
35	5	33.3	678	4 US-08-443-866B-2	Sequence 2, Appli
36	5	33.3	840	4 US-08-974-549A-190	Sequence 190, App
37	5	33.3	872	3 US-08-851-843A-8	Sequence 8, Appli
38	5	33.3	872	3 US-08-851-843A-54	Sequence 8, Appli
39	5	33.3	872	4 US-08-974-549A-221	Sequence 221, App
40	5	33.3	872	4 US-08-854-050-8	Sequence 8, Appli
41	5	33.3	872	4 US-08-854-050-54	Sequence 54, Appli
42	5	33.3	872	4 US-09-430-323-8	Sequence 8, Appli
43	5	33.3	872	4 US-09-430-323-54	Sequence 54, Appli
44	5	33.3	979	4 US-08-878-474-5	Sequence 5, Appli
45	5	33.3	1105	4 US-08-999-774A-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-134-001C-3170
Sequence 3170, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
FILE REFERENCE: GNC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3170
LENGTH: 76
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3170

Query Match      40.0%; Score 6; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5 FSHRHA 10
Db      10 FSHRHA 15

RESULT 2
US-08-887-534A-45
Sequence 45, Application US/08887534A
Patent No. 6455323
GENERAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Horun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,534A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-887-534A-45

Query Match 40.0%; Score 5; DB 4; Length 932;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
|||||
Db 621 FSHRHA 626

RESULT 3
US-09-183-706-41
Sequence 41, Application US/09183706
Patent No. 6245525
GENERAL INFORMATION:
APPLICANT: Martelange, Valrie
APPLICANT: De Smet, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/183,706
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 09/122,989
EARLIER FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 41
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-09-183-706-41

Query Match 33.3%; Score 5; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRH 9
|||||
Db 25 FSHRH 29

RESULT 4
US-09-567-995-41
Sequence 41, Application US/09567995
Patent No. 6303756
GENERAL INFORMATION:
APPLICANT: Martelange, Valrie
APPLICANT: De Smet, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/567,995
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/183,706

PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 41
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-09-567-995-41

Query Match 33.3%; Score 5; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRH 9
|||||
Db 25 FSHRH 29

RESULT 5
US-08-338-530A-6
Sequence 6, Application US/08338530A
Patent No. 5922327
GENERAL INFORMATION:
APPLICANT: CRABB, Brendan S.
APPLICANT: STUDEERT, Michael J.
TITLE OF INVENTION: EQUINE HERPESVIRUS GLYCOPROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,530A
FILING DATE: 25-JAN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00253
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40268/120/CSMB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-338-530A-6

Query Match 33.3%; Score 5; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHRHS 14
|||||
Db 43 AHRHS 47

RESULT 6
US-09-267-384-6
Sequence 6, Application US/09267384

Patent No. 6193983
GENERAL INFORMATION:
APPLICANT: CRABB, Brendan S.
APPLICANT: STUDDERT, Michael J.
TITLE OF INVENTION: EQUINE HERPESVIRUS GLYCOPROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,384
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,530
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: WO PCT/AU93/00253
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40268/120/CSMB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-3399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-267-384-6

Query Match 33.3%; Score 5; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 10 AHLRS 14
|||||
Db 43 AHLRS 47

RESULT 7
US-09-134-001C-3950
Sequence 3950, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3950
LENGTH: 70
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3950

Query Match 33.3%; Score 5; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MYFSH 7
|||||
Db 52 MYFSH 56

RESULT 8
US-08-372-952-1
Sequence 1, Application US/08372952
Patent No. 5645837
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 564583715
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,952
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TDU-1440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-952-1

Query Match 33.3%; Score 5; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MYFSH 7
|||||
Db 102 MYFSH 106

RESULT 9
US-08-875-309-1
Sequence 1, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert

APPLICANT: Huang, Ziwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 61806000115
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-309-1

Query Match 33.3%; Score 5; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MYFSH 7
|||||
DB 102 MYFSH 106

RESULT 10
PCT-US96-00310-1
Sequence 1, Application PC/TUS9600310
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Kornogold, Robert
APPLICANT: Huang, Ziwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1752
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00310-1

Query Match 33.3%; Score 5; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MYFSH 7
|||||
DB 102 MYFSH 106

RESULT 11
US-08-815-175-3
Sequence 3, Application US/08815175
Patent No. 5856139
GENERAL INFORMATION:
APPLICANT: Lai, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL PROLINE-RICH ACIDIC PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jingle Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,175
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0225 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 899433
US-08-815-175-3

Query Match 33.3%; Score 5; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 HLRS 15
|||||
DB 92 HLRS 96

RESULT 12
US-08-665-259-1
; Sequence 1, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klingner, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-665-259-1

Query Match 33.3%; Score 5; DB 3; Length 179;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 HLRS 14
|||||
DB 19 HLRS 23

RESULT 13
US-08-762-500-1
; Sequence 1, Application US/08762500

Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klingner, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-762-500-1

Query Match 33.3%; Score 5; DB 3; Length 179;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 HLRS 14
|||||
DB 19 HLRS 23

RESULT 14
US-09-562-737-110
; Sequence 110, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: URSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 110
; LENGTH: 200

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
US-09-562-737-110

Query Match 33.3%; Score 5; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 SHRA 10
|||||
Db 130 SHRA 134

RESULT 15
US-07-940-605A-12
Sequence 12, Application US/07940605A
Patent No. 5540926

GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE//DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-940-605A-12

Query Match 33.3%; Score 5; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 MYFSH 7
|||||
Db 123 MYFSH 127

Search completed: November 27, 2002, 07:32:08
Job time : 4.08494 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:28:06 : Search time 1.38996 Seconds
(Without alignments)
171.849 Million cell updates/sec

Title: US-09-893-615-1

Sequence: 1 WRMYFSHRHRLRP 15

Scoring table:

Gap 60.0 , Gapext 60.0

Searched: 102317 seqs, 15924203 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PCF_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB pep:*
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- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	10	US-09-893-615-1
2	15	100.0	19	10	US-09-893-615-27
3	15	100.0	19	10	US-09-893-615-29
4	15	100.0	19	10	US-09-893-615-33
5	15	100.0	19	10	US-09-893-615-35
6	15	100.0	19	10	US-09-893-615-37
7	15	100.0	19	10	US-09-893-615-65
8	6	40.0	899	10	US-09-815-242-12615
9	6	40.0	932	10	US-09-815-242-12615
10	6	40.0	943	10	US-09-815-242-11834
11	5	33.3	26	10	US-09-864-761-34696
12	5	33.3	26	10	US-09-925-299-1380
13	5	33.3	36	10	US-09-923-831-41
14	5	33.3	48	10	US-09-864-761-45980
15	5	33.3	119	10	US-09-740-288A-10
16	5	33.3	135	10	US-09-949-192-21
17	5	33.3	149	12	US-10-061-690-3
18	5	33.3	254	10	US-09-815-242-5110
19	5	33.3	266	10	US-09-911-826A-6

20	5	33.3	374	10	US-09-740-288A-12	Sequence 12, Appl
21	5	33.3	379	10	US-09-740-288A-26	Sequence 26, Appl
22	5	33.3	387	10	US-09-916-109-6	Sequence 6, Appl1
23	5	33.3	415	10	US-09-740-288A-28	Sequence 28, Appl1
24	5	33.3	425	12	US-10-052-586-570	Sequence 570, App
25	5	33.3	444	8	US-08-812-393A-2	Sequence 2, Appl1
26	5	33.3	460	10	US-09-925-297-584	Sequence 584, App
27	5	33.3	467	10	US-09-870-130-5	Sequence 5, Appl1
28	5	33.3	469	9	US-10-001-835-168	Sequence 168, App
29	5	33.3	483	10	US-09-916-109-4	Sequence 4, Appl1
30	5	33.3	500	12	US-10-006-867-84	Sequence 84, Appl1
31	5	33.3	872	9	US-09-843-676-8	Sequence 8, Appl1
32	5	33.3	872	9	US-09-843-676-54	Sequence 54, Appl1
33	5	33.3	937	10	US-09-949-192-19	Sequence 19, Appl1
34	5	33.3	979	10	US-09-803-187A-5	Sequence 5, Appl1
35	5	33.3	1017	10	US-09-897-056-5	Sequence 5, Appl1
36	5	33.3	1025	10	US-09-897-056-7	Sequence 7, Appl1
37	5	33.3	1038	10	US-09-752-639-151	Sequence 151, App
38	5	33.3	1038	10	US-09-984-198-151	Sequence 151, App
39	5	33.3	1275	10	US-09-749-140-6	Sequence 6, Appl1
40	5	33.3	1285	10	US-09-925-301-1394	Sequence 1394, App
41	5	33.3	1474	10	US-09-873-403-5	Sequence 5, Appl1
42	5	33.3	1474	12	US-10-052-817-2	Sequence 2, Appl1
43	4	26.7	7	9	US-10-080-100-54	Sequence 54, Appl1
44	4	26.7	8	9	US-10-080-100-17	Sequence 17, Appl1
45	4	26.7	18	10	US-09-922-261-358	Sequence 358, App

ALIGNMENTS

RESULT 1
US-09-893-615-1
Sequence 1, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPGONIN AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESS: FUNNEN, LRP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995, 0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-893-615-1

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
DB 1 WRMYFSHRHAHLRSP 15

RESULT 2
US-09-893-615-27
Sequence 27, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudt, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-893-615-27

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
DB 3 WRMYFSHRHAHLRSP 17

RESULT 3
US-09-893-615-29
Sequence 29, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.

Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudt, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-893-615-29

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
DB 3 WRMYFSHRHAHLRSP 17

RESULT 4
US-09-893-615-33
Sequence 33, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995,0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-893-615-33
Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WRMYFSHRAHLRSP 15
|||||
DB 3 WRMYFSHRAHLRSP 17
RESULT 5
US-09-893-615-35
Sequence 35, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995,0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-893-615-35

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WRMYFSHRAHLRSP 15
|||||
DB 3 WRMYFSHRAHLRSP 17
RESULT 6
US-09-893-615-37
Sequence 37, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995,0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-893-615-37
Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WRMYFSHRAHLRSP 15
|||||
DB 3 WRMYFSHRAHLRSP 17
RESULT 7
US-09-893-615-65
Sequence 65, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.

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; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
; POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Elnaudi, Carol P
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 04995.0041-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-893-615-65

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WRWFSRHAHLRSP 15
Db 3 WRWFSRHAHLRSP 17

RESULT 8
US-09-815-242-5356
; Sequence 5356, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5356
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5356

Query Match 40.0%; Score 6; DB 10; Length 899;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSHRHA 10
Db 607 FSHRHA 612

RESULT 9
US-09-815-242-12615
; Sequence 12615, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12615
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12615

Query Match 40.0%; Score 6; DB 10; Length 932;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSHRHA 10
Db 621 FSHRHA 626

RESULT 10
US-09-815-242-11834
; Sequence 11834, Application US/09815242
```

```
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11834
LENGTH: 943
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11834

Query Match
Best Local Similarity 40.0%; Score 6; DB 10; Length 943;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSHRHA 10
|||||
Db 631 FSHRHA 636

RESULT 11
US-09-864-761-34696
Sequence 34696, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34696
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL078621.19
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EST_HUMAN HIT: BF059228.1, EVALUATE 2.20e-02
US-09-864-761-34696

Query Match
Best Local Similarity 33.3%; Score 5; DB 10; Length 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HLRSP 15
|||||
Db 1 HLRSP 5

RESULT 12
US-09-925-299-1380
Sequence 1380, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1380
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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LOCATION: (15)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (19)
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NAME/KEY: SITE
LOCATION: (21)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (24)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-923-299-1380

Query Match 33.3%; Score 5; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 HRRHH 11
DB 1 HRRHH 5

RESULT 13
US-09-923-831-41
Sequence 41, Application US/09923831
Patent No. US2002015142A1
GENERAL INFORMATION:
APPLICANT: Martelange, Val,rie
APPLICANT: De Smet, Charles
APPLICANT: Boon-Fallieur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/923,831
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 09/183,706
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 41
LENGTH: 36
TYPE: PR1
ORGANISM: Homo sapiens
US-09-923-831-41

Query Match 33.3%; Score 5; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSHRH 9
DB 25 FSHRH 29

RESULT 14
US-09-864-761-45980
Sequence 45980, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45980
LENGTH: 48
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC017079.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EST_HUMAN HIT: AA852449.1, EVALU = 5.00e-15
US-09-864-761-45980

Query Match 33.3%; Score 5; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MYFSH 7
DB 44 MYFSH 48

RESULT 15
US-09-740-288A-10
Sequence 10, Application US/09740288A
Patent No. US20010039042A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/09/740,288A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 119

Wed Nov 27 08:54:09 2002

; TYPE: PRT
; ORGANISM: Argemone mexicana
US-09-740-288A-10

Query Match 33.3%; Score 5; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 HRAH 11
 |||||
Db 72 HRAH 76

Search completed: November 27, 2002, 07:32:52
Job time : 2.38996 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2002, 05:38:32 : Search time 8.28185 Seconds
(without alignments)
241.342 Million cell updates/sec

Title: US-09-893-615-2
Perfect score: 91
Sequence: 1 MWMHRRIPLQLAGR 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	91	100.0	15	AAW12276	Synthetic library
2	91	100.0	15	AAW71334	A glycolipid sugar
3	91	100.0	15	AAW94702	Lipoteichoic acid
4	91	100.0	15	AAW17987	Beta-2GPI Ab bindi
5	91	100.0	15	ABW73358	Exemplary pharmino
6	91	100.0	19	AAW94729	Sequence 15mer 2nd
7	91	100.0	19	AAW94710	Sequence 15mer 2-8/
8	91	100.0	19	AAW94721	Sequence 15mer 2-19
9	91	100.0	19	AAW94705	Sequence 15mer 2-1/
10	91	100.0	19	AAW94709	Sequence 15mer 2-7/

11	91	100.0	37	17	AAW12287
12	80	87.9	19	20	AAW94708
13	69	75.8	15	17	AAW12277
14	56	61.5	11	17	AAW03372
15	56	61.5	15	17	AAW03374
16	51	56.0	159	22	ABG15894
17	50	54.9	11	17	AAW03373
18	50	54.9	15	17	AAW03375
19	50	54.9	139	22	ABB27778
20	50	54.9	139	22	ABB32949
21	50	54.9	139	22	ABB18423
22	50	54.9	139	22	AAW53750
23	50	54.9	139	22	AAW56133
24	50	54.9	139	22	AAW14004
25	50	54.9	139	22	AAW26410
26	50	54.9	139	22	AAW01745
27	50	54.9	139	23	ABG35783
28	49	53.8	157	22	AAW84592
29	49	53.8	157	23	ABW77573
30	46.5	51.1	74	21	AAW54412
31	46	50.5	11	17	AAW03370
32	46	50.5	15	17	AAW03371
33	46	50.5	71	22	AAW06299
34	46	50.5	536	21	AAW84592
35	44.5	48.9	285	23	AAW51648
36	44.5	48.9	298	15	AAW48755
37	44.5	48.9	298	17	AAW02727
38	44.5	48.9	343	23	ABW08348
39	44	48.4	305	22	ABW09714
40	43.5	47.8	74	23	ABP02393
41	43.5	47.8	385	22	AAW93386
42	43	47.3	51	22	AAW56677
43	43	47.3	51	22	AAW29377
44	43	47.3	117	22	AAW64601
45	43	47.3	367	22	ABW11448

ALIGNMENTS

RESULT 1
AAW12276
ID AAW12276 standard; peptide; 15 AA.

AAW12276;

15-APR-1997 (first entry)

Synthetic library peptide #1 which binds anti-T. gondii p30 antibody.

Toxoplasma gondii: surface protein: antibody; screening; peptide library; diagnostic assay; immunisation; phage; fusion protein; envelop.

Synthetic.

EP724016-A1.

31-JUL-1996.

29-JAN-1996; 96EP-0420030.

30-JAN-1995; 95FR-0001297.

(JOLI/) JOLIVET-REYNARD C.

(INMR) BIO MERIDEX.

Jolivet-Reynard C;

WPI: 1996-343531/35.

New polypeptide reactive with anti-p30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic acid, vectors and transformed cells

Synthetic template
Sequence 15mer2-5/
Synthetic library
Peptide #6 which b
Peptide #8 which b
Novel human diagno
Peptide #7 which b
Peptide #9 which b
Human peptide #429
Peptide #435 encod
Protein #422 encod
Human brain expres
Human bone marrow
Peptide #438 encod
Peptide #447 encod
Peptide #427 encod
Human peptide enco
Human AFP protein
Human mast cell re
Zea mays protein f
Peptide #4 which b
Peptide #5 which b
Human foetal prote
Amino acid sequen
Rat GPCR polypept
Human thoracic aor
Human thoracic aor
RTA-like G protein
Novel human diagno
Human ORFX protein
Human polypeptide,
Human brain expres
Peptide #3414 enco
Protonibacterium
Drosophila/melanog

XX Example 2; Page 7; 33pp; French.
PS
CC The invention relates to novel peptides which bind to antibodies which
CC recognize the Toxoplasma gondii P30 envelope protein. A peptide library
CC was generated to express pentadecapeptides on the surface of a
CC filamentous phage as a fusion protein with the PIII protein. The library
CC was screened with immobilised anti-T. gondii P30 protein antibody 1E1E7.
CC Phages which bind this antibody were recovered and amplified by one
CC round of infection in E. coli. The resultant phages were rescreened with
CC the immobilised antibody and the second round screen isolated 58
CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA
CC from 30 colonies was isolated and sequenced to determine the sequence of
CC the pentadecapeptide encoded. The peptide sequences AAW12276-86 were
CC identified. Of the 30 colonies studied, this peptide sequence was
CC encoded 11 times. A template peptide sequence (AAW12287) corresponding
CC to the sequence across the phage PIII sequence and putative
CC pentadecapeptide was used to generate a series of overlapping
CC pentadecapeptides. These peptides were used to determine the best
CC peptide sequence which binds the 1E1E7 antibody. Peptides AAW03367-75
CC were isolated. The new peptides can then be used in diagnostic assays to
CC detect T. gondii antibodies in a sample or to purify anti-P30 antibodies
CC or for active immunisation against T. gondii.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 91; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WHMRHRIPQLAAGR 15
DB 1 WHMRHRIPQLAAGR 15
RESULT 2
AAW1334
ID AAW1334 standard; peptide; 15 AA.
XX
AC AAW1334;
XX
DT 25-NOV-1998 (first entry)
XX
DE A glycolipid sugar chain peptide.
XX
KM Glycolipid sugar chain; inhibitory; adhesion; metastasis; cancer cell.
XX
OS Synthetic.
XX
PN JP10237099-A.
XX
PD 08-SEP-1998.
XX
PF 26-FEB-1997; 97JP-0042311.
XX
PR 26-FEB-1997; 97JP-0042311.
XX
PA (IMMO) IMMUNO JAPAN INC.
XX
DR WPI; 1998-537488/46.
XX
PT New peptide which reacts specifically with antibody against
PT glyco-lipid sugar chains - useful for inhibition of cancer
PT metastasis
PS Claim 8; Page 3; 7pp; Japanese.
XX
XX AAW1332-36 represent glycolipid sugar chain replica peptides. They
CC react specifically with an antibody against glycolipid sugar chains
CC and inhibit adhesion and metastasis of cancer cells to a target cell.
CC The peptides can be used to prevent cancer metastasis.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 91; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WHMRHRIPQLAAGR 15
DB 1 WHMRHRIPQLAAGR 15
RESULT 3
AAW94702
ID AAW94702 standard; peptide; 15 AA.
XX
AC AAW94702;
XX
DT 22-APR-1999 (first entry)
XX
DE Lipoteichoic acid epitope peptide mimic for Mab 96-110.
XX
KM Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
KM immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM Mab 96-110.
XX
OS Staphylococcus sp.
XX
PN WO9857994-A2.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX
DR WPI; 1999-095329/08.
XX
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Claim 16; Page 120; 150pp; English.
XX
CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic acid
CC of gram positive bacteria, where the Mab is a chimeric immunoglobulin
CC comprising at least part of a human immunoglobulin constant region and
CC at least part of a non-human immunoglobulin variable region having
CC specificity to lipoteichoic acid of gram positive bacteria. The
CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
CC the bacteria and enhance protection from lethal infection. The antibodies
CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
CC acid antibody or characterised by amino acids corresponding to one or
CC more of the complementarity determining regions (CDRs) of the variable
CC region of the antibody) can be used for treating or preventing infections
CC caused by gram positive bacteria. They can also be used for the diagnosis
CC of gram positive bacterial infections. The present sequence represents a
CC specifically claimed lipoteichoic acid epitope peptide mimic that can be
CC bound by the antibody of the invention (Mab 96-110).
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 91; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WHMRHRIPQLAAGR 15
DB 1 WHMRHRIPQLAAGR 15

DB 1 MHWRHRIPLQLAAGR 15

RESULT 6
AAW94729

ID AAW94729 standard; Protein; 19 AA.

AC AAW94729;

DT 22-APR-1999 (first entry)

DE Sequence 15mer 2nd.1 resulting from library panning experiments.

KM Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;

KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

OS Staphylococcus sp.

PN WO9857994-A2.

PD 23-DEC-1998.

PF 16-JUN-1998; 98WO-US12402.

PR 16-JUN-1997; 97US-0049871.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Fischer GW, Schuman RF, Stinson JL, Wong H;

DR N-PSDB; AAX05555.

PS MPI: 1999-095329/08.

PT New antibodies to lipoteichoic acid of gram positive bacteria - used

PT to develop products for the diagnosis, prevention and treatment of

PT infections caused by gram positive bacteria

PT Example 5; Fig 8; 150pp; English.

CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic

CC acid of gram positive bacteria, where the Mab is a chimeric

CC immunoglobulin comprising at least part of a human immunoglobulin

CC constant region and at least part of a non-human immunoglobulin variable

CC region having specificity to lipoteichoic acid of gram positive bacteria.

CC The antibodies bind to whole bacteria and enhance phagocytosis and

CC killing of the bacteria and enhance protection from lethal infection. The

CC antibodies or peptides (encoded by a DNA of the variable region of

CC anti-lipoteichoic acid antibody or characterised by amino acids

CC corresponding to one or more of the complementarity determining regions

CC (CDRs) of the variable region of the antibody) can be used for treating

CC or preventing infections caused by gram positive bacteria. They can also

CC be used for the diagnosis of gram positive bacterial infections.

CC Sequences AAW94726-34 represent common peptide sequences resulting from

CC all library panning experiments. Three series of panning experiments were

CC conducted to identify peptide sequences to which antibody of the

CC invention (Mab 96-110) bound strongly. The translated sequences provide

CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

SQ Sequence 19 AA;

Query Match 100.0%; Score 91; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHWRHRIPLQLAAGR 15

DB 3 MHWRHRIPLQLAAGR 17

RESULT 7
AAW94710

ID AAW94710 standard; Protein; 19 AA.

AC AAW94710;

DT 22-APR-1999 (first entry)

DE Sequence 15mer 2-8/0 resulting from 15mer library panning experiment.

KM Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;

KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

OS Staphylococcus sp.

PN WO9857994-A2.

PD 23-DEC-1998.

PF 16-JUN-1998; 98WO-US12402.

PR 16-JUN-1997; 97US-0049871.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Fischer GW, Schuman RF, Stinson JL, Wong H;

DR N-PSDB; AAX05336.

PS MPI: 1999-095329/08.

PT New antibodies to lipoteichoic acid of gram positive bacteria - used

PT to develop products for the diagnosis, prevention and treatment of

PT infections caused by gram positive bacteria

PT Example 5; Fig 6A-B; 150pp; English.

CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic

CC acid of gram positive bacteria, where the Mab is a chimeric

CC immunoglobulin comprising at least part of a human immunoglobulin

CC constant region and at least part of a non-human immunoglobulin variable

CC region having specificity to lipoteichoic acid of gram positive bacteria.

CC The antibodies bind to whole bacteria and enhance phagocytosis and

CC killing of the bacteria and enhance protection from lethal infection. The

CC antibodies or peptides (encoded by a DNA of the variable region of

CC anti-lipoteichoic acid antibody or characterised by amino acids

CC corresponding to one or more of the complementarity determining regions

CC (CDRs) of the variable region of the antibody) can be used for treating

CC or preventing infections caused by gram positive bacteria. They can also

CC be used for the diagnosis of gram positive bacterial infections.

CC Sequences AAW94703-22 represent common peptide sequences resulting from a 15mer library

CC panning second experiment. Three series of panning experiments were

CC conducted to identify peptide sequences to which antibody of the

CC invention (Mab 96-110) bound strongly. The translated sequences provide

CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

SQ Sequence 19 AA;

Query Match 100.0%; Score 91; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHWRHRIPLQLAAGR 15

DB 3 MHWRHRIPLQLAAGR 17

RESULT 8
AAW94721

ID AAW94721 standard; Protein; 19 AA.

AC AAW94721;

DT 22-APR-1999 (first entry)

DE Sequence 15mer2-19/0 resulting from 15mer library panning experiment.
 XX
 XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW Mab 96-110; panning.
 XX
 XX Staphylococcus sp.
 OS
 PN MO9857994-A2.
 XX
 PD 23-DEC-1998.
 XX
 PF 16-JUN-1998; 98WO-US12402.
 XX
 PR 16-JUN-1997; 97US-0049871.
 XX
 XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 PA Fischer GW, Schuman RF, Stinson JL, Mong H;
 PI
 XX WPI; 1999-095329/08.
 DR N-PSDB; AAX05347.
 XX
 XX
 PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX
 XX Example 5; Fig 6A-B; 150pp; English.
 XX
 XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 XX
 SO Sequence 19 AA;
 Query Match 100.0%; Score 91; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPQLAAGR 15
 DB 3 WHMRHRIPQLAAGR 17

RESULT 9
 AAW94705
 ID AAW94705 standard; Protein; 19 AA.
 XX
 AC AAW94705;
 XX
 DT 22-APR-1999 (first entry)
 XX
 XX Sequence 15mer2-1/0 resulting from 15mer library panning experiment.
 DE Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW Mab 96-110; panning.
 XX

OS Staphylococcus sp.
 XX
 XX MO9857994-A2.
 XX
 PD 23-DEC-1998.
 XX
 PF 16-JUN-1998; 98WO-US12402.
 XX
 PR 16-JUN-1997; 97US-0049871.
 XX
 XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 PA Fischer GW, Schuman RF, Stinson JL, Mong H;
 PI
 XX WPI; 1999-095329/08.
 DR N-PSDB; AAX05351.
 XX
 XX
 PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX
 XX Example 5; Fig 6A-B; 150pp; English.
 XX
 XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 XX
 SO Sequence 19 AA;
 Query Match 100.0%; Score 91; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPQLAAGR 15
 DB 3 WHMRHRIPQLAAGR 17

RESULT 10
 AAW94709
 ID AAW94709 standard; Protein; 19 AA.
 XX
 AC AAW94709;
 XX
 DT 22-APR-1999 (first entry)
 XX
 XX Sequence 15mer2-7/0 resulting from 15mer library panning experiment.
 DE Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW Mab 96-110; panning.
 XX
 XX Staphylococcus sp.
 OS
 XX MO9857994-A2.
 PN
 XX 23-DEC-1998.
 PD

PF 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX
DR WPI: 1999-095329/08.
XX
DR N-PSDB: AAX05535.
XX
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Example 5; Fig 6A-B; 150pp; English.
XX
CC The invention relates to a monoclonal antibody (MAb) to lipoteichoic
CC acid of gram positive bacteria, where the MAb is a chimeric
CC immunoglobulin comprising at least part of a human immunoglobulin
CC constant region and at least part of a non-human immunoglobulin variable
CC region having specificity to lipoteichoic acid of gram positive bacteria.
CC The antibodies bind to whole bacteria and enhance phagocytosis and
CC killing of the bacteria and enhance protection from lethal infection. The
CC anti-lipoteichoic acid antibodies (encoded by a DNA of the variable region of
CC corresponding to one or more of the complementarity determining regions
CC (CDRs) of the variable region of the antibody) can be used for treating
CC or preventing infections caused by gram positive bacteria. They can also
CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
CC panning second experiment. Three series of panning experiments were
CC conducted to identify peptide sequences to which antibody of the
CC invention (Mab 96-110) bound strongly. The translated sequences provide
CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
XX
SQ Sequence 19 AA:

Query Match 100.0%; Score 91; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHRRHRIPQLAAGR 15
DB 3 WHRRHRIPQLAAGR 17

RESULT 11
AAW12287
ID AAW12287 standard; peptide; 37 AA.
XX
AC AAW12287;
XX
DT 15-APR-1997 (first entry)
XX
DE Synthetic template peptide for overlapping peptide series.
XX
KW Toxoplasma gondii; surface protein; antibody; screening; peptide library;
KW diagnostic assay; immunisation; phage; fusion protein; envelop.
XX
OS Synthetic.
XX
PN EP724016-A1.
XX
PD 31-JUL-1996.
XX
PE 29-JAN-1996; 96EP-0420030.
XX
PR 30-JAN-1995; 95FR-0001297.
XX
PA (JOLI/) JOLIVET-REYNAUD C.
PA (INMR) BIO MERIEUX.
XX

PI Jolivet-Reynaud C;
XX
XX WPI: 1996-343531/35.
DR
XX
XX
PT New polypeptide reactive with anti-P30 antibodies against Toxoplasma
PT gondii, useful for diagnosis or immunisation, also new nucleic
PT acid, vectors and transformed cells
XX
XX
PS Example 5; Page 9; 33pp; French.
XX
CC The invention relates to novel peptides which bind to antibodies which
CC recognise the Toxoplasma gondii P30 envelop protein. A peptide library
CC was generated to express pentadecapeptides on the surface of a
CC filamentous phage as a fusion protein with the P11 protein. The library
CC was screened with immobilised anti-T. gondii P30 protein antibody 1E1E7.
CC Phages which bind this antibody were recovered and amplified by one
CC round of infection in E. coli. The resultant phages were rescreened with
CC the immobilised antibody and the second round screen isolated 58
CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA
CC from 30 colonies was isolated and sequenced to determine the sequence of
CC the pentadecapeptide encoded. The peptide sequences AAW12276-86 were
CC identified. Of the 30 colonies studied, this peptide sequence was
CC encoded once. A template peptide sequence (AAW12287) corresponding to
CC the sequence across the phage P11 sequence and putative
CC pentadecapeptides was used to generate a series of overlapping
CC pentadecapeptides. These peptides were used to determine the best
CC peptide sequence which binds the 1E1E7 antibody. Peptides AAW03367-75
CC were isolated. The new peptides can then be used in diagnostic assays to
CC detect T. gondii antibodies in a sample or to purify anti-P30 antibodies
CC or for active immunisation against T. gondii.
XX
SQ Sequence 37 AA:

Query Match 100.0%; Score 91; DB 17; Length 37;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHRRHRIPQLAAGR 15
DB 10 WHRRHRIPQLAAGR 24

RESULT 12
AAW94708
ID AAW94708 standard; protein; 19 AA.
XX
AC AAW94708;
XX
DT 22-APR-1999 (first entry)
XX
DE Sequence 15mer2-5/0 resulting from 15mer library panning experiment.
XX
KW Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110; panning.
XX
OS Staphylococcus sp.
XX
PN W09857994-A2.
XX
PD 23-DEC-1998.
XX
PE 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX
XX WPI: 1999-095329/08.
DR N-PSDB: AAX05534.
XX

PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX
 XX Example 5; Fig 6A-B; 150pp; English.
 PS
 CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 CC
 XX Sequence 19 AA:
 SO
 OY Query Match 87.9%; Score 80; DB 20; Length 19;
 Db Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 HMRHRIPQLAAGR 15
 4 HMRHRIPQLAAGR 17
 DB
 RESULT 13
 AAW12277
 ID AAW12277 standard; peptide: 15 AA.
 XX
 AC AAW12277;
 XX
 DT 15-APR-1997 (first entry)
 XX
 DE Synthetic library peptide #2 which binds anti-T. gondii P30 antibody.
 XX
 KW Toxoplasma gondii; surface protein; antibody; screening; peptide library;
 KW diagnostic assay; immunisation; phage; fusion protein; envelop.
 XX
 OS Synthetic.
 XX
 PN EP724016-A1.
 XX
 PD 31-JUL-1996.
 XX
 PF 29-JAN-1996; 96EP-0420030.
 XX
 PR 30-JAN-1995; 95FR-0001297.
 XX
 PA (JOLI/) JOLIVET-REYNAUD C.
 PA (INMR) BIO MERIEUX.
 XX
 PI Jolivet-Reynaud C;
 XX
 DR WPI; 1996-343531/35.
 XX
 PT New polypeptide reactive with anti-P30 antibodies against Toxoplasma
 PT gondii - useful for diagnosis or immunisation, also new nucleic
 PT acid, vectors and transformed cells
 XX
 PS Example 2; Page 7; 33pp; French.
 CC The invention relates to novel peptides which bind to antibodies which

CC recognise the Toxoplasma gondii P30 envelop protein. A peptide library
 CC was generated to express pentadecapeptides on the surface of a
 CC filamentous phage as a fusion protein with the PIII protein. The library
 CC was screened with immobilised anti-T. gondii P30 protein antibody 1E1E7.
 CC Phages which bind this antibody were recovered and amplified by one
 CC round of infection in E. coli. The resultant phages were rescreened with
 CC the immobilised antibody and the second round screen isolated 58
 CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA
 CC from 30 colonies was isolated and sequenced to determine the sequence of
 CC the pentadecapeptide encoded. The peptide sequences AAW12276-86 were
 CC identified. Of the 30 colonies studied, this peptide sequence was
 CC encoded once. A template peptide sequence (AAW12287) corresponding to
 CC the sequence across the phage PIII sequence and putative
 CC pentadecapeptide was used to generate a series of overlapping
 CC pentadecapeptides. These peptides were used to determine the best
 CC peptide sequence which binds the 1E1E7 antibody. Peptides AAW03367-75
 CC were isolated. The new peptides can then be used in diagnostic assays to
 CC detect T. gondii antibodies in a sample or to purify anti-P30 antibodies
 CC or for active immunisation against T. gondii.
 XX
 XX Sequence 15 AA:
 SO
 OY Query Match 75.8%; Score 69; DB 17; Length 15;
 Db Best Local Similarity 85.7%; Pred. No. 7.2e-05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 2 HMRHRIPQLAAGR 15
 2 HMRHRIPQLAAGR 15
 DB
 RESULT 14
 AAW03372
 ID AAW03372 standard; peptide: 11 AA.
 XX
 AC AAW03372;
 XX
 DT 15-APR-1997 (first entry)
 XX
 DE Peptide #6 which binds anti-Toxoplasma gondii P30 antibody.
 XX
 KW Toxoplasma gondii; surface protein; antibody; screening; peptide library;
 KW diagnostic assay; immunisation; phage; E.coli.
 XX
 OS Synthetic.
 XX
 PN EP724016-A1.
 XX
 PD 31-JUL-1996.
 XX
 PF 29-JAN-1996; 96EP-0420030.
 XX
 PR 30-JAN-1995; 95FR-0001297.
 XX
 PA (JOLI/) JOLIVET-REYNAUD C.
 PA (INMR) BIO MERIEUX.
 XX
 PI Jolivet-Reynaud C;
 XX
 DR WPI; 1996-343531/35.
 XX
 PT New polypeptide reactive with anti-P30 antibodies against Toxoplasma
 PT gondii - useful for diagnosis or immunisation, also new nucleic
 PT acid, vectors and transformed cells
 XX
 PS Claim 7; Page 19; 33pp; French.
 XX
 CC Peptides AAW03367-75 are peptides isolated from a peptide library, which
 CC bind to antibody 1E1E7 which recognises the P30 surface protein from
 CC Toxoplasma gondii. The peptide library was constructed by inserting a
 CC nucleic acid sequence encoding a random pentadecapeptide in the PIII
 CC envelop protein of a filamentous phage. Antibody 1E1E7 was immobilised

CC on the bottom of a Petri dish and the expressed peptide library was
 CC overlaid on the antibody. After washing, phages bound on the antibodies
 CC were recovered and the phage amplified by passage through E. coli. The
 CC phages were rescreened by the same method and 58 bacterial colonies were
 CC recovered. Of these, 30 were further studied and the nucleic acid
 CC encoding the pentadecapeptide was isolated. The nucleic acids encoded
 CC the peptides AAW12276-86. A series of overlapping peptides based on the
 CC peptide template AAW12287 was constructed to identify which peptide
 CC sequences bound to the anti-P30 antibody. The peptide scanning isolated
 CC peptides AAW03367-75. The peptides can then be used in diagnostic
 CC assays to detect T. gondii antibodies in a sample or to purify anti-P30
 CC antibodies or for active immunisation against T. gondii.

XX Sequence 11 AA:

Query Match 61.5%; Score 56; DB 17; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 HRIPQLAAGR 15
 |||||
 DB 1 HRIPQLAAGR 11

RESULT 15

AAW03374

ID AAW03374 standard; peptide; 15 AA.

XX AAW03374;

DT 15-APR-1997 (first entry)

DE Peptide #8 which binds anti-Toxoplasma gondii P30 antibody.

KM Toxoplasma gondii: surface protein; antibody: screening; peptide library;
 KM diagnostic assay; immunisation; phage; E.coli.

XX Synthetic.

PN EP724016-A1.

PD 31-JUL-1996.

PF 29-JAN-1996; 96EP-0420030.

PR 30-JAN-1995; 95FR-0001297.

PA (JOLI/) JOLIVET-REYNAUD C.

PA (INMR) BIO MERIEUX.

XX Jolivet-Reynaud C;

PI WPI: 1996-343531/35.

DR N-PSDB; AAT131330.

XX New polypeptide reactive with anti-P30 antibodies against Toxoplasma
 PT gondii - useful for diagnosis or immunisation, also new nucleic
 PT acid, vectors and transformed cells

XX Claim 7; Page 20; 33pp: French.

XX Peptides AAW03367-75 are peptides isolated from a peptide library, which
 CC bind to antibody 1E17 which recognises the P30 surface protein from
 CC Toxoplasma gondii. The peptide library was constructed by inserting a
 CC nucleic acid sequence encoding a random pentadecapeptide in the pIII
 CC envelope protein of a filamentous phage. Antibody 1E17 was immobilised
 CC on the bottom of a Petri dish and the expressed peptide library was
 CC overlaid on the antibody. After washing, phages bound on the antibodies
 CC were recovered and the phage amplified by passage through E. coli. The
 CC phages were rescreened by the same method and 58 bacterial colonies were
 CC recovered. Of these, 30 were further studied and the nucleic acid
 CC encoding the pentadecapeptide was isolated. The nucleic acids encoded
 CC the peptides AAW12276-86. A series of overlapping peptides based on the

CC peptide template AAW12287 was constructed to identify which peptide
 CC sequences bound to the anti-P30 antibody. The peptide scanning isolated
 CC peptides AAW03367-75. The peptides can then be used in diagnostic
 CC assays to detect T. gondii antibodies in a sample or to purify anti-P30
 CC antibodies or for active immunisation against T. gondii.

XX Sequence 15 AA:

Query Match 61.5%; Score 56; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 HRIPQLAAGR 15
 |||||
 DB 1 HRIPQLAAGR 11

Search completed: November 27, 2002, 07:17:50
 Job time : 11.2819 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:15:05 ; Search time 4.1197 Seconds
(without alignments)
350.688 Million cell updates/sec

Title: US-09-893-615-2

Perfect score: 91

Sequence: 1 WHMRHRIQLAAGR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	51.6	649	2 C75112	hypothetical prote
2	46.5	51.1	354	2 T36559	probable epoxide h
3	46.5	51.1	391	2 T13182	integrase - Lactob
4	46	50.5	96	4 ODEC31	hypothetical prote
5	45	49.5	516	2 H87369	tryptophan halogen
6	44.5	48.9	270	2 C83167	probable transcrip
7	44.5	48.9	343	2 A35639	G protein-coupled
8	44.5	48.9	356	2 F70636	probable epib prot
9	44	48.4	636	2 D82679	hypothetical prote
10	44	48.4	1839	1 RRMPEM	genome polypeptide
11	43	47.3	152	2 G81175	dAMP pyrophosphohy
12	43	47.3	152	2 H81930	probable nucleosid
13	43	47.3	222	2 T35942	probable ABC-type
14	43	47.3	330	2 G87401	epoxide hydrolase
15	43	47.3	434	2 E82162	paraquat-inducible
16	43	47.3	615	2 T37981	probable exocyst c
17	43	47.3	716	2 AC2449	ABC transporter AT
18	43	47.3	1298	2 A48999	protein-lysine k
19	42	46.2	207	2 A75475	probable acetyltra
20	42	46.2	289	2 T08176	glucose-1-phosphat
21	42	46.2	410	2 T50718	hypothetical prote
22	42	46.2	436	2 B70510	probable acyltrans
23	42	46.2	437	1 E64553	conserved hypothet
24	42	46.2	641	2 C84726	probable receptor-
25	42	46.2	782	2 S62583	probable transcrip
26	42	46.2	1101	2 AB2481	hypothetical prote
27	42	46.2	1189	2 I39711	cell protein - Agr
28	41.5	45.6	642	2 D75516	acetyl-CoA synthas
29	41	45.1	158	2 S39754	pathogenesis-relat

30	41	45.1	232	2 S58353	CD1b protein - she
31	41	45.1	249	2 E87597	transcription regu
32	41	45.1	291	2 C71362	hypothetical prote
33	41	45.1	322	2 B70957	probable epib prot
34	41	45.1	333	2 S47246	gene Cbl protein -
35	41	45.1	354	2 SC4212	nitrilase (EC 3.5.
36	41	45.1	389	1 S36653	kpsd protein - Sac
37	41	45.1	435	2 F83888	GTP-binding protei
38	41	45.1	502	2 E87596	tryptophan halogen
39	41	45.1	503	2 H87438	tryptophan halogen
40	41	45.1	509	2 G87596	tryptophan halogen
41	41	45.1	580	2 T36393	L-aspartate oxidase
42	41	45.1	650	2 D71021	hypothetical prote
43	41	45.1	716	2 AH2319	glycyl-tRNA synthet
44	41	45.1	1227	2 AG2504	hypothetical prote
45	40.5	44.5	321	2 C84664	epoxide hydrolase

ALIGNMENTS

RESULT 1

C75112 hypothetical protein PAB1903 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: C75112

R:Anonymous, Genoscope

A:Description: The EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s

A:Reference number: A75001

A:Accession: C75112

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-649 <KAW>

A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49612.1; PID:g545

C:Genetics: Experimental source: strain Orsay

C:Gene: PAB1903

C:Superfamily: hypothetical protein YPI09c

Query Match 51.6% Score 47; DB 2; Length 649;

Best Local Similarity 61.5% Pred. No. 11;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 WHMRHRIQLAAG 14

Db 563 NMHGRIPKLAVG 575

RESULT 2

T36559 Probable epoxide hydrolase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T36559

R:Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A

A:Submitted to the EMBL Data Library, June 1999

A:Reference number: Z21584

A:Accession: T36559

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-354 <SEP>

A:Cross-references: EMBL:AL079353; PIDN:CAB45554.1; GSPDB:GN00070; SCOEDB:SC17.08c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC17.08c

C:Superfamily: troplnesterase

Query Match 51.1% Score 46.5; DB 2; Length 354;

Best Local Similarity 53.3% Pred. No. 7.3;

Matches 8; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 1 WH-WRRIPLOLAG 14
 1: ||||:|
 Db 62 WYSMRHQLPALAAG 76

RESULT 3

Integrase - Lactobacillus phage phi-gle
 C:Species: Lactobacillus phage phi-gle
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
 C:Accession: T13182
 R:Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Takeo, Gene 187, 45-53, 1997
 A:Title: Genome structure of the Lactobacillus temperate phage phi gle: the whole genome
 A:Reference number: 217631; MUID:97225795; PMID:9073065
 A:Accession: T13182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-391 <KOD>
 A:Cross-references: EMBL:X98106; NID:91926320; PIDN:CAA6758.1; PID:91926326
 C:Genetics:
 A:Gene: Int
 C:Superfamily: phage L54a excisionase

Query Match 51.1%; Score 46.5; DB 2; Length 391;
 Best Local Similarity 38.1%; Pred. No. 8.1;
 Matches 8; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

OY 1 WHWR-----HRIPLQLAG 14
 |||||
 Db 12 WHWRINTDGRVINSAG 32

RESULT 4

hypothetical protein C-96 rsfa 3'-region - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 29-Sep-1999 #sequence_revision 29-Sep-1999 #text_change 29-Sep-1999
 C:Accession: A04448
 R:Schneider, J.; Isono, K.
 Nucleic Acids Res. 10, 1857-1865, 1982
 A:Title: The DNA sequence of the gene rsfa of Escherichia coli coding for ribosomal prot
 A:Reference number: A04448; MUID:62196865; PMID:6281725
 A:Accession: A04448
 A:Molecule type: DNA
 A:Residues: 1-96 <SCH>
 A:Cross-references: GB:V00352; GB:J01681; GB:J01682; NID:942899
 C:Comment: This is the hypothetical translation of a sequence that was not reported as a
 C:Genetics:
 A:Map position: 20 min

Query Match 50.5%; Score 46; DB 4; Length 96;
 Best Local Similarity 66.7%; Pred. No. 2.4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WHWRHRIPL 9
 |||||
 Db 1 WHWRHYITM 9

RESULT 5

tryptophan halogenase, probable [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: H87369
 R:Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: H87369

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE005673; NID:913422252; PIDN:AAK22956.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0972
 C:Superfamily: Rhizobium plasmid PNGR234a y4xg protein

Query Match 49.5%; Score 45; DB 2; Length 516;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 WRHRIPLQLAG 14
 |||||
 Db 272 WRHRIPLQHRAG 283

RESULT 6

probable transcription regulator PA3830 [imported] - Pseudomonas aeruginosa (strain P
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: C83167
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337; PMID:10584043
 A:Accession: C83167
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-270 <STO>
 A:Cross-references: GB:AE004800; GB:AE004091; NID:9949999; PIDN:AMG07217.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3830

Query Match 48.9%; Score 44.5; DB 2; Length 270;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

OY 2 WHRRHRIPL-----QLAAG 14
 |||||
 Db 213 WHRHQVRLAALPRLAAG 230

RESULT 7

G protein-coupled receptor RTA - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
 C:Accession: A35639
 R:Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Marcus, D.R.; Lynch
 Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
 A:Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue
 A:Reference number: A35639; MUID:90222168; PMID:2105324
 A:Accession: A35639
 A:Molecule type: mRNA
 A:Residues: 1-343 <ROS>
 A:Cross-references: GB:M35297; NID:9206809; PIDN:AAA2087.1; PID:9206810; GB:M32098
 C:Superfamily: mas transforming protein
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein
 F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.9%; Score 44.5; DB 2; Length 343;
 Best Local Similarity 57.1%; Pred. No. 15;
 Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 1 WHRRHRIPLQLAG 14
 |||||
 Db 150 WYWRRR-PKRUSAG 162

RESULT 8

F70636

probable ephB protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: F70636

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

R:Conor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

R:Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.

R:Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295087; PMID:9634230

A:Accession: F70636

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-356 <COL>

A:Cross-references: GB:284498; GB:AL123456; NID:93261701; PIDN:CAB06523.1; PID:g1806224

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: ephB

C:Superfamily: triphosphatase

Query Match	48.9%	Score 44.5;	DB 2;	Length 356;
Best Local Similarity	53.3%	Pred. No. 15;		
Matches	8;	Conservative	2;	Mismatches 4;
				Indels 1;
				Gaps 1;

Oy	1	WH-WRHRIPLQIAG 14
	1:	
	40	WYSMRHRIPLAGAG 54

RESULT 9

DB2679

hypothetical protein XF1451 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: DB2679

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

R:Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB2515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number AS9328 below

A:Accession: DB2679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-636 <SIM>

A:Cross-references: GB:AE003975; GB:AE003849; NID:99106468; PIDN:AAF84260.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

R:Bitones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H

R:as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A

Rodrigues, V.; Rosa, A.J.; de M. de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: AS9328

A:Contents: annotation

C:Genetics:

A:Gene: XF1451

Db	207	WRRHSVPLQ 216
----	-----	---------------

RESULT 10

RRWPEM

genome polypeptide - eggplant mosaic virus

N:Alternative names: RNA nucleotidyltransferase (RNA-directed); RNA replicase

N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C:Species: eggplant mosaic virus

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 19-Jan-2001

C:Accession: J00102

R:Osorio-Keese, M.E.; Keese, P.; Glibbs, A.

R:Virology 172, 547-554, 1989

A:Title: Nucleotide sequence of the genome of eggplant mosaic tymovirus.

A:Reference number: J00102; MUID:90021185; PMID:2800336

A:Accession: J00102

A:Molecule type: genomic RNA

A:Residues: 1-1839 <OSO>

A:Cross-references: EMBL:J04374

C:Superfamily: eggplant mosaic virus RNA-directed RNA polymerase

C:Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis

F:965-972/Region: nucleotide-binding motif A (P-loop)

F:1027-1032/Region: nucleotide-binding motif B

F:971/Binding site: ATP (lys) #status predicted

Query Match	48.4%	Score 44;	DB 1;	Length 1839;
Best Local Similarity	63.6%	Pred. No. 93;		
Matches	7;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;

Oy	3	WRRHRIPLQIA 13
	1	
	1094	WRRHRIPLQIAS 1104

RESULT 11

GB1175

dATP pyrophosphohydrolase NMB0642 [imported] - Neisseria meningitidis (strain MC58 se

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: GB1175

R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

R:Hikey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

R:Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappaport, R.

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: AB1000; MUID:20175755; PMID:10710307

A:Accession: GB1175

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-152 <TEMT>

A:Cross-references: GB:AE002419; GB:AE002098; NID:97225863; PIDN:AAF41065.1; PID:9722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0642

Query Match	47.3%	Score 43;	DB 2;	Length 152;
Best Local Similarity	85.7%	Pred. No. 11;		
Matches	6;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;

Oy	2	HWRHRIPLQ 8
	1	
	84	HWRHRIPLQ 90

RESULT 12

HB1930

probable nucleoside triphosphate pyrophosphohydrolase NMA0852 [imported] - Neisseria

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: HB1930

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

R:Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H81930
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB8413.1; PID:g737956
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: nlpA; NMA0852

Query Match 47.3%; Score 43; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 HMRHRIP 8
|||||
DB 84 HMRHRYP 90

RESULT 13
T35942
probable ABC-type transport system ATP-binding protein - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T35942
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21551
A:Accession: T35942
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-222 <SEE>
A:Cross-references: EMBL:AL035206; PIDN:CAA22764.1; GSPDB:GN00070; SCOPDB:SC9B5.22
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOPDB:SC9B5.22
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 47.3%; Score 43; DB 2; Length 222;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 HMRHRIP 8
|||||
DB 68 HMRHRAP 74

RESULT 14
G87401
epoxide hydrolase [Imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: G87401
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87401
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <STO>
A:Cross-references: GB:AE005673; NID:g13422557; PIDN:AAK23211.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCI229
C:Superfamily: trophoblastase

Query Match 47.3%; Score 43; DB 2; Length 330;
Best Local Similarity 61.5%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 WMRHRIPQIAAGR 15
|||||
DB 50 WMRHIALAAGR 62

RESULT 15
E82162
paragut-inducible protein A VC1753 [Imported] - *Vibrio cholerae* (strain N16961 serog
C:Species: *Vibrio cholerae*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82162
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Olin, H.; Dragol, I.; Sellers
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-434 <HEI>
A:Cross-references: GB:AE004252; GB:AE003852; NID:g9656263; PIDN:AAF94903.1; GSPDB:GN
C:Genetics:
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
A:Gene: VC1753
A:Map position: 1
C:Superfamily: hypothetical protein H11671

Query Match 47.3%; Score 43; DB 2; Length 434;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 WMRHRIPLOLAG 14
|||||
DB 204 WMRHFLPAOTPOG 217

Search completed: November 27, 2002, 07:24:13
Job time : 10.112 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 05:39:34 : Search time 2.14286 Seconds

(without alignments)
290.334 Million cell updates/sec

Title: US-09-893-615-2

Perfect score: 91

Sequence: 1 MHMRHRIPLQLAGR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	48.9	343	1 RTA_RAT	P23749 rattus norv
2	44.4	48.4	1839	1 POLR_EPMV	P20126 eggplant mo
3	43.3	47.3	615	1 EX70_SCHPO	Q10339 schizosacch
4	43.3	47.3	1298	1 VGR3_HUMAN	P35916 homo sapien
5	42.2	46.2	437	1 Y269_HELIX	P56131 hellobacte
6	42.2	46.2	782	1 YAKB_SCHPO	Q09942 schizosacch
7	41.1	45.1	158	1 PRL_ASPDF	Q05736 asparagus o
8	41.1	45.1	232	1 C1B3_SHEEP	P80943 ovis aries
9	41.1	45.1	291	1 Y126_TREPA	O83163 treponema p
10	41.1	45.1	333	1 C1B2_SHEEP	Q29432 ovis aries
11	41.1	45.1	389	1 KSS5_ECOLI	P42218 escherichia
12	41.1	45.1	734	1 PSAB_GUTTH	O78507 guillardi
13	40.5	44.5	4485	1 DYHG_CHIRE	Q39575 chlamydomon
14	40.4	44.0	135	1 LEG7_HUMAN	P47929 homo sapien
15	40.4	44.0	315	1 T2S1_STRAL	O53608 streptomyce
16	40.4	44.0	344	1 VPO_BP2	P25480 bacterioph
17	40.4	44.0	506	1 POPB_SCHPO	Q09855 schizosacch
18	40.4	44.0	526	1 ANPD_RHOCA	Q07983 rhodobacter
19	40.4	44.0	661	1 PSAB_PROHO	P58387 prochloroth
20	40.4	44.0	730	1 PSAB_SYNY2	P29125 synechocyst
21	40.4	44.0	732	1 PSAB_SYNY3	P17155 synechococc
22	40.4	44.0	733	1 PSAB_ODOSI	P49480 odontella s
23	40.4	44.0	734	1 PSAB_ANTMA	Q33332 antirrhinum
24	40.4	44.0	734	1 PSAB_ARATH	P56767 arabidopsis
25	40.4	44.0	734	1 PSAB_CYACA	Q9146 cyanidium c
26	40.4	44.0	734	1 PSAB_EUGRA	O19431 euglena gra
27	40.4	44.0	734	1 PSAB_LOTJA	P58385 lotus japon
28	40.4	44.0	734	1 PSAB_MARPO	P66408 marcanthia
29	40.4	44.0	734	1 PSAB_MESVI	Q9mur7 mesostigma
30	40.4	44.0	734	1 PSAB_NEPOL	Q9tkw1 nephroselm
31	40.4	44.0	734	1 PSAB_OENHO	Q9tmr7 oenothera h
32	40.4	44.0	734	1 PSAB_ORYSA	P12156 oryza sativ
33	40.4	44.0	734	1 PSAB_PEA	P05311 pisum sativ

ALIGNMENTS

RESULT 1	RTA_RAT	STANDARD:	PRT:	343 AA.
AC	P23749:			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	01-JUL-1993 (Rel. 26, Last annotation update)			
DE	Probable G protein-coupled receptor RTA.			
GN	RTA.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Sprague-Dawley; TISSUE-Aorta;			
RX	MEDLINE=9022216; PubMed=2109324;			
RA	Ross P.C., Figler R.A., Corjay M.H., Barber C.M., Adam N.,			
RA	Harcus D.R., Lynch K.R.;			
RT	"RTA, a candidate G protein-coupled receptor: cloning, sequencing,			
RT	and tissue distribution."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056(1990).			
CC	-1- FUNCTION: ORPHAN RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: GUT, VAS DEFERENS, UTERUS, AND AORTA BUT ONLY			
CC	BARELY DETECTABLE IN LIVER, KIDNEY, LUNG, AND SALIVARY GLAND. IN			
CC	THE BRAIN, RTA IS MARKEDLY ABUNDANT IN THE CEREBELLUM.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	MOST SIMILAR TO MAS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: M35297; AAA42087.1; -			
DR	EMBL: M35298; AAA42088.1; -			
DR	PIR: A35639; A35639.			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PF00001; 7tm_1; 1.			
DR	PROSITE: PS00237; G-PROTEIN RECP_F1.1; 1.			
DR	PROSITE: PS50262; G-PROTEIN RECP_F1.2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 44			
FT	DOMAIN 45 66			
FT	DOMAIN 67 82			
FT	DOMAIN 83 104			
FT	DOMAIN 105 123			
FT	DOMAIN 124 144			
FT	DOMAIN 145 160			
FT	DOMAIN 161 181			
FT	DOMAIN 182 198			
FT	TRANSMEM 199 220			
FT	TRANSMEM 199 220			

P41640 pinus thunb
P51285 porphyra pu
P58765 psittacus nu
P06512 psittacus ol
P06407 nicotiana t
P58366 triticum ae
P09144 chlamydomon
P04967 zea mays (m
P48113 cyanophora
Q9r6t9 synechococc
P58565 anabaena sp
P31088 anabaena va

```

GT  DOMAIN 221 241 CYTOPLASMIC (POTENTIAL).
FT  TRASMEM 242 263 6 (POTENTIAL).
FT  DOMAIN 264 273 EXTRACELLULAR (POTENTIAL).
FT  TRASMEM 274 294 7 (POTENTIAL).
FT  DOMAIN 295 343 CYTOPLASMIC (POTENTIAL).
FT  CAROHID 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 343 AA: 38364 MW: 8463000770941F4 CRC64;

Query Match 48.9%; Score 44.5; DB 1; Length 343;
Best Local Similarity 57.1%; Pred. No. 4.3;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 1 WHRRRIPQLAAG 14
    1:11111:1:11
DB 150 WYRRRR-PKRLSNG 162

RESULT 2
POLR_EPMV STANDARD: PRT; 1839 AA.
ID POLR_EPMV
AC P20126;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replicase polypeptide (EC 2.7.7.48).
OS Eggplant mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
OX NCBI_Taxid=12151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90021185; PubMed=2800336;
RA Osorio-Keese M.E., Keese P., Gibbs A.;
RT "Nucleotide sequence of the genome of eggplant mosaic tymovirus.";
RL Virology 172:547-554(1989).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
    [RNA] (N).
-----
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-----
CC EMBL: J04374; AAA3039.1; -
DR PIR: J00102; RRMPEM.
DR MEROPS: C21.001; -
DR InterPro: IPR001788; RNA_dep_RNApol2.
DR InterPro: IPR000606; VIRAL_helicase1.
DR Pfam: PF00978; RNA_dep_RNApol2; 1.
DR Pfam: PF01443; VIRAL_helicase1; 1.
KW Transferrase; RNA-directed RNA polymerase; Polypeptide; ATP-binding.
FT NP BIND 965 972 ATP (BY SIMILARITY).
SQ SEQUENCE 1839 AA: 204731 MW: FDBDC1F5115E7661 CRC64;

Query Match 48.4%; Score 44; DB 1; Length 1839;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 WHRRRIPQLAAG 13
    1:11111:1:1
DB 1094 WSHRRIPKOLAS 1104

RESULT 3
EX70_SCHPO STANDARD: PRT; 615 AA.
ID EX70_SCHPO
AC Q10339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 70 kDa exocyst complex protein.

```

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GN EXO70 OR SPBC582.02 OR SPBC106.20.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_Taxid=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean C.,
RA Mooney P., Mould S., Mungall K., Murphy L., Niblett D., Odell J.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolckaert G., Aert R., Robben J., Grymoperez B.,
RA Welfjens I., Vanscreels E., Rieger M., Schaefer M., Meller Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garçon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpukovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
-----
RN [2]
RP IDENTIFICATION.
RX MEDLINE=21843682; PubMed=11854409;
RA Wang H., Tang X., Liu J., Trautmann S., Balasundaram D., McCollum D.,
RA Balasubramanian M.K.;
RT "The multiprotein exocyst complex is essential for cell separation in
    Schizosaccharomyces pombe.";
RL Mol. Biol. Cell 13:515-529(2002).
CC -1- FUNCTION: Required for exocytosis (By similarity).
CC -1- SUBUNIT: Sec3, sec5, sec6, sec8, sec10, sec15 and exo70 are
    component of exocyst complex.
CC -1- SIMILARITY: BELONGS TO THE EXO70 FAMILY.
-----
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-----
CC EMBL: AL096788; CAB4665.1; -
CC DR EMBL: AL110295; CAB53736.1; -
DR InterPro: IPR004140; Exo70.
DR Pfam: PF03081; Exo70; 1.
KW Transport; protein transport.
SQ SEQUENCE 615 AA: 69041 MW: 20A137C4D815BA23 CRC64;

Query Match 47.3%; Score 43; DB 1; Length 615;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 WHRRRIPQLAAG 15
    1:11111:1:1
DB 407 WGRHREINDLSAR 421

```

RESULT 4
VGR3_HUMAN STANDARD: PRT: 1298 AA.
AC P35916;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
DE (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).
GN FLT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93241723; PubMed=8386825;
RA Galland F., Karaymshava A., Pebusque M.-J., Borg J.-P., Rotlapel R.,
RT Dubreuil P., Rosnet O., Birnbaum D.;
RT "The FLT4 gene encodes a transmembrane tyrosine kinase related to the
RT vascular endothelial growth factor receptor.";
RT Oncogene 8:1233-1240(1993).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=93007958; PubMed=1327515;
RX Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,
RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,
RT Alltalo R., Alltalo K.;
RT "FLT4 receptor tyrosine kinase contains seven immunoglobulin-like
RT loops and is expressed in multiple human tissues and cell lines.";
RL Cancer Res. 52:5738-5743(1992).
RN [3]
RP ERRATUM.
RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,
RA Alltalo R., Alltalo K.;
RL Cancer Res. 53:3845-3845(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA Lee J., Gray A., Yuan J., Luch S.M., Avraham H., Wood W.I.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 761-1190 FROM N.A.
RX MEDLINE=92119639; PubMed=1310071;
RA Aprelikova O., Pajusola K., Partanen J., Armstrong E., Alltalo R.,
RA Bailey S.K., McMahon J., Masumth J., Huebner K., Alltalo K.;
RT "FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-
RT qter.";
RT Cancer Res. 52:746-748(1992).
CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
CC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PLACENTA, LUNG, HEART, AND KIDNEY. DOES NOT
CC SEEM TO BE EXPRESSED IN PANCREAS AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: X69878; CAA49505.1; -;
DR EMBL: X68203; CAA48290.1; ALT_INIT.
DR EMBL: U63143; AAB85215.1; -;
DR PIR: S36130; S36130.
DR HSP: P1362; 1PGR.
DR Genew; HGNC:3767; FLT4.

DR MM: 136352; -;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR001824; RTK_inseil.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_5.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 2.
DR SMART: SM00410; Ig_Like; 2.
DR SMART: SM00408; Igc2; 2.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_LIT; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase: Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
KW Glycoprotein.
FT SIGNAL 1 23
FT CHAIN 24 1298
FT
FT DOMAIN 24 775
FT TRANSMEM 776 797
FT DOMAIN 798 1298
FT DOMAIN 44 118
FT DOMAIN 151 213
FT DOMAIN 245 317
FT DOMAIN 351 403
FT DOMAIN 438 541
FT DOMAIN 571 660
FT DOMAIN 692 758
FT DOMAIN 845 1173
FT NP_BIND 851 859
FT BINDING 879 879
FT ACT_SITE 1037 1037
FT DISULFID 51 111
FT DISULFID 158 206
FT DISULFID 252 310
FT DISULFID 445 534
FT DISULFID 578 653
FT DISULFID 699 751
FT CARBOHYD 33 33
FT CARBOHYD 104 104
FT CARBOHYD 166 166
FT CARBOHYD 251 251
FT CARBOHYD 299 299
FT CARBOHYD 411 411
FT CARBOHYD 515 515
FT CARBOHYD 527 527
FT CARBOHYD 594 594
FT CARBOHYD 683 683
FT CARBOHYD 690 690
FT CARBOHYD 758 758
FT MOD_RES 1068 1068
FT CONFLICT 24 24
FT CONFLICT 745 745
FT CONFLICT 752 753
FT CONFLICT 890 890
FT CONFLICT 1128 1128
FT CONFLICT 1146 1146
FT CONFLICT 1164 1164
SQ SEQUENCE 1298 AA; 145598 MW; 3DC469ED3C8B3B1 CRC64;
Query Match 47.3%; Score 43; DB 1; Length 1298;
Best local Similarity 46.7%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 WHRRRIPLQLAAGR 15
DB 458 WHRRPWTCKMFAQR 472

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RESULT 5
Y269_HELPY
ID Y269_HELPY STANDARD: PRT: 437 AA.
AC P56131:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein HP0269.
GN HP0269.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Colton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- SIMILARITY: BELONGS TO THE UPF0004 FAMILY.
CC -----
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CC -----
CC EMBL: AE000546; AAD07337.1; -
CC DR TIGR: HP0269; -
CC DR InterPro: IPR001861; UPF0004.
CC DR Pfam: PF00919; UPF0004. 1.
CC DR TIGRfams: TIGR00089; UPF0004. 1.
CC DR PROSITE: PS01278; UPF0004. 1.
CC KW Hypothetical protein; Complete proteome.
CC SO SEQUENCE 437 AA; 49423 MW; 3ECD46B6C1CEB3F CRC64;

Query Match 46.2%; Score 42; DB 1; Length 437;
Best Local Similarity 38.5%; Pred. No. 14;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 WRRHPIQLAAGR 15
   1:|||||:
Db 341 WKERVPLEVSSSR 353

RESULT 6
YAKB_SCHPO
ID YAKB_SCHPO STANDARD: PRT: 782 AA.
AC 009922:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative transcriptional regulatory protein C1F7.11c.
GN SPAC1F7.11c.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxID=4896;
RN [1]

```

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RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Haldago J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Nibbelk D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Trivey A., Walsh S.V., Warren F., Whitehead S.,
RA Woodward J., Voickeys G., Aert R., Robben J., Gymnopoulos B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambuit R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sphakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE 21NUCLEAR
CC CLUSTER DOMAIN.
CC -----
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CC -----
CC EMBL: Z67998; CA91958.1; -
CC DR HSSP: P12351; 1HWT.
CC DR InterPro: IPR001138; Fungal_TRN.
CC DR Pfam: PF00172; zn-clus. 1.
CC DR SMART: SM00066; GAL4. 1.
CC DR PROSITE: PS00463; ZN2_CY6_FUNGAL_1; 1.
CC DR PROSITE: PS50048; ZN2_CY6_FUNGAL_2; 1.
CC KW Hypothetical protein; Transcription regulation; DNA-binding;
CC KW Nuclear protein; Zinc; Metal-binding.
CC FT DNA_BIND 22 50
CC SO SEQUENCE 782 AA; 89377 MW; B0BDAEC986B1C7F CRC64;

Query Match 46.2%; Score 42; DB 1; Length 782;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 HMRHRIP 8
   1:|||||
Db 189 HMRHRIP 195

RESULT 7
PRL_ASPOF
ID PRL_ASPOF STANDARD: PRT: 158 AA.
AC 005736:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1 (AOPR1).
GN PRL.
OS Asparagus officinalis (Garden asparagus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
 CC Asparagus
 CC NCBI_TaxID=4686;
 RN (1)
 RN MEDLINE=93329716; PubMed=1627770;
 RX Warner S.A.J., Scott R., Draper J.;
 RT "Characterisation of a wound-induced transcript from the monocot
 RT asparagus that shares similarity with a class of intracellular
 RT pathogenesis-related (PR) proteins.";
 RL Plant Mol. Biol. 19:555-561(1992).
 RN (12)
 RN MEDLINE=94035138; PubMed=8220442;
 RX Warner S.A.J., Scott R., Draper J.;
 RT "Isolation of an asparagus intracellular PR gene (Aopri) wound-
 RT responsive promoter by the inverse polymerase chain reaction and its
 RT characterization in transgenic tobacco.";
 RL Plant J. 3:191-201(1993).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- INDUCTION: BY WOUNDING AND ELICITOR TREATMENTS.
 CC -1- SIMILARITY: BELONGS TO THE BETVI FAMILY OF PATHOGENESIS-RELATED
 CC PROTEINS.
 CC -----
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 CC -----
 DR EMBL: X62103; CAA44013.1;
 DR EMBL: X64452; CAA45784.1;
 DR EMBL: A26571; CAA01827.1;
 DR PIR: S22533; S22533.
 DR PIR: S39754; S39754.
 DR HSSP: 024248; 1E09.
 DR InterPro: IPR000916; Bel_V-I.
 DR Pfam: PF00407; Bel_V-I; 1.
 DR PRINTS: PR00634; BETALERGEN.
 DR PROSITE: PS00451; PATHOGENESIS_BETVI; 1.
 KW Pathogenesis-related protein.
 KW SEQUENCE 158 AA; 16921 MW; C9B9354812B00C20 CRC64;
 SQ
 Query Match 45.1%; Score 41; DB 1; Length 158;
 Best Local Similarity 46.2%; Pred. No. 7.5;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 3 WRRRIPLQLAAGR 15
 DB 6 WSHEVAVNVAAGR 18
 DB
 RESULT 8
 CIB3_SHEEP
 ID CIB3_SHEEP STANDARD; PRT: 232 AA.
 AC P80943;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE T-cell surface glycoprotein CD1b-3 (CD1b-3 antigen) (SCDIT10)
 DE (Fragment).
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN (1)
 RN MEDLINE=96269982; PubMed=8662069;
 RX Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;

RT "The sheep CD1 gene family contains at least four CD1B homologues.";
 RL Immunogenetics 44:86-96(1996).
 CC -1- FUNCTION: NOT KNOWN.
 CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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 CC -----
 DR EMBL: X90567; CAA62187.1;
 DR HSSP: P11609; 1CD1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003597; IG-cl.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00407; Igcl; 1.
 KW Glycoprotein; Immunoglobulin domain; Transmembrane; Multigene family.
 KW FT DOMAIN 1 201 EXTRACELLULAR (POTENTIAL).
 KW FT TRANSMEM 202 222 POTENTIAL.
 KW FT DOMAIN 223 232 CYTOPLASMIC (POTENTIAL).
 KW FT DISULFID 19 83 BY SIMILARITY.
 KW FT CARBOHD 123 178 N-LINKED (GLCNAC...) (POTENTIAL).
 KW SEQUENCE 232 AA; 26023 MW; C96DB3840B56158 CRC64;
 SQ
 Query Match 45.1%; Score 41; DB 1; Length 232;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 1 WRRRIPLQLAAG 14
 DB 158 WRRRIPLQLAAG 171
 DB
 RESULT 9
 Y126_TREPA
 ID Y126_TREPA STANDARD; PRT: 291 AA.
 AC O83163;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Hypothetical protein TP0126.
 GN TP0126.
 OS Treponema pallidum.
 CC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 CC NCBI_TaxID=160;
 RN (1)
 RN MEDLINE=96332770; PubMed=9665876;
 RX Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton K.A.,
 RA Sodergren E., Hardson J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khakl H., Richardson D., Howell J.K., Childsbarrow M., Uetebach T.,
 RA McDonald L., Artlach P., Bowman C., Cotton M.D., Fujil C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-386(1998).
 CC -1- SIMILARITY: SOME, TO T. PALLIDUM TP0733.
 CC -----
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 CC -----
 DR EMBL: AE001198; M665118.1; -.
 DR TIGR: TP0126; -.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 74 96 POTENTIAL.
 FT TRANSMEM 188 210 POTENTIAL.
 SO SEQUENCE 291 AA; 31921 MW; 496381BD06E67A3 CRC64;
 Query Match 45.18; Score 41; DB 1; Length 291;
 Best Local Similarity 58.38; Pred. No. 14;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 WHRRIPLOLAG 14
 Db 206 WRRPLPVGAG 217
 RESULT 10
 C1B2_SHEEP STANDARD; PRT; 333 AA.
 AC Q29422;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE T-cell surface glycoprotein CD1b-2 precursor (CD1b-2 antigen)
 DE (SCD1b-42) (Antigen IAH-CC14);
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID:9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=96269982; Pubmed=8662069;
 RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
 RT "The sheep CD1 gene family contains at least four CD1B homologues";
 RT Immunogenetics 44:86-96(1996).
 RL [2]
 RN SEQUENCE OF 21-33.
 RX MEDLINE=99115506; Pubmed=9914336;
 RA Rind S.M., Hopkins J., Dutia B.M.;
 RT "Amino-terminal sequencing of sheep CD1 antigens and identification of
 RT a sheep CD1 gene";
 RT Immunogenetics 49:225-230(1999).
 CC -1- FUNCTION: NOT KNOWN.
 CC -1- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -----
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 CC -----
 DR EMBL: Z36891; CAA85360.1; -.
 DR HSSP: P11609; ICD1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00407; IgC1; 1.
 KW Glycoprotein; Signal; Immunoglobulin domain; Transmembrane;
 KW Multigene family.
 FT SIGNAL 1 20
 FT CHAIN 21 333 T-CELL SURFACE GLYCOPROTEIN CD1b-2.
 FT DOMAIN 21 302 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 303 323 POTENTIAL.
 FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 120 184 BY SIMILARITY.
 FT DISULFID 224 279 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 333 AA; 37039 MW; 861BAE9617DB9BA1 CRC64;
 Query Match 45.18; Score 41; DB 1; Length 333;
 Best Local Similarity 50.08; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 WHRRIPLOLAG 14
 Db 259 WTVRLRVTLNVAAG 272
 RESULT 11
 KSS5_ECOLI STANDARD; PRT; 389 AA.
 AC P42218;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Capsule polysaccharide export protein kpsS.
 GN KPS.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K5;
 RX MEDLINE=9388530; Pubmed=8397187;
 RA Pazzanti C., Rosenow C., Boulinos G.J., Bronner D., Jann K.;
 RA Roberts I.S.;
 RT "Molecular analysis of region 1 of the Escherichia coli K5 antigen
 RT gene cluster: a region encoding proteins involved in cell surface
 RT expression of capsular polysaccharide";
 RT J. Bacteriol. 175:5978-5983(1993).
 RL J. Bacteriol. 175:5978-5983(1993).
 CC -----
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 CC -----
 DR EMBL: X74567; CAA52659.1; -.
 DR Polysaccharide transport; Transport.
 KW SEQUENCE 389 AA; 46381 MW; 73058122C28027DE CRC64;
 Query Match 45.18; Score 41; DB 1; Length 389;
 Best Local Similarity 62.38; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 WHRRIP 8
 Db 174 WHRRHP 181
 RESULT 12
 PSAB_GUTH STANDARD; PRT; 734 AA.
 AC Q78507;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Photosystem I P700 chlorophyll A apoprotein A2 (psab) (PSI-B).
 GN PSAB.
 OS Guillardia theta (Cryptomonas phl).

OG Chloroplast.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Gulliardia.
 OX NCBI_TaxID=55329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99128221; PubMed-9929392;
 RA Douglas S.E., Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, Gulliardia theta:
 complete sequence and conserved synteny groups confirm its common
 RT ancestry with red algae."
 RT J. Mol. Evol. 48:236-244(1999).
 CC -1- FUNCTION: Psaa and psab bind P700, the primary electron donor of
 CC photosystem I (PSI), as well as the electron acceptors A0, A1, and
 CC FX. PSI functions as a plastocyanin/cytochrome c6-ferredoxin
 CC oxidoreductase.
 CC -1- COFACTOR: P700 is a chlorophyll A dimer, A0 is chlorophyll A, A1
 CC is a phytylquinone and FX is a 4Fe-4S iron-sulfur center.
 CC -1- SUBUNIT: A psaa/B heterodimer binds the P700 chlorophyll special
 CC pair and subsequent electron acceptors. The PSI reaction center of
 CC higher plants and algae is composed of one at least 11 subunits.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
 CC thylakoid membrane.
 CC -1- SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF041468; AAC35698.1; -
 DR HSSP: P25897; IJBO.
 DR InterPro: IPR001280; PSI_Psaa/B.
 DR Pfam: PF00223; psaa_psab; 1.
 DR PRINTS: PR00257; PHOTOSPSAB.
 DR PROSITE: PS00419; PHOTOSYSTEM_I_PSAAB; 1.
 KW Chloroplast; Thylakoid; Transmembrane; Metal-binding; Iron;
 KW Iron-sulfur; 4Fe-4S; Chlorophyll.
 FT TRANSMEM 46 69 I (POTENTIAL).
 FT TRANSMEM 135 158 II (POTENTIAL).
 FT TRANSMEM 175 199 III (POTENTIAL).
 FT TRANSMEM 273 291 IV (POTENTIAL).
 FT TRANSMEM 330 353 V (POTENTIAL).
 FT TRANSMEM 369 395 VI (POTENTIAL).
 FT TRANSMEM 417 439 VII (POTENTIAL).
 FT TRANSMEM 517 535 VIII (POTENTIAL).
 FT TRANSMEM 575 596 IX (POTENTIAL).
 FT TRANSMEM 643 665 X (POTENTIAL).
 FT TRANSMEM 707 727 XI (POTENTIAL).
 FT METAL 559 568 IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
 FT METAL 568 559 IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
 FT BINDING 654 654 P700 SPECIAL PAIR CHLOROPHYLL AXIAL
 FT BINDING 654 654 LIGAND (BY SIMILARITY).
 FT BINDING 662 662 A0 CHLOROPHYLL (BY SIMILARITY).
 FT BINDING 670 670 A0 CHLOROPHYLL (BY SIMILARITY).
 FT BINDING 671 671 A1 PHYTYLQUINONE (BY SIMILARITY).
 FT BINDING 700 700 A1 PHYTYLQUINONE (BY SIMILARITY).
 SQ SEQUENCE 734 AA; 82328 MW; 823FEAA29E159BD4 CRC64;

Query Match 45.1%; Score 41; DB 1; Length 734;
 Best Local Similarity 46.7%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 WHMRHRIPLAAGR 15
 DB 594 WHMRHRIPLAAGR 608

RESULT 13
 DYHG_CHLRE

ID DYHG_CHLRE STANDARD; PRT; 4485 AA.
 AC Q39575;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Dynein gamma chain, flagellar outer arm.
 GN ODA2 OR ODA-2.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-1132D;
 RX MEDLINE-94274766; PubMed-7516341;
 RA Wilkerson C.G., King S.M., Wilman G.B.;
 RT "Molecular analysis of the gamma heavy chain of Chlamydomonas
 RT flagellar outer-arm dynein."
 RT J. Cell Sci. 107:497-506(1994).
 CC -1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
 CC FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
 CC DYNEIN HAS ATPASE ACTIVITY.
 CC -1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
 CC GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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 CC -----
 DR EMBL: U15303; AAA50455.1; -
 DR InterPro: IPR004273; Dynein_heavy.
 DR InterPro: IPR001230; Preyln_sile.
 DR Pfam: PR03028; Dynein_heavy; 1.
 KW Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
 KW Coiled coil.
 FT DOMAIN 449 469 COILED COIL (POTENTIAL).
 FT DOMAIN 804 838 COILED COIL (POTENTIAL).
 FT DOMAIN 1093 1114 COILED COIL (POTENTIAL).
 FT DOMAIN 1275 1297 COILED COIL (POTENTIAL).
 FT DOMAIN 1699 1727 COILED COIL (POTENTIAL).
 FT DOMAIN 1917 1945 MICROTUBULE-BINDING (POTENTIAL).
 FT DOMAIN 3077 3099 COILED COIL (POTENTIAL).
 FT DOMAIN 3196 3227 COILED COIL (POTENTIAL).
 FT DOMAIN 3265 3343 COILED COIL (POTENTIAL).
 FT DOMAIN 3569 3663 COILED COIL (POTENTIAL).
 FT NP_BIND 1819 1826 ATP (POTENTIAL).
 FT NP_BIND 2099 2106 ATP (POTENTIAL).
 FT NP_BIND 2425 2432 ATP (POTENTIAL).
 FT NP_BIND 2802 2809 ATP (POTENTIAL).
 SQ SEQUENCE 4485 AA; 512836 MW; 974B79328B403677 CRC64;

Query Match 44.5%; Score 40.5; DB 1; Length 4485;
 Best Local Similarity 60.0%; Pred. No. 2,5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 W-HMRHRIPL 9
 DB 2373 W-HMRHRIPL 2382

RESULT 14
 LEGT_HUMAN STANDARD; PRT; 135 AA.
 AC P47929;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Galectin-7 (HKL-14) (P17).

GN LGALST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 7-19; 75-82; 111-117 AND 120-132.
 RC TISSUE-Epidermis; PubMed=7534301;
 RX MEDLINE=95197604; PubMed=7534301;
 RA Madson P., Rasmussen H.H., Flint T., Gromov P., Kruse T.A., Honore B.,
 RA Vorum H., Cells J.E.;
 RA "Cloning, expression, and chromosome mapping of human galectin-7.",
 RL J. Biol. Chem. 270:5823-5829(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Epidermis;
 RX MEDLINE=95246905; PubMed=7729568;
 RA Magnaldo T., Bernard F., Darmon M.;
 RA "Galectin-7, a human 14-kDa S-lectin, specifically expressed in
 RT keratinocytes and sensitive to retinoic acid.",
 RL Dev. Biol. 168:259-271(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=98434364; PubMed=9760227;
 RA Leonidas D.D., Vatzaki E.H., Vorum H., Cells J.E., Madson P.,
 RA Acharya K.R.;
 RA "Structural basis for the recognition of carbohydrates by human
 RT galectin-7.",
 RL Biochemistry 37:13930-13940(1998).
 CC -1- FUNCTION: COULD BE INVOLVED IN CELL-CELL AND/OR CELL-MATRIX
 CC INTERACTIONS NECESSARY FOR NORMAL GROWTH CONTROL.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED BY A NON-CLASSICAL SECRETORY
 CC PATHWAY.
 CC -1- TISSUE SPECIFICITY: MAINLY IN STRATIFIED SQUAMOUS EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO THE GALAPRIN (S-LECTIN) FAMILY.
 CC -----
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 CC -----
 CC EMBL; L07769; AAA67899.1; -;
 DR EMBL; U06643; AAA86820.1; -;
 DR PDB; 1BK2; 04-NOV-98.
 DR PDB; 2GAL; 04-NOV-98.
 DR PDB; 3GAL; 04-NOV-98.
 DR PDB; 4GAL; 04-NOV-98.
 DR PDB; 5GAL; 04-NOV-98.
 DR Aarhus/Ghent-2DPAGE; 17; IEF.
 DR GeneW; HGNC:6568; LGALST.
 DR MIM; 600615; -;
 DR InterPro; IPR001079; Galectin.
 DR Pfam; PF00337; Gal-binding_lectin; 1.
 DR SMART; SM00276; GLECT; 1.
 DR PROSITE; PS00309; GALAPRIN; 1.
 KW Galectin; Lectin; 3D-structure.
 FT INIT_MET 0
 FT BINDING 69 75
 SQ SEQUENCE 135 AA; 14944 MW; 4E7CEA54036EF806 CRC64;
 Query Match 44.0%; Score 40; DB 1; Length 135;
 Best Local Similarity 75.0%; Pred. No. 9.3;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 HWRHRIPL 9
 DB 108 HRRHRLPL 115

RESULT 15
 ID T2SL_STRAL STANDARD; PRT; 315 AA.
 AC 053608;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Type II restriction enzyme SalI (EC 3.1.21.4) (Endonuclease SalI)
 DE (R. SalI).
 GN SALIR.
 OS Streptomyces albus G.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
 CX NCBI_TaxID=1962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95129852; PubMed=7828868;
 RA Rodicio M.R., Quinton-Jager T., Moran L.S., Slatko B.E., Wilson G.G.;
 RA "Organization and sequence of the SalI restriction-modification
 RT system.",
 RL Gene 151:167-172(1994).
 CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE ATTCGAC AND
 CC CLEAVES AFTER G-1.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -----
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 CC -----
 CC DR EMBL; U01232; AAA81886.1; -;
 DR REBASE; 1588; SALI
 DR Hydrolyase; Endonuclease; Nuclease; Restriction system.
 KW SEQUENCE 315 AA; 35337 MW; DAYC3CAB8B924F07 CRC64;
 Query Match 44.0%; Score 40; DB 1; Length 315;
 Best Local Similarity 57.1%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Search completed: November 27, 2002, 07:18:55
 Job time : 5.14286 secs

OY 1 HWRHRIPLQIAG 14
 DB 301 WYWEHRIDLEAAG 314

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OM protein - protein search, using sw model

Run on: November 27, 2002, 06:27:07 : Search time 8.33977 Seconds

(without alignments)
370.599 Million cell updates/sec

Title: US-09-893-615-2

Perfect score: 91

Sequence: 1 WHMRHRIPIQLAAGR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-REMBL_21:*
2: SP-archaea:*
3: SP-fungi:*
4: SP-human:*
5: SP_invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP-virus:*
16: SP_bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	52.7	62	10	08S754
2	48	52.7	402	10	09FSM9
3	47	51.6	526	5	09UDW3
4	47	51.6	649	17	09V0U1
5	46.5	51.1	354	16	09XA39
6	46.5	51.1	391	9	003969
7	46.5	51.1	802	16	08UW3
8	45.5	50.0	211	17	029897
9	45.5	50.0	505	10	022236
10	45	49.5	126	16	09KYN3
11	45	49.5	516	16	09A9K8
12	45	49.5	595	17	08ZM38
13	45	49.5	649	17	08U137
14	44.5	48.9	4083	3	09C1M7
15	44.5	48.9	270	16	09HXH2
16	44.5	48.9	319	11	0912B6

17	44.5	48.9	343	11	08VCJ6	08vcj6 mus musculus
18	44.5	48.9	356	16	P95276	P95276 mycobacteri
19	44.5	48.9	467	11	099PO2	099pq2 mus musculus
20	44.5	48.9	483	11	08VDX5	08vdx5 mus musculus
21	44	48.4	522	13	09YGX4	09ygx4 brachydanto
22	44	48.4	636	16	09PDC8	09pdc8 xylella fas
23	43	47.3	152	16	09KOG3	09kog3 neisseria m
24	43	47.3	152	16	09JVG2	09jvg2 neisseria m
25	43	47.3	186	6	09BGP1	09bgi1 macaca fasc
26	43	47.3	222	16	09ZBF8	09zbf8 streptomyce
27	43	47.3	322	5	08SZE2	08sze2 drosophila
28	43	47.3	330	16	09A8W9	09a8w9 caulobacter
29	43	47.3	334	2	052445	052445 pseudomonas
30	43	47.3	367	5	09VPE8	09vpe8 drosophila
31	43	47.3	434	16	09KR89	09kr89 vibrio chol
32	43	47.3	444	3	09C197	09c197 amantia mus
33	43	47.3	466	4	09HBV5	09hbv5 homo sapien
34	43	47.3	491	4	09BZB7	09bzb7 homo sapien
35	43	47.3	527	5	09VGT1	09vgt1 drosophila
36	43	47.3	561	11	P70166	P70166 mus musculus
37	43	47.3	566	4	09BZB8	09bzb8 homo sapien
38	43	47.3	716	16	08YLZ5	08ylz5 anabaena sp
39	43	47.3	930	2	09AQSO	09aqso bacillus sp
40	42.5	46.7	639	16	09K4H5	09k4h5 streptomyce
41	42	46.2	207	16	09RW71	09rw71 deinococcus
42	42	46.2	266	2	09RNV1	09rnx1 mycobacteri
43	42	46.2	289	10	042702	042702 chlamydomon
44	42	46.2	292	16	09K3Q1	09k3q1 streptomyce
45	42	46.2	296	2	09RMP1	09rmp1 mycobacteri

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	62 AA.
ID 08S754			
AC 08S754:			
DT 01-JUN-2002 (TREMBLrel. 21, Created)			
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE Hypothetical 7.3 kDa protein.			
GN OSJNB0081F12.14.			
OS Oryza sativa (Rice).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC Ehrhartoideae; Oryzaceae; Oryza.			
OX NCBI_TaxID=4530;			
ON [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=NIPONBARE;			
RA McCombie W.R., de la Bastide M., Spiegel L., Kirchoff K., Preston R.,			
RA Kuit K., Nascimento L., Bell M., Balija V., Baker J., Vii M.D.,			
RA Zuluveran T., Santos L., Miller B., Cummins D.M., Shah R., King L.,			
RA Bahret A., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedila N.;			
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone			
RT OCSJNB0081F12, from chromosome 10, complete sequence."			
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AC090488; AAM01014.1;			
KW Hypothetical protein.			
SQ SEQUENCE 62 AA; 7306 MW; 4B14DB22ABDD41 CRC64;			
Query Match	52.7%	Score 48;	DB 10; Length 62;
Best Local Similarity	53.3%	Pred. No. 2.5;	
Matches 8; Conservative	1;	Mismatches 6;	Indels 0; Gaps 0;
OY 1 WHMRHRIPIQLAAGR 15			
DB 45 WHMRHRIPIQLAAGR 59			
RESULT 2			
09FSM9			

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ID Q9FSM9 PRELIMINARY: PRT: 402 AA.
AC Q9FSM9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 44.1 kDa protein.
GN H0711G06.21.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J.,
RA Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen L.,
RA Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,
RA Lei H.Y., Zhang Y.J., Meng R., Li C., Lu Y., Chen X.C., Zhang Y.,
RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
RT "Oryza sativa indica (Guangluai14) genomic DNA, chromosome 4, BAC
RT clone: H0711G06 (+H0113C06).";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL442115; CAC09515.1;
DR InterPro: IPR004324; BT1.
DR InterPro: IPR003880; Pantine_attach.
DR Pfam: PF03092; BT1; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 402 AA: 44120 MW: E2A00524DB4CC3EF CRC64;

Query Match 52.7%; Score 48; DB 10; Length 402;
Best Local Similarity 39.1%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 5; Indels 8; Gaps 1;

OY 1 HWRHRI-----PQLAAGR 15
DB 276 WWHHREGHLLSGPIQARPCR 298

RESULT 3
O9U0W3
ID O9U0W3 PRELIMINARY: PRT: 526 AA.
AC O9U0W3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Possible CAMP-dependent protein kinase subunit.
GN I7276.06.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann W., Wandolt R., Ivens A.C., Murphy L., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL133436; CAB62823.1;
DR InterPro: IPR000595; CNMP_binding.
DR InterPro: IPR001064; Crystallin.
DR SMART: SM00100; CNMP; 1.
DR PROSITE: PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE: PS00442; CNMP_BINDING_3; 2.
DR PROSITE: PS00223; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
RA Kinase.

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SQ SEQUENCE 526 AA: 57561 MW: 5CA989A7980BDAAB CRC64;
Query Match 51.6%; Score 47; DB 5; Length 526;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 HWRHRIPLQLAG 14
DB 378 WPLHLQIPIMHVG 391

RESULT 4
O9V0U1
ID O9V0U1 PRELIMINARY: PRT: 649 AA.
AC O9V0U1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein PAB1903.
GN PAB1903.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome
RT structure and evolution.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248285; CAB49612.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 649 AA: 75585 MW: C4918F2188EAB1E5 CRC64;

Query Match 51.6%; Score 47; DB 17; Length 649;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 HWRHRIPLQLAG 14
DB 563 NMHGIPKLAVG 575

RESULT 5
O9XA39
ID O9XA39 PRELIMINARY: PRT: 354 AA.
AC O9XA39;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE putative epoxide hydrolase.
GN SC03574 OR SCH17.08C.
GN Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K.D., Harris D.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapalte D., Elchner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;

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RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Karlavage A.R., Graham D.E., Kyrleides N.C.,
 RA Fleischmann R.D., Dougenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kikness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Relch C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon *Archaeoglobus fulgidus*.";
 RL Nature 390:364-370(1997).
 DR EMBL: AE001080; AAB90884.1; -.
 DR TIGR: AF0350; -.
 DR InterPro: IPR002781; DUF81.
 DR Pfam: PF01925; DUF81; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 SQ SEQUENCE 211 AA; 23303 MW; 927825BC1EFCEB46 CRC64.

Query Match 50.5%; Score 46; DB 17; Length 211;
 Best Local Similarity 59.1%; Pred. No. 15;
 Matches 13; Conservative 1; Mismatches 0; Indels 8; Gaps 3;

Oy 1 WHW--RH-----RIPLOL-AAG 14
 ||| | : ||||| |||
 Db 25 WHWRLRYNAPCPRIPLQLPAG 46

RESULT 9

ID 022236 PRELIMINARY; PRT; 505 AA.
 AC 022236;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Hypothetical 58.5 kDa protein.
 GN T32N15.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-CV. COLUMBIA;
 RC de la Bastide M.R., Parnell L.D., Kaplan N., Gnoj L., Hameed A.,
 RA Schütz K., Hasegawa A., Gottesman T., Shohdy N., Granat S., Jensen K.,
 RA Johnson A.F., Lochl M., Dedhia N., Martienssen R., McCombie W.R.;
 RT "A. thaliana BAC T32N15 from chromosome V."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC002534; AAB70030.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 505 AA; 58451 MW; 627A823D89032D0 CRC64.

Query Match 50.0%; Score 45.5; DB 10; Length 505;
 Best Local Similarity 57.1%; Pred. No. 40;
 Matches 8; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

Oy 1 WHWHR--RIPLOL 11
 ||||| | : ||| |
 Db 22 WHWRLHYRVPGLT 35

RESULT 10

ID 09KYN3 PRELIMINARY; PRT; 126 AA.
 AC 09KYN3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Putative membrane protein.
 GN SC07352 OR SC9H11.06.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M45;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL356592; CAB92195.1; -.
 SQ SEQUENCE 126 AA; 13263 MW; 2EB8D083378B22D CRC64.

Query Match 49.5%; Score 45; DB 16; Length 126;
 Best Local Similarity 64.7%; Pred. No. 14;
 Matches 11; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Oy 1 WHWHR-IPLOLA-GR 15
 ||||| | : ||| |
 Db 88 WDMRRPAPQQAALGR 104

RESULT 11

ID 09A9K8 PRELIMINARY; PRT; 516 AA.
 AC 09A9K8;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Tryplothophan halogenase, putative.
 GN CC0972.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OC NCBI_TaxID=155892;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-ATCC 19089 / CB15;
 RC MEDLINE=21173698; PubMed=11259647;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phake N.D., Ely B.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smil J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Uutterback T., Tran K., Wolf A., Yamathayan J., Ernoileva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AE005774; AAK22956.1; -.
 DR TIGR: CC0972; -.
 KW Complete proteome.
 SQ SEQUENCE 516 AA; 57489 MW; 775AE107AD7CF0EC CRC64.

Query Match 49.5%; Score 45; DB 16; Length 516;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 WHRIPLOLAG 14
 ||||| | : ||| |
 Db 272 WHRIPLOLRAG 283

RESULT 12

OBZM38 PRELIMINARY; PRT; 595 AA.
 ID 08ZM38
 AC 08ZM38;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein PAE1989.
 GN PAE1989.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Filt-Gibson S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 DR EMBL: AE009851; AAL63864.1; -.
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR002500; PAPS_reduct.
 DR Pfam: PF00307; fer4; 2.
 DR Pfam: PF01507; PAPS_reduct; 1.
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; 2.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 595 AA; 67145 MW; D91343AB940C4896 CRC64;

Query Match

Best Local Similarity 49.5%; Score 45; DB 17; Length 595;
 Matches 8; Conservative 66.7%; Pred. No. 55;
 Mismatches 4; Indels 0; Gaps 0;

OY 1 WHMRHRIPLQLA 12
 DB 442 WRWGRIPGDLA 453

RESULT 13

OBUI37 PRELIMINARY; PRT; 649 AA.
 ID 08UI37
 AC 08UI37;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein PF1392.
 GN PF1392.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weis R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE010242; AAL81516.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 649 AA; 75072 MW; B66A4194DFD81F1A CRC64;

Query Match

Best Local Similarity 49.5%; Score 45; DB 17; Length 649;
 Matches 8; Conservative 61.5%; Pred. No. 60;
 Mismatches 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 WHMRHRIPLQLAG 14
 : | | | | | | | |

DB 563 NWIHGIPKLAVG 575

RESULT 14

O9C1M7 PRELIMINARY; PRT; 4083 AA.
 ID 09C1M7
 AC 09C1M7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dynein heavy chain 1.
 GN DHCI.
 OS Ashbya gossypii (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Eremotheciaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21102174; PubMed=1181180;
 RA Alberti-Segui C., Dietrich F., Altmann-Johl R., Hoepfner D.,
 RA Philippsen P.;
 RT "Cytoplasmic dynein is required to oppose the force that moves nuclei
 towards the hyphal tip in the filamentous ascomycete Ashbya
 gossypii.";
 RL J. Cell Sci. 114:975-986(2001).
 DR EMBL: AF287477; AAK20175.1; -.
 DR InterPro: IPR003593; AAA_Atpase.
 DR InterPro: IPR004273; Dynein_heavy.
 DR Pfam: PF03028; Dynein_heavy; 1.
 DR SMART: SM00382; AAA; 3.
 KW ATP-binding
 SQ SEQUENCE 4083 AA; 466243 MW; 09DD11DAEF1225E1 CRC64;

Query Match

Best Local Similarity 49.5%; Score 45; DB 3; Length 4083;
 Matches 5; Conservative 50.0%; Pred. No. 3; 1e+02;
 Mismatches 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 WHMRHRIPLQ 10
 DB 3631 WHWFYQIPTE 3640

RESULT 15

O9HXH2 PRELIMINARY; PRT; 270 AA.
 ID 09HXH2
 AC 09HXH2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Probable transcriptional regulator.
 GN PA3830.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.V., Conliffe S.N., Folger K.R., Kas A., Lartbig I.T.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RT Nature 406:959-964(2000).
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XTILS FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC EMBL: AE004800; AAG07217.1; -.
 CC InterPro: IPR000005; HTHARAC.
 DR Pfam: PF00165; HTH_Arac; 2.

DR PRINTS: PRO0032; HTHARAC.
DR SMART: SM00342; HTH_ARAC; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
RW DNA-binding; transcription regulation; Complete proteome.
SQ SEQUENCE 270 AA; 29965 MW; 9DCA2B27481E0C80 CRC64;

Query Match 48.9%; Score 44.5; DB 16; Length 270;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 9; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

QY 2 HWRHRIPL----QLAG 14
||||:|
Db 213 HWRHGVRLAALPRLAG 230

Search completed: November 27, 2002, 07:22:47
Job time : 16.3398 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:17:51 ; Search time 2.72201 Seconds
(without alignments)
162.139 Million cell updates/sec

Title: US-09-893-615-2

Sequence: 1 WHRRRPIQLAAGR 15

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents-AA:

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCYUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	15	2	US-08-592-646A-28
2	91	100.0	15	2	US-08-592-646A-48
3	91	100.0	15	4	US-09-165-422-28
4	91	100.0	15	4	US-09-165-422-48
5	91	100.0	37	2	US-08-592-646A-59
6	91	100.0	37	4	US-09-165-422-59
7	86	94.5	15	2	US-08-592-646A-27
8	86	94.5	15	4	US-09-165-422-27
9	80	87.9	15	2	US-08-592-646A-26
10	80	87.9	15	2	US-08-592-646A-29
11	80	87.9	15	4	US-09-165-422-26
12	80	87.9	15	4	US-09-165-422-29
13	76	83.5	15	2	US-08-592-646A-25
14	76	83.5	15	4	US-09-165-422-25
15	72	79.1	15	2	US-08-592-646A-24
16	72	79.1	15	2	US-08-592-646A-30
17	72	79.1	15	4	US-09-165-422-24
18	72	79.1	15	4	US-09-165-422-30
19	69	75.8	15	2	US-08-592-646A-49
20	69	75.8	15	4	US-09-165-422-49
21	68	74.7	15	2	US-08-592-646A-23
22	68	74.7	15	4	US-09-165-422-23
23	63	69.2	15	2	US-08-592-646A-22
24	63	69.2	15	4	US-09-165-422-22
25	61	67.0	15	2	US-08-592-646A-31
26	61	67.0	15	4	US-09-165-422-31
27	59	64.8	15	2	US-08-592-646A-21

ALIGNMENTS

28	59	64.8	15	4	US-09-165-422-21	Sequence 21, Appl
29	56	61.5	11	2	US-08-592-646A-7	Sequence 7, Appl
30	56	61.5	11	4	US-09-165-422-7	Sequence 7, Appl
31	56	61.5	15	2	US-08-592-646A-9	Sequence 9, Appl
32	56	61.5	15	4	US-09-165-422-9	Sequence 9, Appl
33	52	57.1	15	2	US-08-592-646A-20	Sequence 20, Appl
34	52	57.1	15	4	US-09-165-422-20	Sequence 20, Appl
35	51	56.0	15	2	US-08-592-646A-43	Sequence 43, Appl
36	51	56.0	15	2	US-08-592-646A-44	Sequence 44, Appl
37	51	56.0	15	4	US-09-165-422-43	Sequence 43, Appl
38	51	56.0	15	4	US-09-165-422-44	Sequence 44, Appl
39	50	54.9	11	2	US-08-592-646A-8	Sequence 8, Appl
40	50	54.9	11	4	US-09-165-422-8	Sequence 8, Appl
41	50	54.9	15	2	US-08-592-646A-10	Sequence 10, Appl
42	50	54.9	15	2	US-08-592-646A-41	Sequence 41, Appl
43	50	54.9	15	2	US-08-592-646A-45	Sequence 45, Appl
44	50	54.9	15	4	US-09-165-422-10	Sequence 10, Appl
45	50	54.9	15	4	US-09-165-422-41	Sequence 41, Appl

RESULT 1
US-08-592-646A-28
Sequence 28, Application US/08592646A
Patent No. 585135

GENERAL INFORMATION:

APPLICANT: JOLIVET-RENAUD, Colette

TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA

TITLE OF INVENTION: GONDII AND APPLICATIONS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIVIER & BERRIDGE, PLC

STREET: P. O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,646A

FILING DATE: 26-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPA 36923

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703 836-6400

TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-592-646A-28

Query Match 100.0%, Score 91, DB 2, Length 15;

Best Local Similarity 100.0%, Pred. No. 1.8e-08;

Matches 15, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 WHRRRPIQLAAGR 15
DB 1 WHRRRPIQLAAGR 15

RESULT 2
US-08-592-646A-48
Sequence 48, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-48

Query Match 100.0%; Score 91; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WHMRRHPLQLAAGR 15
Db 1 WHMRRHPLQLAAGR 15

RESULT 3
US-09-165-422-28
Sequence 28, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422

FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-165-422-28

Query Match 100.0%; Score 91; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WHMRRHPLQLAAGR 15
Db 1 WHMRRHPLQLAAGR 15

RESULT 4
US-09-165-422-48
Sequence 48, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-165-422-48

Query Match 100.0%; Score 91; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHHRHRIPIQLAGR 15
DB 1 WHHRHRIPIQLAGR 15

RESULT 5

US-08-592-646A-59
Sequence 59, Application US/08592646A

Patent No. 5851535

GENERAL INFORMATION:

APPLICANT: JOLIVET-REYNAUD, Colette

TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA

TITLE OF INVENTION: GONDII AND APPLICATIONS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIVIER & BERRIDGE, PLC

STREET: P.O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,646A

FILING DATE: 26-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703 836-6400

TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-592-646A-59

OY 1 WHHRHRIPIQLAGR 15
DB 10 WHHRHRIPIQLAGR 24

RESULT 6

US-09-165-422-59
Sequence 59, Application US/09165422

Patent No. 6372897

GENERAL INFORMATION:

APPLICANT: JOLIVET-REYNAUD, Colette

TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA

TITLE OF INVENTION: GONDII AND APPLICATIONS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIVIER & BERRIDGE, PLC

STREET: P.O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-165-422-59

Query Match 100.0%; Score 91; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHHRHRIPIQLAGR 15
DB 10 WHHRHRIPIQLAGR 24

RESULT 7
US-08-592-646A-27
Sequence 27, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVIER & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-592-646A-27

Query Match 94.5%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRRHPIQLAAG 14
DB 2 WHMRRHPIQLAAG 15

RESULT 8

US-09-165-422-27

Sequence 27, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Query Match 94.5%; Score 86; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRRHPIQLAAG 14
DB 2 WHMRRHPIQLAAG 15

RESULT 9

US-08-592-646A-26

Sequence 26, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC

STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 87.9%; Score 80; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRRHPIQLAAG 13
DB 3 WHMRRHPIQLAAG 15

RESULT 10

US-08-592-646A-29

Sequence 29, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-29

Query Match 87.9%; Score 80; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HMRHRIPQLAAGR 15
| | | | | | | | | | | | | | | | |
Db 1 HMRHRIPQLAAGR 14

RESULT 11
US-09-165-422-26
Sequence 26, Application US/09165422
Patent No. 6372897

GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-165-422-26

Query Match 87.9%; Score 80; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HMRHRIPQLAA 13
| | | | | | | | | | | | | | | | |
Db 3 HMRHRIPQLAA 15

RESULT 12
US-09-165-422-29
Sequence 29, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette

TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-165-422-29

Query Match 87.9%; Score 80; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HMRHRIPQLAAGR 15
| | | | | | | | | | | | | | | | |
Db 1 HMRHRIPQLAAGR 14

RESULT 13
US-08-592-646A-25
Sequence 25, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-25

Query Match 83.5%; Score 76; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHRRRIPQLA 12
Db 4 WHRRRIPQLA 15

RESULT 14
US-09-165-422-25
Sequence 25, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-165-422-25

Query Match 83.5%; Score 76; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHRRRIPQLA 12
Db 4 WHRRRIPQLA 15

RESULT 15
US-08-592-646A-24
Sequence 24, Application US/08592646A
Patent No. 3651535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
CONDIT AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-24

Query Match 79.1%; Score 72; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHRRRIPQL 11
Db 5 WHRRRIPQL 15

Search completed: November 27, 2002, 07:25:10
Job time : 2.72201 secs


```

XX Example 2: Page 7: 33pp; French.
PS
CC The invention relates to novel peptides which bind to antibodies which
CC recognise the Toxoplasma gondii P30 envelop protein. A peptide library
CC was generated to express pentadecapeptides on the surface of a
CC filamentous phage as a fusion protein with the PIII protein. The library
CC was screened with immobilised anti-T. gondii P30 protein antibody 1E1E7.
CC Phages which bind this antibody were recovered and amplified by one
CC round of infection in E. coli. The resultant phages were rescreened with
CC the immobilised antibody and the second round screen isolated 58
CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA
CC from 30 colonies was isolated and sequenced to determine the sequence of
CC the pentadecapeptide encoded. The peptide sequences AAW12276-86 were
CC identified. Of the 30 colonies studied, this peptide sequence was
CC encoded 11 times. A template peptide sequence (AAW12287) corresponding
CC to the sequence across the phage PIII sequence and putative
CC pentadecapeptide was used to generate a series of overlapping
CC pentadecapeptides. These peptides were used to determine the best
CC peptide sequence which binds the 1E1E7 antibody. Peptides AAW03367-75
CC were isolated. The new peptides can then be used in diagnostic assays to
CC detect T. gondii antibodies in a sample or to purify anti-P30 antibodies
CC or for active immunisation against T. gondii.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPLOLAAGR 15
Db 1 WHMRHRIPLOLAAGR 15
|||||
RESULT 2
AAW71334
ID AAW71334 standard; peptide: 15 AA.
XX
AC AAW71334;
XX
DT 25-NOV-1998 (first entry)
XX
DE A glycolipid sugar chain peptide.
XX
KM Glycolipid sugar chain; inhibit; adhesion; metastasis; cancer cell.
XX
OS Synthetic.
XX
PN JP10237099-A.
XX
PD 08-SEP-1998.
XX
PF 26-FEB-1997; 97JP-0042311.
XX
PR 26-FEB-1997; 97JP-0042311.
XX
PA (IMMO ) IMMUNO JAPAN INC.
XX
DR WPI; 1998-537488/46.
XX
PT New peptide which reacts specifically with antibody against
PT glyco-lipid sugar chains - useful for inhibition of cancer
PT metastasis
PS Claim 8: Page 3; 7pp; Japanese.
XX
XX AAW71332-36 represent glycolipid sugar chain replica peptides. They
CC react specifically with an antibody against glycolipid sugar chains
CC and inhibit adhesion and metastasis of cancer cells to a target cell.
CC The peptides can be used to prevent cancer metastasis.
XX
SQ Sequence 15 AA;

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```

Query Match 100.0%; Score 15; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPLOLAAGR 15
Db 1 WHMRHRIPLOLAAGR 15
|||||
RESULT 3
AAW94702
ID AAW94702 standard; peptide: 15 AA.
XX
AC AAW94702;
XX
DT 22-APR-1999 (first entry)
XX
DE Lipoteichoic acid epitope peptide mimic for Mab 96-110.
XX
KM Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
KM immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM Mab 96-110.
XX
OS Staphylococcus sp.
XX
PN WO9857994-A2.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX
DR WPI; 1999-095329/08.
XX
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Claim 16; Page 120; 150pp; English.
XX
CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic acid
CC of gram positive bacteria, where the Mab is a chimeric immunoglobulin
CC comprising at least part of a human immunoglobulin constant region and
CC at least part of a non-human immunoglobulin variable region having
CC specificity to lipoteichoic acid of gram positive bacteria. The
CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
CC the bacteria and enhance protection from lethal infection. The antibodies
CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
CC acid antibody or characterised by amino acids corresponding to one or
CC more of the complementarity determining regions (CDRs) of the variable
CC region of the antibody) can be used for treating or preventing infections
CC caused by gram positive bacteria. They can also be used for the diagnosis
CC of gram positive bacterial infections. The present sequence represents a
CC specifically claimed lipoteichoic acid epitope peptide mimic that can be
CC bound by the antibody of the invention. (Mab 96-110).
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 15; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPLOLAAGR 15
Db 1 WHMRHRIPLOLAAGR 15
|||||

```


RESULT 4
AAB17987
ID AAB17987 standard; Peptide: 15 AA.
XX
AC AAB17987;
XX
DT 31-OCT-2000 (first entry)
XX
DE Beta-2GPI Ab binding peptide sequence SEQ ID NO:1099.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer; KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; KW immunosuppressive; EPO; TPO; CTLM4; mimetic; IL-1; TNF; antagonist; KW MMP; inhibitor; erythropoietin; thrombopoietin; Interleukin 1; KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; KW vascular endothelial growth factor; matrix metalloproteinase; KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
PD
PD 04-MAY-2000.
XX
PE 25-OCT-1999; 99WO-US25044.
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
P1 Felge U, Liu C, Cheetham J, Boone TC;
DR WPI: 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and PT pharmacologically active peptides, useful for treating cancer and PT autoimmune diseases -
XX
PS Claim 39; Page 598; 608pp; English.
CC The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)-a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 CC where P1, P2, P3, and P4 = are each independently sequences of CC pharmacologically active peptides; L1, L2, L3, and L4 = are each CC independently linkers; and a, b, c, d, e, and f = are each independent CC 0 or 1, provided that at least 1 of a and b is 1. The composition can CC have cytosolic, antiasthmatic, thrombolytic and immunosuppressive CC activities. DNAs, vectors and host cells from the present invention can CC be used for producing pharmaceutical compositions. The compositions are CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases. CC The use of an Fc domain (rather than a Fab domain) can provide a longer CC half-life or incorporate functions such as Fc receptor binding, protein CC A binding, complement fixation, and possibly placental transfer. AAA69443 CC to AAA69556 and AAB16955 to AAB18003 represent nucleotide and amino acid CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 15 AA:
Query Match 100.0%; Score 15; DB 21; Length 15; Best Local Similarity 100.0%; Prod. No. 1.4e-08; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 1 WHMRRIRPLQLAAGR 15 DB 1 WHMRRIRPLQLAAGR 15
RESULT 5
AAB77358

ID	ABBR73358 standard; Peptide; 15 AA.
XX	
AC	ABBR73358;
XX	
DT	05-APR-2002 (first entry)
DE	Exemplary pharmacologically active peptide SEQ ID NO:1097.
XX	
KM	Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KM	EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KM	TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KM	TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KM	MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KM	cystostatic; antirheumatic; antifertility; antidiabetic; ophthalmological;
KM	antianemic; anorectic; antifertility; haemostatic; dermatological;
KM	neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KM	cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KM	sleep disorder; neurological degenerative disease; anaemia;
KM	thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KM	Fanconi's syndrome.
OS	Synthetic.
XX	
PX	WO200183525-A2.
PD	
XX	08-NOV-2001.
PF	
XX	02-MAY-2001; 2001WO-US14310.
PR	
XX	03-MAY-2000; 2000US-0563286.
PA	(AMGE-) AMGEN INC.
PI	
DR	Felge U, Liu C, Cheetham JC, Boone TC, Gudes JM; WPI: 2002-13013/17.
PT	
XX	
PT	Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility - XX
PS	Claim 39; Page 62; 176pp; English.
XX	
CC	The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antifertility, antidiabetic, ophthalmological, antianemic, anorectic, antiinfertility, haemostatic, dermatological and neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (II), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anemia. The TPO-mimetic comprising compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopenia, aplastic anaemia, metastatic tumour which result in thrombocytopenia, systemic lupus erythematosus, and Fanconi's syndrome. ABB722403 to ABB73426 and AB135695 to AB135777 represent amino acid and nucleic acid sequences used in the exemplification of the present invention. CC
Sequence	15 AA:
Query Match	100.0%: Score 15; DB 23; Length 15;
Best local Similarity	100.0%: Pred. NO. 1.4e-06;
Matches	15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 WHRRIRIPQLAAGR 15

Db 1 MHNRHRIPLQLAAGR 15

RESULT 6
AAW94729
ID AAW94729 standard; Protein; 19 AA.

XX AAW94729;

XX 22-APR-1999 (first entry)

XX Sequence 15mer 2nd.1 resulting from library panning experiments.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;

XX Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

XX Mab 96-110; panning.

XX Staphylococcus sp.

XX MO9857994-A2.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-US12402.

XX 16-JUN-1997; 97US-0049871.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Fischer GW, Schuman RF, Stinson JL, Wong H;

XX MPI: 1999-095329/08.

XX N-PSDB; AAX05555.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used

XX to develop products for the diagnosis, prevention and treatment of

XX infections caused by gram positive bacteria

XX Example 5; Fig 8; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic

XX acid of gram positive bacteria, where the Mab is a chimeric

XX immunoglobulin comprising at least part of a human immunoglobulin

XX constant region and at least part of a non-human immunoglobulin variable

XX region having specificity to lipoteichoic acid of gram positive bacteria.

XX The antibodies bind to whole bacteria and enhance phagocytosis and

XX killing of the bacteria and enhance protection from lethal infection. The

XX antibodies or peptides (encoded by a DNA of the variable region of

XX anti-lipoteichoic acid antibody or characterised by amino acids

XX corresponding to one or more of the complementarity determining regions

XX (CDRs) of the variable region of the antibody) can be used for treating

XX or preventing infections caused by gram positive bacteria. They can also

XX be used for the diagnosis of gram positive bacterial infections.

XX Sequences AAW94726-34 represent common peptide sequences resulting from

XX all library panning experiments. Three series of panning experiments were

XX conducted to identify peptide sequences to which antibody of the

XX invention (Mab 96-110) bound strongly. The translated sequences provide

XX lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

XX Sequence 19 AA;

XX Query Match 100.0%; Score 15; DB 20; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-08;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHNRHRIPLQLAAGR 15

DB 3 MHNRHRIPLQLAAGR 17

RESULT 7
AAW94710

ID AAW94710 standard; Protein; 19 AA.

XX AAW94710;

XX 22-APR-1999 (first entry)

XX Sequence 15mer 2-8/0 resulting from 15mer library panning experiment.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;

XX Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

XX Mab 96-110; panning.

XX Staphylococcus sp.

XX MO9857994-A2.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-US12402.

XX 16-JUN-1997; 97US-0049871.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Fischer GW, Schuman RF, Stinson JL, Wong H;

XX MPI: 1999-095329/08.

XX N-PSDB; AAX05536.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used

XX to develop products for the diagnosis, prevention and treatment of

XX infections caused by gram positive bacteria

XX Example 5; Fig 6A-B; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic

XX acid of gram positive bacteria, where the Mab is a chimeric

XX immunoglobulin comprising at least part of a human immunoglobulin

XX constant region and at least part of a non-human immunoglobulin variable

XX region having specificity to lipoteichoic acid of gram positive bacteria.

XX The antibodies bind to whole bacteria and enhance phagocytosis and

XX killing of the bacteria and enhance protection from lethal infection. The

XX antibodies or peptides (encoded by a DNA of the variable region of

XX anti-lipoteichoic acid antibody or characterised by amino acids

XX corresponding to one or more of the complementarity determining regions

XX (CDRs) of the variable region of the antibody) can be used for treating

XX or preventing infections caused by gram positive bacterial infections.

XX Sequences AAW94705-22 represent common peptide sequences resulting from a 15mer library

XX panning second experiment. Three series of panning experiments were

XX conducted to identify peptide sequences to which antibody of the

XX invention (Mab 96-110) bound strongly. The translated sequences provide

XX lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

XX Sequence 19 AA;

XX Query Match 100.0%; Score 15; DB 20; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-08;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHNRHRIPLQLAAGR 15

DB 3 MHNRHRIPLQLAAGR 17

RESULT 8
AAW94721
ID AAW94721 standard; Protein; 19 AA.

XX AAW94721;

XX 22-APR-1999 (first entry)

DE	Sequence 15mer2-19/0 resulting from 15mer library panning experiment.
XX	
KM	Monoclonal antibody: Mab; lipoteichoic acid; gram positive; bacteria;
KM	immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM	Mab 96-110; panning.
XX	
OS	Staphylococcus sp.
XX	
PN	MO9857994-A2.
XX	
PD	23-DEC-1998.
XX	
PF	16-JUN-1998; 98WO-US12402.
XX	
PR	16-JUN-1997; 97US-0049871.
XX	
PA	(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX	
PI	Fischer GW, Schuman RF, Stinson JL, Wong H;
DR	WPI; 1999-095329/08.
DR	N-PSDB; AAX05547.
XX	
PT	New antibodies to lipoteichoic acid of gram positive bacteria - used
PT	to develop products for the diagnosis, prevention and treatment of
XX	
PS	infections caused by gram positive bacteria
XX	
PS	Example 5; Fig 6A-B; 150pp; English.
XX	
CC	The invention relates to a monoclonal antibody (Mab) to lipoteichoic
CC	acid of gram positive bacteria, where the Mab is a chimeric
CC	immunoglobulin comprising at least part of a human immunoglobulin
CC	constant region and at least part of a non-human immunoglobulin variable
CC	region having specificity to lipoteichoic acid of gram positive bacteria.
CC	The antibodies bind to whole bacteria and enhance phagocytosis and
CC	killing of the bacteria and enhance protection from lethal infection. The
CC	antibodies or peptides (encoded by a DNA of the variable region of
CC	anti-lipoteichoic acid antibody or characterised by amino acids
CC	corresponding to one or more of the complementarity determining regions
CC	(CDRs) of the variable region of the antibody) can be used for treating
CC	or preventing infections caused by gram positive bacteria. They can also
CC	be used for the diagnosis of gram positive bacterial infections.
CC	Sequences AAW94705-22 represent sequences resulting from a 15mer library
CC	panning second experiment. Three series of panning experiments were
CC	conducted to identify peptide sequences to which antibody of the
CC	invention (Mab 96-110) bound strongly. The translated sequences provide
CC	lipoteichoic acid epitope peptide mimics to which Mabs6-110 bound.
XX	
SO	Sequence 19 AA:
XX	
Query Match	100.0%; Score 15; DB 20; Length 19;
Best Local Similarity	100.0%; Pred. No. 1,7e-08;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 WHWRRHRIPLQLAAGR 15
DB	3 WHWRRHRIPLQLAAGR 17
XX	
RESULT 9	
AAW94705	
ID	AAW94705 standard; Protein; 19 AA.
XX	
AC	AAW94705;
XX	
DT	22-APR-1999 (first entry)
XX	
DE	Sequence 15mer2-1/0 resulting from 15mer library panning experiment.
XX	
KM	Monoclonal antibody: Mab; lipoteichoic acid; gram positive; bacteria;
KM	immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM	Mab 96-110; panning.
XX	

OS	Staphylococcus sp.
XX	
PN	W09857994-A2.
XX	
PD	23-DEC-1998.
XX	
PF	16-JUN-1998; 98WO-US12402.
XX	
PR	16-JUN-1997; 97US-0049871.
XX	
PA	(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX	
PI	Fischer GW, Schuman RF, Stinson JL, Wong H;
XX	
DR	WPI; 1999-095329/08.
XX	N-PSDB; AAX05531.
PT	New antibodies to lipoteichoic acid of gram positive bacteria - used
PX	to develop products for the diagnosis, prevention and treatment of
XX	infections caused by gram positive bacteria
PS	Example 5: Fig 6A-B; 150pp; English.
XX	
CC	The invention relates to a monoclonal antibody (Mab) to lipoteichoic
CC	acid of gram positive bacteria, where the Mab is a chimeric
CC	immunoglobulin comprising at least part of a human immunoglobulin
CC	constant region and at least part of a non-human immunoglobulin variable
CC	region having specificity to lipoteichoic acid of gram positive bacteria.
CC	The antibodies bind to whole bacteria and enhance phagocytosis and
CC	killing of the bacteria and enhance protection from lethal infection. The
CC	antibodies or peptides (encoded by a DNA of the variable region of
CC	anti-lipoteichoic acid antibody or characterised by amino acids
CC	(CPRS) of the variable region of the complementarity determining regions
CC	or preventing infections caused by gram positive bacteria. They can also
CC	be used for the diagnosis of gram positive bacterial infections.
CC	Sequences AAW94705-22 represent sequences resulting from a 15mer library
CC	panning second experiment. Three series of panning experiments were
CC	conducted to identify peptide sequences to which antibody of the
CC	invention (Mab 96-110) bound strongly. The translated sequences provide
CC	lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
XX	
SQ	Sequence 19 AA:
	Query Match 100.0%; Score 15; DB 20; Length 19;
	Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 WHRRHRIPQLAAGR 15
DB	3 WHRRHRIPQLAAGR 17
RESULT 10	
ID	AAW94709
XX	AAW94709 standard; Protein; 19 AA.
AC	AAW94709;
XX	
DT	22-APR-1999 (first entry)
XX	
DE	Sequence 15mer2-7/0 resulting from 15mer library panning experiment.
XX	
KM	Monoclonal antibody: Mab; lipoteichoic acid; gram positive; bacteria;
KW	Immunoglobulin; Phagocytosis; Infection; epitope; peptide mimic;
XX	Mab 96-110; panning.
OS	Staphylococcus sp.
XX	
PN	W09857994-A2.
XX	
PD	23-DEC-1998.
XX	

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PF 16-JUN-1998: 98WO-US12402.
XX
PR 16-JUN-1997: 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
DR WPI; 1999-095329/08.
DR N-PSDB; AAX05535.
XX
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Example 5; Fig 6A-B; 150pp; English.
XX
CC The invention relates to a monoclonal antibody (MAb) to lipoteichoic
CC acid of gram positive bacteria, where the MAb is a chimeric
CC immunoglobulin comprising at least part of a human immunoglobulin
CC constant region and at least part of a non-human immunoglobulin variable
CC region having specificity to lipoteichoic acid of gram positive bacteria.
CC The antibodies bind to whole bacteria and enhance phagocytosis and
CC killing of the bacteria and enhance protection from lethal infection. The
CC antibodies or peptides (encoded by a DNA of the variable region of
CC anti-lipoteichoic acid antibody or characterised by amino acids
CC corresponding to one or more of the complementarity determining regions
CC (CDRs) of the variable region of the antibody) can be used for treating
CC or preventing infections caused by gram positive bacteria. They can also
CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAW94703-22 represent sequences resulting from a 15mer library
CC panning second experiment. Three series of panning experiments were
CC conducted to identify peptide sequences to which antibody of the
CC invention (Mab 96-110) bound strongly. The translated sequences provide
CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
XX
SQ Sequence 19 AA:
Query Match 100.0%; Score 15; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHMHRIRIQLAAGR 15
   |||||
DB 3 WHMHRIRIQLAAGR 17

RESULT 11
AAW12287
ID AAW12287 standard; peptide; 37 AA.
XX
AC AAW12287;
XX
DT 15-APR-1997 (first entry)
XX
DE Synthetic template peptide for overlapping peptide series.
XX
KM Toxoplasma gondii; surface protein; antibody; screening; peptide library;
KM diagnostic assay; immunisation; phage; fusion protein; envelop.
XX
OS Synthetic.
XX
PN EF724016-A1.
XX
PD 31-JUL-1996.
XX
PF 29-JAN-1996: 96EP-0420030.
XX
PR 30-JAN-1995: 95FR-0001297.
XX
PA (JOLI/) JOLIVET-REYNAUD C.
PA (INMR) BIO MERIEUX.
XX

```

```

PI Jolivet-Reynaud C;
XX
DR WPI; 1996-343531/35.
XX
PT New polypeptide reactive with anti-P30 antibodies against Toxoplasma
PT gondii - useful for diagnosis or immunisation, also new nucleic
PT acid, vectors and transformed cells
XX
PS Example 5; Page 9; 33pp; French.
XX
CC The invention relates to novel peptides which bind to antibodies which
CC recognise the Toxoplasma gondii P30 envelop protein. A peptide library
CC was generated to express pentadecapeptides on the surface of a
CC filamentous phage as a fusion protein with the PIII protein. The library
CC was screened with immobilised anti-T. gondii P30 protein antibody 1E17.
CC Phages which bind this antibody were recovered and amplified by one
CC round of infection in E. coli. The resultant phages were rescreened with
CC the immobilised antibody and the second round screen isolated 58
CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA
CC from 30 colonies was isolated and sequenced to determine the sequence of
CC the pentadecapeptide encoded. The peptide sequences AAW12276-86 were
CC identified. Of the 30 colonies studied, this peptide sequence was
CC encoded once. A template peptide sequence (AAW12287) corresponding to
CC the sequence across the phage PIII sequence and putative
CC pentadecapeptide was used to generate a series of overlapping
CC pentadecapeptides. These peptides were used to determine the best
CC peptide sequence which binds the 1E17 antibody. Peptides AAW03367-75
CC were isolated. The new peptides can then be used in diagnostic assays to
CC detect T. gondii antibodies in a sample or to purify anti-P30 antibodies
CC or for active immunisation against T. gondii.
XX
SQ Sequence 37 AA:
Query Match 100.0%; Score 15; DB 17; Length 37;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHMHRIRIQLAAGR 15
   |||||
DB 10 WHMHRIRIQLAAGR 24

RESULT 12
AAW94708
ID AAW94708 standard; Protein; 19 AA.
XX
AC AAW94708;
XX
DT 22-APR-1999 (first entry)
XX
DE Sequence 15mer2-5/0 resulting from 15mer library panning experiment.
XX
KM Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
KM immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM Mab 96-110; Panning.
XX
OS Staphylococcus sp.
XX
PN W09857994-A2.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998: 98WO-US12402.
XX
PR 16-JUN-1997: 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
DR WPI; 1999-095329/08.
DR N-PSDB; AAX05534.
XX

```

PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT Infections caused by gram positive bacteria
 XX
 XX Example 5; Flg 6A-B; 150pp; English.
 PS
 CC The invention relates to a monoclonal antibody (MAb) to lipoteichoic
 CC acid of gram positive bacteria, where the MAb is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-72 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 CC
 XX
 SQ Sequence 19 AA:
 Query Match 93.3%; Score 14; DB: 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 HMRHRIPQLAAGR 15
 |||||
 DB 4 HMRHRIPQLAAGR 17
 RESULT 13
 AAW03372
 ID AAW03372 standard; peptide: 11 AA.
 XX
 AC AAW03372:
 XX
 DT 15-APR-1997 (first entry)
 XX
 DE Peptide #6 which binds anti-Toxoplasma gondii P30 antibody.
 XX
 KW Toxoplasma gondii; surface protein; antibody; screening; peptide library;
 KW diagnostic assay; immunisation; phage; E.coli.
 XX
 OS Synthetic.
 XX
 PN EP724016-A1.
 XX
 PD 31-JUL-1996.
 XX
 PE 29-JAN-1996; 96EP-0420030.
 XX
 PR 30-JAN-1995; 95FR-0001297.
 XX
 PA (JOLI/) JOLIVET-REYNAUD C.
 PA (INMR) BIO MERIEUX.
 XX
 PI Jolivet-Reynaud C;
 XX
 DR WPI; 1996-343531/35.
 DR N-PSDB; AAT31328.
 XX
 PT New polypeptide reactive with anti-P30 antibodies against Toxoplasma
 PT gondii - useful for diagnosis or immunisation, also new nucleic
 PT acid, vectors and transformed cells
 XX
 PS Claim 7; Page 19; 33pp; French.
 XX

CC Peptides AAW03367-75 are peptides isolated from a peptide library, which
 CC bind to antibody 1E1E7 which recognises the P30 surface protein from
 CC Toxoplasma gondii. The peptide library was constructed by inserting a
 CC nucleic acid sequence encoding a random pentadecapeptide in the P30
 CC envelope protein of a filamentous phage. Antibody 1E1E7 was immobilised
 CC on the bottom of a Petri dish and the expressed peptide library was
 CC overlaid on the antibody. After washing, phages bound on the antibodies
 CC were recovered and the phage amplified by passage through E. coli. The
 CC phages were rescreened by the same method and 58 bacterial colonies were
 CC recovered. Of these, 30 were further studied and the nucleic acid
 CC encoding the pentadecapeptide was isolated. The nucleic acids encoded
 CC the peptides AAW12276-86. A series of overlapping peptides based on the
 CC peptide template AAW12287 was constructed to identify which peptide
 CC sequences bound to the anti-P30 antibody. The peptide scanning isolated
 CC peptides AAW03367-75. The peptides can then be used in diagnostic
 CC assays to detect T. gondii antibodies in a sample or to purify anti-P30
 CC antibodies or for active immunisation against T. gondii.
 CC
 XX
 SQ Sequence 11 AA:
 Query Match 73.3%; Score 11; DB: 17; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 HRIPQLAAGR 15
 |||||
 DB 1 HRIPQLAAGR 11
 RESULT 14
 AAW03374
 ID AAW03374 standard; peptide: 15 AA.
 XX
 AC AAW03374:
 XX
 DT 15-APR-1997 (first entry)
 XX
 DE Peptide #8 which binds anti-Toxoplasma gondii P30 antibody.
 XX
 KW Toxoplasma gondii; surface protein; antibody; screening; peptide library;
 KW diagnostic assay; immunisation; phage; E.coli.
 XX
 OS Synthetic.
 XX
 PN EP724016-A1.
 XX
 PD 31-JUL-1996.
 XX
 PE 29-JAN-1996; 96EP-0420030.
 XX
 PR 30-JAN-1995; 95FR-0001297.
 XX
 PA (JOLI/) JOLIVET-REYNAUD C.
 PA (INMR) BIO MERIEUX.
 XX
 PI Jolivet-Reynaud C;
 XX
 DR WPI; 1996-343531/35.
 DR N-PSDB; AAT31330.
 XX
 PT New polypeptide reactive with anti-P30 antibodies against Toxoplasma
 PT gondii - useful for diagnosis or immunisation, also new nucleic
 PT acid, vectors and transformed cells
 XX
 PS Claim 7; Page 20; 33pp; French.
 XX
 CC Peptides AAW03367-75 are peptides isolated from a peptide library, which
 CC bind to antibody 1E1E7 which recognises the P30 surface protein from
 CC Toxoplasma gondii. The peptide library was constructed by inserting a
 CC nucleic acid sequence encoding a random pentadecapeptide in the P30
 CC envelope protein of a filamentous phage. Antibody 1E1E7 was immobilised
 CC on the bottom of a Petri dish and the expressed peptide library was
 CC overlaid on the antibody. After washing, phages bound on the antibodies

CC were recovered and the phage amplified by passage through *E. coli*. The
CC phages were rescreened by the same method and 58 bacterial colonies were
CC recovered. Of these, 30 were further studied and the nucleic acid
CC encoding the pentadecapeptide was isolated. The nucleic acids encoded
CC the peptides AWM12276-86. A series of overlapping peptides based on the
CC peptide template AWM12287 was constructed to identify which peptide
CC sequences bound to the anti-P30 antibody. The peptide scanning isolated
CC peptides AAW03367-75. The peptides can then be used in diagnostic
CC assays to detect *T. gondii* antibodies in a sample or to purify anti-P30
CC antibodies or for active immunisation against *T. gondii*.
XX
SO Sequence 15 AA:
Query Match 73.3%; Score 11; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 HRIPQLAAGR 15
DB 1 HRIPQLAAGR 11
RESULT 15
ABB83482
ID ABB83482 standard; Protein; 529 AA.
XX
AC ABB83482;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human cytoskeleton-associated protein, CSAP-11.
XX
KW Human: cytoskeleton-associated protein; CSAP; CSAP-11;
KW cell proliferative disorder; viral infection; neurological disorder;
KW transgenic animal; antiatherosclerotic; antiproliferative; antiinflammatory;
KW virucide; anticonvulsant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; cytoskeletal.
XX
OS Homo sapiens.
XX
PN W0200253719-A2.
XX
PD 11-JUL-2002.
XX
PF 04-JAN-2002; 2002WC-US00178.
XX
PR 04-JAN-2001; 2001US-260085P.
PR 13-FEB-2001; 2001US-268554P.
PR 14-FEB-2001; 2001US-269111P.
PR 23-FEB-2001; 2001US-271211P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lu DAM, Baughn MR, Yao MG, Ding L, Honchell CD, Yue H, Tang YT;
PI Warren BA, Duggan BM, Xu Y, Walla NK, Griffin JA, Stewart EA;
PI Gandhi AR, Khan FA, Thangavelu K, Ison CH, Azimzal Y, Hattalia AJA;
PI Gietzen KJ, Lai PG, Sanjanwala MM, Elliott VS;
XX
DR WPI: 2002-583611/62.
DR N-PSDB; ABB85320.
XX
XX
PT Novel isolated human cytoskeleton-associated protein for diagnosing,
PT treating or preventing atherosclerosis, psoriasis, leukemia, epilepsy,
PT ischemic cerebrovascular disease, cerebral neoplasms and Alzheimer's
PT disease
XX
PS Claim 1; Page 134-135; 167pp; English.
XX
CC The present sequence is the protein sequence for a human
CC cytoskeleton-associated protein (CSAP). The CSAP and its coding sequence
CC are useful in the diagnosis, treatment and prevention of a cell
CC proliferative disorder such as actinic keratosis, atherosclerosis,
CC psoriasis, primary thrombocythaemia, leukaemia; a viral infection such as

CC those caused by adenoviruses (acute respiratory disease, pneumonia),
CC arenaviruses (lymphocytic choriomeningitis); and a neurological disorder
CC such as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral
CC neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease or
CC amyotrophic lateral sclerosis. The CSAP coding sequence is also useful
CC for creating knock out or knock in humanised animals or transgenic
CC animals to model human diseases.
XX
SO Sequence 529 AA:
Query Match 46.7%; Score 7; DB 23; Length 529;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 LQLAAGR 15
DB 332 LQLAAGR 338
Search completed: November 27, 2002, 07:27:57
Job time : 7.32819 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:25:20 : Search time 2.25869 Seconds
(without alignments)
638.431 Million cell updates/sec

Title: US-09-893-615-2

Perfect score: 15

Sequence: 1 MWMRRIRPLQLAAGR 15

Scoring table: OLIGO

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	40.0	82	B83740	hypothetical prote
2	6	40.0	111	H91187	hypothetical prote
3	6	40.0	142	S57954	probable molybdenu
4	6	40.0	203	F69381	flagellin (flaB1-1
5	6	40.0	220	S60210	fomA protein - Str
6	6	40.0	254	H69057	hypothetical prote
7	6	40.0	309	AB3446	hypothetical expor
8	6	40.0	330	D87068	hypothetical prote
9	6	40.0	334	D95982	hypothetical prote
10	6	40.0	342	S50400	hypothetical expor
11	6	40.0	344	D75486	hypothetical prote
12	6	40.0	347	JC5788	probable UDP-glucos
13	6	40.0	367	1	tsec-1 protein (A
14	6	40.0	413	2	DNM-directed DNA p
15	6	40.0	413	2	alpha-1-antitrypsin
16	6	40.0	413	2	alpha-1-antitrypsin
17	6	40.0	440	2	lysine carboxypept
18	6	40.0	450	2	phosphotransferase
19	6	40.0	492	2	conserved hypotet
20	6	40.0	510	2	conserved hypotet
21	6	40.0	522	2	lysine carboxypept
22	6	40.0	536	2	lysine carboxypept
23	6	40.0	558	2	phosphotransferase
24	6	40.0	585	2	conserved hypotet
25	6	40.0	603	2	glucose inhibited
26	6	40.0	666	2	glucose inhibited
27	6	40.0	691	2	sporulation protei
28	6	40.0	778	2	hypothetical prote
29	6	40.0	803	2	hypothetical prote

30	6	40.0	1111	2	T01239	hypothetical prote
31	6	40.0	1144	2	A81983	probable DNA-direc
32	6	40.0	1144	2	H81037	DNA polymerase III
33	6	40.0	1937	2	T03224	probable polyketid
34	5	33.3	18	2	PT0239	Ig heavy chain CDR
35	5	33.3	26	2	H90667	hypothetical prote
36	5	33.3	29	2	S03947	hydrogen dehydroge
37	5	33.3	65	2	AF2770	hypothetical prote
38	5	33.3	70	2	A69842	hypothetical prote
39	5	33.3	77	2	A83548	transcription regu
40	5	33.3	79	2	T20201	hypothetical prote
41	5	33.3	81	2	AG0142	molybdopterin (mpt
42	5	33.3	81	2	T10320	hypothetical prote
43	5	33.3	84	2	E70841	hypothetical prote
44	5	33.3	93	2	D6497	hypothetical prote
45	5	33.3	93	2	A72126	hypothetical prote

ALIGNMENTS

RESULT 1

B83740
hypothetical protein BH0722 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B83740
R:Takami, H.; Nakasone, K.; Takaki, Y.; Meeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H.
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <STO>
A:Cross-references: GB:BA001509; GB:BA000004; MID:g10173176; PIDN:BA804441.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0722

Query Match 40.0%; Score 6; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAAG 14
DB 18 LQLAAG 23

RESULT 2

H91187
hypothetical protein ECS4472 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: H91187
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasaara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <HAV>
A:Cross-references: PIDN:BA000007; PIDN:BA837895.1; PID:g13363947; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS4472

Query Match 40.0%; Score 6; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PLOLAA 13
|||||
Db 89 PLOLAA 94

RESULT 3

S57954

probable molybdenum-pterin-binding-protein - Azotobacter vinelandii

C:Species: Azotobacter vinelandii

C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999

C:Accession: S57954

R:Mouncey, N.J.; Mitchenell, L.A.; Pau, R.N.

submitted to the EMBL Data Library, June 1995

A:Description: Mutational analysis of genes of the mod locus involved in molybdate trans

A:Reference number: S57954

A:Accession: S57954

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <MOU>

A:Cross-references: EMBL:249882; NID:g899220; PIDN:CAA90038.1; PID:g899221

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 142;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAAG 14
|||||
Db 47 LQLAAG 52

RESULT 4

F69381

flagellin (flaB1-1) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999

C:Accession: F69381

R:Klen, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sultmon, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uitterlind, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MID:98049343; PMID:9389475

A:Accession: F69381

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-203 <MLE>

A:Cross-references: GB:AE001030; GB:AE000782; NID:g2689353; PIDN:AAB90186.1; PID:g264953

C:Superfamily: archaeal flagellin

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 203;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAAG 14
|||||
Db 85 LQLAAG 90

RESULT 5

S60210

foma protein - Streptomyces wedmorensis

C:Species: Streptomyces wedmorensis

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2002

C:Accession: S60210

R:Hidaka, T.; Goda, M.; Kuzuyama, T.; Takai, N.; Hidaka, M.; Seto, H.

Mol. Gen. Genet. 249, 274-280, 1995

A:Title: Cloning and nucleotide sequence of fosfomycin biosynthetic genes of Streptomyces

A:Reference number: S60207; MID:96091152; PMID:7500951

A:Accession: S60210

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-220 <HID>
A:Cross-references: EMBL:038561; NID:g1060999; PID:g1061005
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Gene: foma

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 220;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PLOLAA 13
|||||
Db 53 PLOLAA 58

RESULT 6

H69057

hypothetical protein MTH1434 - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000

C:Accession: H69057

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.

; Ott, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,

Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MID:98037514; PMID:9371463

A:Accession: H69057

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-254 <MTH>

A:Cross-references: GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAB85909.1; PID:g262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1434

A:Start codon: GTG

C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH1434

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 254;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAAG 14
|||||
Db 196 LQLAAG 201

RESULT 7

AB3446

hypothetical exported protein BME11552 (imported) - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AB3446

R:DelVecchio, V.G.; Kapetral, V.; Redkar, R.J.; Patra, G.; Muter, C.; Los, T.; Ivanov

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lec

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A:Reference number: AD3252; PMID:11756688

A:Accession: AB3446

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-309 <KUR>

A:Cross-references: GB:AE008917; PIDN:AAL52733.1; PID:g17983563; GSPDB:GNO0190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME11552

A:Map position: I

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 309;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RPLQL 11

Db 251 R1P1QL 256

RESULT 8

hypothetical protein ML1274 (imported) - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87068
R: Cole, S.T.; Eigmeier, K.; Parhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R: Davis, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A: Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sg
A: Title: Massive gene decay in the leprosy bacillus.
A: Reference number: A86909; M0ID:21128732; PMID:11234002
A: Accession: D87068
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-330 <STO>
A: Cross-references: GB:AL450380; M0ID:913093207; PIDN:CAC31655.1; GSPDB:GN00147
C: Genetics:
A: Gene: ML1274

Query Match 40.0%; Score 6; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 R1R1PL 9
Db 121 R1R1PL 126

RESULT 9

hypothetical exported protein (imported) - Sinorhizobium meliloti (strain 1021) magaplas
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: D95982
R: Finn, T.M.; Weldner, S.; Wong, K.; Buhrmaster, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A: Title: The complete sequence of the 1.683-kb PSYMB megaplasmid from the N2-fixing endo
A: Reference number: A95842; M0ID:21396508; PMID:11481431
A: Accession: D95982
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-334 <KUR>
A: Cross-references: GB:AL591985; PIDN:CAC49524.1; PID:915141011; GSPDB:GN00167
A: Experimental source: strain 1021, megaplasmid psymb
R: Gallibert, F.; Finn, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A: Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hepault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welis, D.H.; Wong, K.; Yeh, K.
A: Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A: Reference number: A96039; M0ID:21368234; PMID:11474104
A: Contents: annotation
C: Genetics:
A: Gene: SMB20998
A: Genome: plasmid

Query Match 40.0%; Score 6; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 R1P1QL 11
Db 276 R1P1QL 281

RESULT 10

S50400
hypothetical protein YMR144w - yeast (Saccharomyces cerevisiae)
N: Alternate names: hypothetical protein YK375.13
C: Species: Saccharomyces cerevisiae
C: Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C: Accession: S50400
R: Radcock, K.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A: Reference number: S50388
A: Accession: S50400
A: Molecule type: DNA
A: Residues: 1-342 <BAD>
A: Cross-references: EMBL:247071; M0ID:9606429; PIDN:CA87358.1; PID:9606442; GSPDB:GNC
C: Genetics:
A: Gene: MIPS:YMR144w
A: Cross-references: SGD:S0004752
A: Map position: 13R

Query Match 40.0%; Score 6; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQ1AAG 14
Db 274 LQ1AAG 279

RESULT 11

probable UDP-glucose 4-epimerase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75486
R: White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A: Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A: Reference number: A75250; M0ID:20036896; PMID:10567266
A: Accession: D75486
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-344 <WHI>
A: Cross-references: GB:AE001927; GB:AE000513; M0ID:96458409; PIDN:AF10287.1; PID:9645
A: Experimental source: strain R1
C: Genetics:
A: Gene: DR0711
A: Map position: 1
C: Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolc

Query Match 40.0%; Score 6; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 Q1AAGR 15
Db 210 Q1AAGR 215

RESULT 12

tsec-1 protein (A and B) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 05-Nov-1999
C:Accession: J05788; J05789
R: Chen, L.; Sato, M.; Inoko, H.; Kimura, M.
Biochem. Biophys. Res. Commun. 240, 261-268, 1997
A: Title: Molecular cloning and analysis of novel cDNAs specifically expressed in adult
A: Reference number: J05788; M0ID:98049818; PMID:9388464
A: Accession: J05788
A: Molecule type: mRNA
A: Residues: 1-347 <CHE>
A: Cross-references: DDBJ:AB000619; M0ID:92749770; PIDN:BAA24108.1; PID:d1025015; PID:9

A:Experimental source: testis
A:Accession: J05789
A:Molecule type: mRNA
A:Residues: 1-347 <CH2>
A:Cross-references: DDBJ:AB000619; NID:g2749770; PIDN:BAA24108.1; PID:dl025015; PID:g274
A:Experimental source: testis
C:Comment: This protein plays a role in mammalian spermatogenesis.
F:38-80,201-332/Domain: coiled-coil #status predicted <CDC>

Query Match 40.0%; Score 6; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LQLAGR 15
|||||
DB 36 LQLAGR 41

RESULT 13

DJPS3P
DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Pseudomonas putida
C:Species: Pseudomonas putida
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999
C:Accession: JY0002
R:Fujita, M.Q.; Yoshikawa, H.; Ogasawara, N.
Mol. Gen. Genet. 215, 381-387, 1989
A:Title: Structure of the dnaA region of Pseudomonas putida: conservation among three ba
A:Reference number: JY0002; MUID:89218947; PMID:2540413
A:Accession: JY0002
A:Molecule type: DNA
A:Residues: 1-367 <FUD>
A:Cross-references: GB:X14791; NID:g45689; PIDN:CAA32894.1; PID:g45691
C:Genetics:
A:Gene: dnaA
C:Superfamily: DNA-directed DNA polymerase III beta chain
C:Keywords: DNA replication initiation; nucleotidyltransferase

Query Match 40.0%; Score 6; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAG 14
|||||
DB 284 LQLAG 289

RESULT 14

JX0267
alpha-1-antitrypsin S-1 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C:Accession: JX0267
R:Salto, A.; Sanojara, H.
J. Biochem. 113, 456-461, 1993
A:Title: Rabbit plasma alpha-1-antitrypsin S-1: cloning, sequencing, expression, and
A:Reference number: JX0267; MUID:93293795; PMID:8514734
A:Accession: JX0267
A:Molecule type: mRNA
A:Residues: 1-413 <SAI>
A:Cross-references: GB:D16104; NID:g286191; PIDN:BAA03678.1; PID:g303762
A:Experimental source: liver
A:Note: Part of this sequence, including the amino end of the mature protein, was confir
C:Superfamily: antithrombin III
C:Keywords: glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-413/Product: alpha-1-antitrypsin S-1 #status experimental <MAT>
F:65,102,266/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 40.0%; Score 6; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAG 14

DB 129 LQLAG 134
|||||

RESULT 15

A54968
alpha-1-antitrypsin precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 16-Jul-1999
C:Accession: A54968
R:Ray, B.K.; Gao, X.; Ray, A.
J. Biol. Chem. 269, 22080-22086, 1994
A:Title: Expression and structural analysis of a novel highly inducible gene encoding
A:Reference number: A54968; MUID:94350954; PMID:8071331
A:Accession: A54968
A:Molecule type: preliminary
A:Status: preliminary
A:Residues: 1-413 <RAY>
A:Cross-references: GB:L12139; NID:g405551; PIDN:AAA57133.1; PID:g601905
C:Superfamily: antithrombin III

Query Match 40.0%; Score 6; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAG 14
|||||
DB 129 LQLAG 134

Search completed: November 27, 2002, 07:31:20
Job time : 6.25869 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:36:38 ; Search time 1259.04 Seconds
(without alignments)
7350.598 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318
Sequence: 1 CAAATGTTCTCTCCACTC.....GGACCATGCTGGAATATAGA 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_hg:*
- 3: gb_in:*
- 4: gb_com:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_com:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_un:*
- 28: em_vl:*
- 29: em_vl:*
- 30: em_hg_hum:*
- 31: em_hg_inv:*
- 32: em_hg_other:*
- 33: em_hg_mus:*
- 34: em_hg_pln:*
- 35: em_hg_rtd:*
- 36: em_hg_mam:*
- 37: em_hg_vrt:*
- 38: em_sy:*
- 39: em_hggo_hum:*
- 40: em_hggo_mus:*
- 41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303.6	95.5	321	10	MMIG013
2	301.6	94.8	318	10	AF178620
3	301	94.7	318	10	AF178619
4	300.4	94.5	321	6	AR096128
5	300.4	94.5	321	6	AR210527
6	300.4	94.5	384	6	AR000010
7	300.4	94.5	384	6	AR060923
8	300.4	94.5	384	6	AR211055
9	300.4	94.5	384	6	AR032417
10	300.4	94.5	384	6	BD004717
11	300.4	94.5	9209	6	AR000007
12	300.4	94.5	9209	6	AR060920
13	300.4	94.5	9209	6	AR211052
14	300.4	94.5	9209	6	AR032414
15	300.4	94.5	9209	6	BD004714
16	300.4	94.5	18986	6	AR051652
17	300.4	94.5	18986	6	AR092290
18	298.8	94.0	384	6	AR015962
19	298.8	94.0	1370	10	MUSICKAAR
20	297.2	93.5	9209	6	AR015961
21	295.6	93.0	318	6	AR096196
22	295.6	93.0	318	6	AR210595
23	295.6	93.0	335	6	AR096195
24	295.6	93.0	335	6	AR210594
25	295.6	93.0	403	6	109200
26	295.6	93.0	403	10	MUSICKCNA
27	295.6	93.0	477	10	S76823
28	294.2	92.5	345	10	MUSICKVA2A
29	294	92.5	403	6	105923
30	292.6	92.0	309	10	MMIGVKPA
31	292.4	91.9	302	10	MUSICKAPE
32	290.8	91.4	350	10	AV058906
33	290.8	91.4	384	10	MMU05285
34	290.8	91.4	403	6	108812
35	290.8	91.4	732	6	AS1863
36	290.8	91.4	732	6	AR33237
37	290.8	91.4	732	6	AR085831
38	290.8	91.4	732	6	AR182961
39	289.4	91.0	318	12	AF277092
40	289.4	91.0	765	6	AX057984
41	289.4	91.0	1239	6	AX057945
42	289.4	91.0	1280	6	AX057947
43	288.2	90.6	435	6	A17967
44	288	90.6	360	10	AF029237
45	287.6	90.4	705	6	AB3197

ALIGNMENTS

RESULT 1
LOCUS MMIG013
DEFINITION Mouse hybridoma 2d3 mRNA for Immunoglobulin kappa light chain V region.
ACCESSION X58586 Y00794
VERSION X58586.1 GI:51562
KEYWORDS Ig kappa light chain; Ig variable region; Immunoglobulin.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Meek, K.
TITLE Direct Submission

JOURNAL Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern Medical School, 5323 Harry Hines Blvd. Microbiology, Dallas Texas 75235, USA

REFERENCE 2 (bases 1 to 321)

AUTHORS Meek,K., Hasemann,C., Pollok,B., Alkan,S.S., Bralt,M., Slaoui,M., Urdalo,J. and Capra,J.D.

TITLE Structural characterization of antidiabetic antibodies. Evidence that Ab2s are derived from the germ-line differently than Ab1s

JOURNAL J. Exp. Med. 169 (2), 519-533 (1989)

MEDLINE 89094248

PUBMED 2492056

FEATURES

Source

1..321

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/cell_line="Hybridoma 2D3-K"

1..321

/gene="IG kappa light chain"

<1..>321

/gene="IG kappa light chain"

/note="variable region"

/evidence="experimental"

<1..>321

/gene="IG kappa light chain"

/note="variable region"

/codon_start=1

/product="IG kappa light chain"

/protein_id="CAA1461.1"

/db_xref="GI:938245"

/translation="QIVLSQSPAILLSAPEKYVMTCRASSSVYMHVYQKRGSSPK PWISATSNLASGVPARFSGSGTSLSLTISRYEADNATYYCHOWSSNPPTGGGTR LEIKR"

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/gene="IG kappa light chain"

/product="IG kappa light chain"

/note="variable region"

BASE COUNT 78 a 92 c 80 g 71 t

ORIGIN

Query Match 95.5% Score 303.6; DB 10; Length 321;
Best Local Similarity 97.2%; Pred. NO.3.8e-90;
Matches 309; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CAATTGTTCTCTCCAGTCTCCAGCAATCCTGTCGATCTCCAGGGGAAAGTCA 60
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Db 1 CAATTGTTCTCTCCAGTCTCCAGCAATCCTGTCGATCTCCAGGGGAAAGTCA 60

QY 61 ATGACTTGACAGGGCCAGCTCAAGTGAATTAATGACATGCACTGGTACCAAGCCAGCA 120
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Db 61 ATGACTTGACAGGGCCAGCTCAAGTGAATTAATGACATGCACTGGTACCAAGCCAGCA 120

QY 121 TCTCTCCCAAAACCTGGATTTCGCCACATCAACCTGGCTTCGAGTCCCTGCTGC 180
|||||
Db 121 TCTCTCCCAAAACCTGGATTTCGCCACATCAACCTGGCTTCGAGTCCCTGCTGC 180

QY 181 TTCTAGTGGACATGGGTCTGGAGCTCTTACTCTCTCAACATCAGACAGAGGAGCTGAA 240
|||||
Db 181 TTCTAGTGGACATGGGTCTGGAGCTCTTACTCTCTCAACATCAGAGTGGAGGCTGAA 240

QY 241 GATCTGCGCACTTATTAATGCGCAGCAGTGAAGTAAACCCAGCTTGGAGGGGG 300
|||||
Db 241 GATCTGCGCACTTATTAATGCGCAGCAGTGAAGTAAACCCAGCTTGGAGGGGG 300

QY 301 ACCATGCTGGAATTAAGA 318
|||||
Db 301 ACCATGCTGGAATTAAGA 318

RESULT 2
AF178620 318 bp mRNA linear ROD 22-MAY-2000
LOCUS AF178620
DEFINITION Mus musculus 39-9 Immunoglobulin light chain variable region mRNA,

partial cds.
AF178620
AF178620.1 GI:5853223

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
Puterman,C., Deocharan,B. and Diamond,B.
TITLE Molecular analysis of the autoantibody response in peptide-induced autoimmunity

JOURNAL J. Immunol. 164 (5), 2542-2549 (2000)

MEDLINE 20143847

PUBMED 10679092

REFERENCE 2 (bases 1 to 318)

AUTHORS Puterman,C., Deocharan,B. and Diamond,B.

TITLE Direct Submission

JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA

FEATURES

Source

1..318

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/cell_line="39-9"

/cell_type="hybridoma"

/note="from peptide-immunized mouse"

<1..>318

/note="IG kappa: anti-peptide antibody"

/codon_start=1

/product="Immunoglobulin light chain variable region"

/protein_id="A054373.1"

/db_xref="GI:5853224"

/translation="GIYLFQSPAILLSAPEKYVMTCRASSSVYMHVYQKRGSSPK PWIATSNLASGVPARFSGSGTSLSLTISRYEADNATYYCHOWSSNPPTGGGTR LEIKR"

BASE COUNT 75 a 89 c 81 g 73 t

ORIGIN

Query Match 94.8% Score 301.6; DB 10; Length 318;
Best Local Similarity 97.2%; Pred. NO.1.0e-89;
Matches 307; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AATTGTTCTCTCCAGTCTCCAGCAATCCTGTCGATCTCCAGGGGAAAGTCA 62
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Db 3 AATTGTTCTCTCCAGTCTCCAGCAATCCTGTCGATCTCCAGGGGAAAGTCA 62

QY 63 GACTTGACAGGGCCAGCTCAAGTGAATTAATGACATGCACTGGTACCAAGCCAGATC 122
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Db 63 GACTTGACAGGGCCAGCTCAAGTGAATTAATGACATGCACTGGTACCAAGCCAGATC 122

QY 123 CTCCCAAAACCTGGATTTCGCCACATCAACCTGGCTTCGAGTCCCTGCTGC 182
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Db 123 CTCCCAAAACCTGGATTTCGCCACATCAACCTGGCTTCGAGTCCCTGCTGC 182

QY 183 CAGTGGAGTGGGTCTGGAGCTCTTACTCTCTCAACATCAGACAGAGGAGCTGAGA 242
|||||
Db 183 CAGTGGAGTGGGTCTGGAGCTCTTACTCTCTCAACATCAGAGTGGAGGCTGAGA 242

QY 243 TGCTGCCACTTATTAATGCGCAGCAGTGAAGTAAACCCAGCTTGGAGGGGGAC 302
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Db 243 TGCTGCCACTTATTAATGCGCAGCAGTGAAGTAAACCCAGCTTGGAGGGGGAC 302

QY 303 CATGCTGGAATTAAGA 318
|||||
Db 303 CATGCTGGAATTAAGA 318

RESULT 3
AF178619 318 bp mRNA linear ROD 22-MAY-2000
LOCUS AF178619
DEFINITION Mus musculus 8-3 Immunoglobulin light chain variable region mRNA,

partial cds.
ACCESSION AF178619
VERSION AF178619.1 GI:5853221
KEYWORDS
SOURCE
ORGANISM Mus musculus.
Mus musculus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 318)
AUTHORS Puterman, C., Desocharan, B. and Diamond, B.
TITLE Molecular analysis of the autoantibody response in peptide-induced autoimmunity
JOURNAL J. Immunol. 164 (5), 2542-2549 (2000)
MEDLINE 20143847
PUBMED 10679092
REFERENCE 2 (bases 1 to 318)
AUTHORS Puterman, C., Desocharan, B. and Diamond, B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
FEATURES
source
1. .318
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="8-3"
/cell_type="hybridoma"
/note="from peptide-immunized mouse"
<1. .>318
/note="1Gm kappa; anti-peptide antibody"
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAB54372.1"
/db_xref="GI:3835222"
/translation="KIVISQSPALLSAPGQKVTMTGRASSSVYMLMYQKPPSPK PWISATSNLASGVAPRFSGSGTSYSLTISRVAEDAAATYCCQWSNPFTFGGTR LEIK"
BASE COUNT 76 a 92 c 78 g 72 t
ORIGIN
Query Match 94.7%; Score 301; DB 10; Length 318;
Best Local Similarity 96.8%; Pred. No. 2.8e-89;
Matches 307; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2 AAATGTTCTCTCCAGCTCCAGCAATCCTGTCGATCTCCAGGGAAGGTCAACA 61
DB 2 AAATGTTATCTCCAGCTCCAGCAATCCTGTCGATCTCCAGGGAAGGTCAACA 61
QY 62 TGACTTGAGGGCCAGCTCAAGTGAATTAATGATGATGATGATGATGATGATGAT 121
DB 62 TGACTTGAGGGCCAGCTCCAGTGTCAATGATGATGATGATGATGATGATGAT 121
QY 122 CCTCCCCAAACCTGGAATTCCTGACATCCACCTGCTTGAGAGTCCCTGCTGCT 181
DB 122 CCTCCCCAAACCTGGAATTCCTGACATCCACCTGCTTGAGAGTCCCTGCTGCT 181
QY 182 TCAGTGGAGTGGGCTGGGACCTTACTCTCTACATATAGAGAGAGAGTGAAG 241
DB 182 TCAGTGGAGTGGGCTGGGACCTTACTCTCTACATATAGAGAGAGAGTGAAG 241
QY 242 ATGCTGCACCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
DB 242 ATGCTGCACCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 302 CCATGCTGGAATAAGA 318
DB 302 CCAAGCTGGAATAAAA 318
RESULT 4
AR096128
LOCUS AR096128 321 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 6005091.

AR096128
VERSION AR096128.1 GI:10024649
KEYWORDS
SOURCE
ORGANISM Unknown.
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 321)
AUTHORS Gross, M. Stuart., Nichols, A. John., Padlan, E. Agustin., Patel, A. Haridhai., and Sylvester, D. Robert.
TITLE Nucleic acids encoding immunoglobulin domains
JOURNAL Patent: US 6005091-A 6 21-DEC-1999;
FEATURES
source
1. .321
/organism="unknown"
BASE COUNT 78 a 92 c 79 g 72 t
ORIGIN
Query Match 94.5%; Score 300.4; DB 6; Length 321;
Best Local Similarity 96.5%; Pred. No. 4.5e-89;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 CAAATGTTCTCTCCAGCTCCAGCAATCCTGTCGATCTCCAGGGAAGGTCAACA 60
DB 1 CAAATGTTCTCTCCAGCTCCAGCAATCCTGTCGATCTCCAGGGAAGGTCAACA 60
QY 61 ATGACTTGAGGGCCAGCTCAAGTGAATTAATGATGATGATGATGATGATGATGAT 120
DB 61 ATGACTTGAGGGCCAGCTCAAGTGAATTAATGATGATGATGATGATGATGATGAT 120
QY 121 TCCGCCCAAAACCTGGATTTCTGCAATCCAGCTGGGCTTGGAGTCCCTGCTGGC 180
DB 121 TCCGCCCAAAACCTGGATTTCTGCAATCCAGCTGGGCTTGGAGTCCCTGCTGGC 180
QY 181 TTCAGTGGCAGTGGGCTGGGACCTTACTCTCTACATATAGAGAGAGAGAGAGAG 240
DB 181 TTCAGTGGCAGTGGGCTGGGACCTTACTCTCTACATATAGAGAGAGAGAGAGAG 240
QY 241 GATGCTGCACCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 GATGCTGCACCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 ACCATGCTGGAATAAGA 318
DB 301 ACCATGCTGGAATAAAA 318
RESULT 5
AR210527
LOCUS AR210527 321 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6391299.
ACCESSION AR210527
VERSION AR210527.1 GI:21513278
KEYWORDS
SOURCE
ORGANISM Unknown.
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 321)
AUTHORS Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev., Gross, M. Stuart., Nichols, A. John., Padlan, E. Agustin., Patel, A. Haridhai., and Sylvester, D. Robert.
TITLE Anti-factor IX/Xa antibodies
JOURNAL Patent: US 6391299-A 6 21-MAY-2002;
FEATURES
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BASE COUNT 78 a 92 c 79 g 72 t
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 QY 61 ATGACTTTCAGGGGCGACGCTCAAGTGAATTAATTCATGACAGTGTACAGAGAACCCAGGA 120
 DB 61 ATGACTTTCAGGGGCGACGCTCAAGTGAATTAATTCATGACAGTGTACAGAGAACCCAGGA 120
 QY 121 TCTTCCCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTCTGTGAGTCCCTGCTCGC 180
 DB 121 TCTTCCCCCAAAACCTGGATTTATGCCACATCCAACTGGCTTCTGTGAGTCCCTGCTCGC 180
 QY 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAATCAGCAGAGTGGAGCTGAA 240
 DB 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAATCAGCAGAGTGGAGCTGAA 240
 QY 241 GATGCTGGCCACTTATTACTGCCAGCAGTGGAGTAAGTAAACCACCGTTCCGAGGGGG 300
 DB 241 GATGCTGGCCACTTATTACTGCCAGCAGTGGAGTAAGTAAACCACCGTTCCGAGGGGG 300
 QY 301 ACCATGCTGGAATAAGA 318
 DB 301 ACCATGCTGGAATAAGA 318
 RESULT 6
 ARO00010 384 bp DNA linear PAT 04-DEC-1998
 LOCUS Sequence 6 from patent US 5736137.
 DEFINITION ARO00010
 ACCESSION ARO00010 GI:3962541
 VERSION ARO00010.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 384)
 AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.
 TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
 JOURNAL Patent: US 5736137-A 6 07-APR-1998;
 FEATURES
 source 1..384
 BASE COUNT 92 a 105 c 93 g 94 t
 ORIGIN
 Query Match 94.5%; Score 300.4; DB 6; Length 384;
 Best Local Similarity 96.5%; Pred. No. 4.5e-89;
 Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAGTCTACA 60
 DB 67 CAAATTGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAGTCTACA 126
 QY 61 ATGACTTTCAGGGGCGACGCTCAAGTGAATTAATTCATGACAGTGTACAGAGAACCCAGGA 120
 DB 127 ATGACTTTCAGGGGCGACGCTCAAGTGAATTAATTCATGACAGTGTACAGAGAACCCAGGA 186
 QY 121 TCTTCCCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTCTGTGAGTCCCTGCTCGC 180
 DB 187 TCTTCCCCCAAAACCTGGATTTATGCCACATCCAACTGGCTTCTGTGAGTCCCTGCTCGC 246
 QY 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAATCAGCAGAGTGGAGCTGAA 240
 DB 247 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAATCAGCAGAGTGGAGCTGAA 306
 QY 241 GATGCTGGCCACTTATTACTGCCAGCAGTGGAGTAAGTAAACCACCGTTCCGAGGGGG 300
 DB 307 GATGCTGGCCACTTATTACTGCCAGCAGTGGAGTAAGTAAACCACCGTTCCGAGGGGG 366
 QY 301 ACCATGCTGGAATAAGA 318

DB 367 ACCAAGCTGGAATAAGA 384
 RESULT 7
 ARO60923 384 bp DNA linear PAT 29-SEP-1999
 LOCUS Sequence 6 from patent US 5843439.
 DEFINITION ARO60923
 ACCESSION ARO60923
 VERSION ARO60923.1 GI:5988614
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 384)
 AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.
 TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
 JOURNAL Patent: US 5843439-A 6 01-DEC-1998;
 FEATURES
 source 1..384
 BASE COUNT 92 a 105 c 93 g 94 t
 ORIGIN
 Query Match 94.5%; Score 300.4; DB 6; Length 384;
 Best Local Similarity 96.5%; Pred. No. 4.5e-89;
 Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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 DB 67 CAAATTGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAGTCTACA 126
 QY 61 ATGACTTTCAGGGGCGACGCTCAAGTGAATTAATTCATGACAGTGTACAGAGAACCCAGGA 120
 DB 127 ATGACTTTCAGGGGCGACGCTCAAGTGAATTAATTCATGACAGTGTACAGAGAACCCAGGA 186
 QY 121 TCTTCCCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTCTGTGAGTCCCTGCTCGC 180
 DB 187 TCTTCCCCCAAAACCTGGATTTATGCCACATCCAACTGGCTTCTGTGAGTCCCTGCTCGC 246
 QY 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAATCAGCAGAGTGGAGCTGAA 240
 DB 247 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAATCAGCAGAGTGGAGCTGAA 306
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 DB 307 GATGCTGGCCACTTATTACTGCCAGCAGTGGAGTAAGTAAACCACCGTTCCGAGGGGG 366
 QY 301 ACCATGCTGGAATAAGA 318
 DB 367 ACCAAGCTGGAATAAGA 384
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 AR211055 384 bp DNA linear PAT 20-JUN-2002
 LOCUS Sequence 6 from patent US 6399061.
 DEFINITION AR211055
 ACCESSION AR211055
 VERSION AR211055.1 GI:21514275
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 384)
 AUTHORS Anderson,D.R., Hanna,N., Newman,R.A., Reff,M.E. and Rastetter,W.H.
 TITLE Chimeric and radiolabeled antibodies specific to human CD20 antigen and use thereof for treatment of B-cell lymphoma
 JOURNAL Patent: US 6399061-A 6 04-JUN-2002;
 FEATURES
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Query Match      94.5%; Score 300.4; DB 6; Length 384;
Best Local Similarity 96.5%; Pred. No. 4.5e-89;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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DB 67 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAAGTCA 126
OY 61 ATGACTTGAGGGCCAGCTCAAGTGAATTAATACATGCTGTACAGAGCAAGCCAGA 120
DB 127 ATGACTTGAGGGCCAGCTCAAGTGAATTAATACATGCTGTACAGAGCAAGCCAGA 186
OY 121 TCCTCCCCAAACCTGGATTTCTGCACATCAACCTGGCTTTCGAGTCCCTGCTGC 180
DB 187 TCCTCCCCAAACCTGGATTTCTGCACATCAACCTGGCTTTCGAGTCCCTGCTGC 246

OY 241 GATGCTGCCACTTATTACTGCGAGAGTGAATTAACCCAGCTTCGAGGGGG 300
DB 307 GATGCTGCCACTTATTACTGCGAGAGTGAATTAACCCAGCTTCGAGGGGG 366
OY 301 ACCATGCTGGAATAAGA 318
DB 367 ACCAAGCTGGAATCAAA 384

RESULT 9
AX032417
LOCUS AX032417 384 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 6 from Patent EP1005870.
ACCESSION AX032417
VERSION AX032417.1 GI:10279390
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
1 (bases 1 to 384)
Rastetter,W.H., Hanna,N., Leonard,J.E., Newman,R.A., Refl,M.E. and
Anderson,D.R.
TITLE
Therapeutic application of chimeric antibodies to human b
lymphocyte restricted differentiation antigen for treatment of b
cell lymphoma
JOURNAL
Patent: EP 1005870-A 6 07-JUN-2000;
IDEC PHARMA CORP (US)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32644"
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Query Match      94.5%; Score 300.4; DB 6; Length 384;
Best Local Similarity 96.5%; Pred. No. 4.5e-89;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAAGTCA 60
DB 67 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAAGTCA 126
OY 61 ATGACTTGAGGGCCAGCTCAAGTGAATTAATACATGCTGTACAGAGCAAGCCAGA 120
DB 127 ATGACTTGAGGGCCAGCTCAAGTGAATTAATACATGCTGTACAGAGCAAGCCAGA 186
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DB 187 TCCTCCCCAAACCTGGATTTCTGCACATCAACCTGGCTTTCGAGTCCCTGCTGC 246
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OY 181 TTCAGTGGCAGTGGGTCTGGACACTTACTCTCACAATACAGACAGTGGAGCTGAA 240
DB 247 TTCAGTGGCAGTGGGTCTGGACACTTACTCTCACAATACAGACAGTGGAGCTGAA 306
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DB 307 GATGCTGCCACTTATTACTGCGAGAGTGAATTAACCCAGCTTCGAGGGGG 366
OY 301 ACCATGCTGGAATAAGA 318
DB 367 ACCAAGCTGGAATCAAA 384

RESULT 10
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LOCUS BD004717 384 bp DNA linear PAT 31-JAN-2002
DEFINITION Chimeric antibody against human B lymphocyte limited
differentiation antibody for remedy of B cell lymphoma and
therapeutic use of radiolabeled antibody.
ACCESSION BD004717
VERSION BD004717.1 GI:18632678
KEYWORDS JP 2001010974-A/5.
SOURCE
Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 384)
Anderson,D.R., Rastetter,W.H., Hanna,N., Leonard,J.E., Newman,R.A.
and Refl,M.E.
TITLE
Chimeric antibody against human B lymphocyte limited
differentiation antibody for remedy of B cell lymphoma and
therapeutic use of radiolabeled antibody
Patent: JP 2001010974-A 5 16-JAN-2001;
IDEC PHARMACEUTICALS CORP
OS Homo sapiens (human)
PN JP 2001010974-A/5
PD 16-JAN-2001
PF 21-APR-2000 JP 2000126317
PR 13-NOV-1992 US 07/978891.03-NOV-1993 US 08/149099 PI
DURRELL R ANDERSON,WILLIAM H RASTETTER,NABIL HANNA, PI JOHN E
LEONARD,
PI ROWLAND A NEWMAN,MITCHELL E REFF
PC A61K39/395,A61K31/375,A61K31/573,A61K31/664,A61K31/704, PC
A61K45/00,A61P35/00.
PC C07K16/28,C07K16/46,G01N33/33//C12N5/10,C12N5/09,C12P21/02,
PC C12P21/08,
PC (C12P21/02,C12R1:91),(C12P21/08,C12R1:91),C12N5/00,C12N5/00
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match      94.5%; Score 300.4; DB 6; Length 384;
Best Local Similarity 96.5%; Pred. No. 4.5e-89;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAAGTCA 60
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OY 61 ATGACTTGAGGGCCAGCTCAAGTGAATTAATACATGCTGTACAGAGCAAGCCAGA 120
DB 127 ATGACTTGAGGGCCAGCTCAAGTGAATTAATACATGCTGTACAGAGCAAGCCAGA 186
OY 121 TCCTCCCCAAACCTGGATTTCTGCACATCAACCTGGCTTTCGAGTCCCTGCTGC 180
DB 187 TCCTCCCCAAACCTGGATTTCTGCACATCAACCTGGCTTTCGAGTCCCTGCTGC 246
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Db	247	TTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAAATCAGCAGTGGAGGCTGAA	306
Oy	241	GATGCTGCCACTTATTACTGGCAGCAGTGGAGTAGTAACCCACCAGTTCGGAGGGGG	300
Db	307	GATGCTGCCACTTATTACTGGCAGCAGTGGAGTAGTAACCCACCAGTTCGGAGGGGG	366
Oy	301	ACCATGCTGGAAATAGAA 318	
Db	367	ACCAAGCTGGAAATCAAA 384	
RESULT 11			
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DEFINITION	Sequence 3 from patent US 5736137.		Linear
ACCESSION	AR000007		
VERSION	AR000007.1	GI:3962538	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 9209)		
	Anderson, D.R., Hanna, N., Leonard, J.E., Newman, R.A., Reff, M.E. and		
	Rastetter, W.H.		
TITLE	Therapeutic application of chimeric and radiolabeled antibodies to		
	human B lymphocyte restricted differentiation antigen for treatment		
JOURNAL	Patent: US 5736137-A 3 07-Apr-1998;		
FEATURES	Location/Qualifiers		
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Query Match 94.5%; Score 300.4; Db 6; Length 9209;			
Best Local Similarity 96.5%; Pred. No. 4,1e-89;			
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;			
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Oy	61	ATGACTTTCAGAGGCGCAGTCAAGTAAATTAATGACATGCACTGGTACCCAGACAGCCAGCA	120
Db	1105	ATGACTTTCAGAGGCGCAGTCAAGTAAATTAATGACATGCACTGGTTCACAGACAGCCAGCA	1164
Oy	121	TCCTCCCTCCCAAAACCTGGATTTCGCGACATCCAACTGGCTTCTGAGTCCCTGCTCGC	180
Db	1165	TCCTCCCTCCCAAAACCTGGATTTCGCGACATCCAACTGGCTTCTGAGTCCCTGCTCGC	1224
Oy	181	TTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAAATCAGCAGTGGAGGCTGAA	240
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Oy	241	GATGCTGCCACTTATTACTGGCAGCAGTGGAGTAGTAACCCACCAGTTCGGAGGGGG	300
Db	1285	GATGCTGCCACTTATTACTGGCAGCAGTGGAGTAGTAACCCACCAGTTCGGAGGGGG	1344
Oy	301	ACCATGCTGGAAATAGAA 318	
Db	1345	ACCAAGCTGGAAATCAAA 1362	
RESULT 12			
LOCUS	AR060920	9209 bp	DNA
DEFINITION	Sequence 3 from patent US 5843439.		Linear
ACCESSION	AR060920		
VERSION	AR060920.1	GI:5988611	

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 9209) Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Refl,M.E. and Rastetter,W.H.
TITLE	Therapeutic application of chimeric and radiolabelled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
JOURNAL	Patent: US 5843439-A 3 01-DEC-1998;
FEATURES	Location/Qualifiers 1..9209
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Query Match	94.5%; Score 300.4; DB 6; Length 9209;
Best Local Similarity	96.5%; Pred. No. 4,1e-89;
Matches 307; Conservative	0; Mismatches 11; Indels 0; Gaps 0;
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Db	1105 ATGACTTCAGAGGGCCAGCTCAAGTAAATTACATGCATGCTGTACCCAGACAGCA 1164
OY	121 TCCTCCCCCAACCTCGATTTCTGCCACATCCAACTGGCTTCTGAGTCCCTGCTGC 180
Db	1165 TCCTCCCCCAACCTCGATTTCTGCCACATCCAACTGGCTTCTGAGTCCCTGCTGC 1224
OY	181 TTCAGTGGAGAGGGGTCTGGAGACTCTTACTCTTCACATGACGACAGATGAGGCTGA 240
Db	1225 TTCAGTGGAGAGGGGTCTGGAGACTCTTACTCTTCACATGACGACAGATGAGGCTGA 1284
OY	241 GATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCACCCAGTTGCGAGGGGG 300
Db	1285 GATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCACCCAGTTGCGAGGGGG 1344
OY	301 ACCATGCTGGGAATTAAGA 318
Db	1345 ACCAAGCTGGGAATCAAA 1362
RESULT 13	
LOCUS	AR211052 9209 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 3 from patent US 6399061.
ACCESSION	AR211052
VERSION	AR211052.1 GI:21514272
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 9209) Anderson,D.R., Hanna,N., Newman,R.A., Refl,M.E. and Rastetter,W.H.
TITLE	Chimeric and radiolabelled antibodies specific to human CD20 antigen and use thereof for treatment of B-cell lymphoma
JOURNAL	Patent: US 6399061-A 3 04-JUN-2002;
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Query Match	94.5%; Score 300.4; DB 6; Length 9209;
Best Local Similarity	96.5%; Pred. No. 4,1e-89;
Matches 307; Conservative	0; Mismatches 11; Indels 0; Gaps 0;
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Db 1105 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCTGTACCAGCAGAACCCAGCA 1164
QY 121 TCCTCCCCCAAAACCTGGATTTCTGTCACATCCAGCTGGCTTGGAGTCCCTGCTGC 180
Db 1165 TCCTCCCCCAAAACCTGGATTTATGTCACATCCAGCTGGCTTGGAGTCCCTGCTGC 1224
QY 181 TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGAGAGTGGAGCTGAA 240
Db 1225 TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGAGAGTGGAGCTGAA 1284
QY 241 GATGCTGCCACTTATTACTGCGCAGAGTGAAGTAAACCCACCCAGCTTGGAGGGGG 300
Db 1285 GATGCTGCCACTTATTACTGCGCAGAGTGAAGTAAACCCACCCAGCTTGGAGGGGG 1344
QY 301 ACCATGCTGGAATAAGA 318
Db 1345 ACCAAGCTGGAATAATCAAA 1362

RESULT 14
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LOCUS AX032414
DEFINITION Sequence 3 from Patent EP1005870.
ACCESSION AX032414
VERSION AX032414.1 GI:10279387
KEYWORDS
ORGANISM unidentified.
SOURCE unclassified.
REFERENCE 1 (bases 1 to 9209)
AUTHORS Rastetter,W.H., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and
TITLE Therapeutic application of chimeric antibodies to human b
lymphocyte restricted differentiation antigen for treatment of b
cell lymphoma
JOURNAL Patent: EP 1005870-A 3 07-JUN-2000;
IDEC PHARMA CORP (US)
FEATURES
source 1..9209
Location/Qualifiers:
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/db_xref="taxon:32644"
BASE COUNT 2239 a 2397 c 2390 g 2183 t
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Best Local Similarity 96.5%; Pred. No. 4,1e-89;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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RESULT 15
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LOCUS BD004714
DEFINITION 9209 bp DNA linear PAT 31-JAN-2002
Chimeric antibody against human B lymphocyte limited
differentiation antibody for remedy of B cell lymphoma and
therapeutic use of radiolabeled antibody.
ACCESSION BD004714
VERSION BD004714.1 GI:18632675
KEYWORDS JP 2001010974-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 9209)
AUTHORS Anderson,D.R., Rastetter,W.H., Hanna,N., Leonard,J.E., Newman,R.A.
and Reff,M.E.
TITLE Chimeric antibody against human B lymphocyte limited
differentiation antibody for remedy of B cell lymphoma and
therapeutic use of radiolabeled antibody
Patent: JP 2001010974-A 2 16-JAN-2001;
IDEC PHARMACEUTICALS CORP
COMMENT OS Homo sapiens (human)
PN JP 2001010974-A/2
PD 16-JAN-2001
PE 21-APR-2000 JP 2000126317
PR 13-NOV-1992 US 07/978891, 03-NOV-1993 US 08/149099 PI
DURELL R ANDERSON, WILLIAM H RASTETTER, NABIL HANNA, PI JOHN E
LEONARD,
PI ROWLAND A NEWMAN, MITCHELL E REFF
PC A6IK39/395, A6IK31/375, A6IK31/573, A6IK31/654, A6IK31/704, PC
A6IK45/00, A6IP35/00,
PC C07K16/28, C07K16/46, G01N33/53//C12N5/10, C12N15/09, C12P21/02,
PC C12P21/08,
PC (C12P21/02, C12R1:91), (C12P21/08, C12R1:91), C12N5/00, C12N15/00
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Query Match 94.5%; Score 300.4; DB 6; Length 9209;
Best Local Similarity 96.5%; Pred. No. 4,1e-89;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 301 ACCATGCTGGAAATPAGA 318
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Total number of hits satisfying chosen parameters: 4370478

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- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300.4	94.5	321	18	AAAT77377
2	300.4	94.5	321	24	ABK24004
3	298.8	94.0	384	15	AAO55106
4	298.4	93.8	19001	19	AAV61793
5	297.2	93.5	449	21	AAA43472
6	297.2	93.5	708	21	AAA63530
7	297.2	93.5	9208	15	AAO65629
8	295.6	93.0	318	18	AAAT79000
9	295.6	93.0	318	24	ABK24005

10	295.6	93.0	335	18	AAAT79899
11	295.6	93.0	335	24	ABK24004
12	295.6	93.0	403	8	AAAT70972
13	295.6	93.0	403	10	AAAT91147
14	295.6	93.0	404	22	AAV82358
15	295.6	93.0	404	22	AAH22071
16	295.6	93.0	426	18	AAAT36317
17	295.6	93.0	426	18	AAAT70869
18	295.6	93.0	426	18	AAAT51043
19	295.6	93.0	426	19	AAV03927
20	295.6	93.0	426	19	AAV18558
21	295.6	93.0	426	19	AAV18594
22	293	92.1	387	13	AAO27350
23	293	92.1	1925	21	AAAT15019
24	292.4	91.9	387	13	AAO20983
25	290.8	91.4	732	17	AAAT42508
26	290.8	91.4	732	20	AAV72081
27	289.4	91.0	765	22	AAO68590
28	289.4	91.0	1239	22	AAO68563
29	289.4	91.0	1280	22	AAO68564
30	288.2	90.6	435	12	AAO15115
31	288.2	90.6	435	14	AAO36613
32	287.6	90.4	705	20	AAV72047
33	287.6	90.4	3217	20	AAV72076
34	286.6	90.1	318	24	AAAT91128
35	284	89.3	765	22	AAO68591
36	283.4	89.1	1590	20	AAAT24806
37	281.8	88.6	321	14	AAO39412
38	281.4	88.5	711	15	AAO55106
39	281.4	88.5	711	18	AAAT65080
40	281.2	88.4	758	21	AAAT60937
41	281.2	88.4	759	22	AAO60426
42	280.2	88.1	711	17	AAAT1728
43	280.2	88.1	711	21	AAAT98748
44	278	87.4	321	10	AAAT91661
45	278	87.4	420	12	AAO11970

ALIGNMENTS

RESULT 1	
AAAT77377	
ID	AAAT77377 standard; cDNA: 321 BP.
XX	
AC	AAAT77377;
XX	
DT	26-DEC-1997 (first entry)
XX	
DE	Mouse anti-human Factor IX antibody BC2 light chain cDNA.
XX	
XX	Thrombosis; therapy: Factor IX; anticoagulant; monoclonal antibody;
KW	humanized antibody; antibody engineering; light chain; CDR;
KW	complementarity determining region; myocardial infarction;
KW	angina; atrial fibrillation; stroke; kidney damage;
KW	pulmonary embolism; deep vein thrombosis; coronary angioplasty;
KW	disseminated intravascular coagulation; artificial organ; sepsis;
XX	shunt; prosthesis; ss.
XX	
OS	Mus musculus.
XX	
PN	WO9726010-A1.
XX	
PD	24-JUL-1997.
XX	
PF	17-JAN-1997; 97WO-US00759.
XX	
PR	24-OCT-1996; 96US-0029119.
XX	
PR	17-JAN-1996; 96US-0010108.
XX	
PA	(SMK) SMITHKLINE BEECHAM CORP.
XX	(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

Anti-Factor IX Mab
Murine BC2 light c
2H7 Vh sequence in
2H7 Vh sequence.
Mouse antibody 2H7
2H7 light chain va
2H7 antibody light
2H7 light chain va
Coding sequence fo
Mouse 2H7 antibody
Mouse 2H7 antibody
Mouse 2H7 antibody
Encodes ASB7 antib
DNA encoding a CD-
Encodes Variable r
Murine ASB7 Light
Plasmid pBE14/ASB7
DNA encoding a fus
DNA encoding a fus
Anti-CD20 single c
IL-2 chimeric anti
Anti-IL2R-alpha an
Plasmid pNG3/ASB7V
IRES-based ASB7 ch
Anti-NKG2D hybrido
DNA encoding a fus
ASB7 F(ab')2 codin
Mab32 Light chain
Sequence encoding
Single-chain anti-
Chimeric L6 anti-t
L6 sFv DNA. Unde
Anti-erbB2 scFv CD
Nucleotide sequenc
Chimeric antibody
Sequence encoding

PI Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
PI Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
XX WPI: 1997-385117/35.
DR P-PSDB: AAM24520.
XX
PT Inhibiting thrombosis with self-limiting antibody to coagulation
PT factor - avoids uncontrolled bleeding by providing only partial
PT inhibition
XX
PS Example 5; Page 64; 150pp; English.
XX
CC This cDNA sequence encodes the light chain variable region (see
CC AAM24520) of mouse anti-human factor IX monoclonal antibody BC2.
CC Claimed humanised antibodies (see AAM24510-18) contain CDRs (see
CC AAM24504-09) of BC2 heavy and light chains inserted into framework
CC regions of selected human antibody sequences. They have self-
CC limiting neutralising activity, and are useful as anticoagulant
CC agents in treatment of thrombosis associated with myocardial
CC infarction, unstable angina, atrial fibrillation, stroke, renal
CC damage, pulmonary embolism, deep vein thrombosis, percutaneous
CC transluminal coronary angioplasty, disseminated intravascular
CC coagulation, sepsis, or artificial organs, shunts or prostheses
CC (claimed). Also claimed are chimeric antibodies (see AAT79900), and
CC Fab and Fab')2 fragments. The claimed antibodies do not cause
CC uncontrolled bleeding (contrast heparin and Warfarin) since they
CC provide only partial inhibition of coagulation.
XX
SQ Sequence 321 BP; 78 A; 92 C; 79 G; 72 T; 0 other;
XX
Query Match 94.5%; Score 300.4; DB 18; Length 321;
Best Local Similarity 96.5%; Pred. No. 3.3e-77;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
QY 1 CAAATTTGTCCTCCAGCTCCAGCAATCCTGTCGATCCAGGGGAAAGGTACA 60
Db 1 CAAATTTGTCCTCCAGCTCCAGCAATCCTGTCGATCCAGGGGAAAGGTACA 60
QY 61 ATGACTTGCGAGGGCCAGCTCAAGTAAATTACATGCACTGTGACCAAGCCAGGA 120
Db 61 ATGACTTGCGAGGGCCAGCTCAAGTAAATTACATGCACTGTGACCAAGCCAGGA 120
QY 121 TCCCTCCGCCAACCCTGGATTTCGCCACATCCAGCTGCTTGAGAGTCCCTGCGC 180
Db 121 TCCCTCCGCCAACCCTGGATTTCGCCACATCCAGCTGCTTGAGAGTCCCTGCGC 180
QY 181 TTCAGTGGCAGAGGGGTGGGACCTTTACTCTCTCAACAATCAGCAGAGTGGAGCTGAA 240
Db 181 TTCAGTGGCAGAGGGGTGGGACCTTTACTCTCTCAACAATCAGCAGAGTGGAGCTGAA 240
QY 241 GATGCTGCCACTTATTTACTGCGCAGCAGTGAAGTAAACCCAGCTTGCGAGGGGG 300
Db 241 GATGCTGCCACTTATTTACTGCGCAGCAGTGAAGTAAACCCAGCTTGCGAGGGGG 300
QY 301 ACCATGCTGGAATTAAGA 318
Db 301 ACCAAGCTGGAATTAAGA 318
XX
RESULT 2
ABK23937
ID ABK23937 standard; cDNA; 321 BP.
XX
AC ABK23937;
XX
DT 09-APR-2002 (first entry)
XX
DE Murine BC2 light chain variable region cDNA.
XX
KM Human: mouse; BC2: animal post-thromboembolic induced ischemia;
KM thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss;
KM thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KM vasotropic; cardiant; PCR primer; anti-respiratory syncytial virus;
XX

KM heavy chain variable region; light chain variable region.
XX
OS Mus sp.
XX
PN WO200187339-A1.
XX
PD 22-NOV-2001.
XX
PF 05-OCT-2000; 2000MO-US27438.
XX
PR 15-MAY-2000; 2000US-0571434.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
XX WPI: 2002-082944/11.
DR P-PSDB: AAU80976.
XX
PT Treating post-thromboembolic induced ischemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator -
XX
PS Example 5; Page 94; 163pp; English.
XX
CC The invention relates to a method for treating an animal
CC post-thromboembolic induced ischemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thromboembolic induced
CC ischemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating thromboembolic
CC post-thromboembolic-induced ischemia, for preventing thromboembolic
CC stroke in an animal, and for reducing a required dose of a thrombolytic
CC agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding
CC antibodies and PCR primers used in the method of the invention.
XX
SQ Sequence 321 BP; 78 A; 92 C; 79 G; 72 T; 0 other;
XX
Query Match 94.5%; Score 300.4; DB 24; Length 321;
Best Local Similarity 96.5%; Pred. No. 3.3e-77;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
QY 1 CAAATTTGTCCTCCAGCTCCAGCAATCCTGTCGATCCAGGGGAAAGGTACA 60
Db 1 CAAATTTGTCCTCCAGCTCCAGCAATCCTGTCGATCCAGGGGAAAGGTACA 60
QY 61 ATGACTTGCGAGGGCCAGCTCAAGTAAATTACATGCACTGTGACCAAGCCAGGA 120
Db 61 ATGACTTGCGAGGGCCAGCTCAAGTAAATTACATGCACTGTGACCAAGCCAGGA 120
QY 121 TCCCTCCGCCAACCCTGGATTTCGCCACATCCAGCTGCTTGAGAGTCCCTGCGC 180
Db 121 TCCCTCCGCCAACCCTGGATTTCGCCACATCCAGCTGCTTGAGAGTCCCTGCGC 180
QY 181 TTCAGTGGCAGAGGGGTGGGACCTTTACTCTCTCAACAATCAGCAGAGTGGAGCTGAA 240
Db 181 TTCAGTGGCAGAGGGGTGGGACCTTTACTCTCTCAACAATCAGCAGAGTGGAGCTGAA 240
QY 241 GATGCTGCCACTTATTTACTGCGCAGCAGTGAAGTAAACCCAGCTTGCGAGGGGG 300
Db 241 GATGCTGCCACTTATTTACTGCGCAGCAGTGAAGTAAACCCAGCTTGCGAGGGGG 300
QY 301 ACCATGCTGGAATTAAGA 318
Db 301 ACCAAGCTGGAATTAAGA 318
XX
RESULT 3
AAO65630
ID AAO65630 standard; DNA; 384 BP.
XX
AC AAO65630;
XX

DT	01-FEB-1995	(first entry)	
XX			
DE	Murine variable region light chain from 2B5.		
XX			
KW	B cell lymphoma chimeric antibody; CD20; peripheral blood cells;		
KW	cell lysis; ss.		
XX			
OS	Mus musculus.		
XX			
PN	W09411026-A.		
XX			
PD	26-MAY-1994.		
XX			
PE	12-NOV-1993; 93WO-US10953.		
XX			
PR	13-NOV-1992; 92US-0978891.		
XX			
PR	03-NOV-1993; 93US-0149099.		
XX			
PA	(IDEC-) IDEC PHARM CORP.		
XX			
PI	Anderson DR, Hanna N, Leonard JF, Newman RA, Rastetter WH;		
PI	Refline;		
XX			
DR	WPI; 1994-183162/22.		
XX			
DR	P-PSDB; AAR55214.		
XX			
PT	Treating B cell lymphoma with chimeric antibody - against CD20,		
PT	causing rapid depletion of peripheral B cells, also new		
XX	antibodies and hybridomas		
XX			
PS	Disclosure; Fig 4; 101pp; English.		
XX			
CC	The sequence is the murine variable region light chain derived from		
CC	murine anti-CD20 monoclonal antibody 2B5.		
CC	See also AA065629-35.		
XX			
SO	Sequence 384 BP; 92 A; 106 C; 92 G; 94 T; 0 other;		
	Query Match	94.0%; Score 298.8; DB 15; Length 384;	
	Best Local Similarity	96.2%; Pred. No. 1e-76;	
	Matches	306; Conservative 0; Mismatches 12; Indels 0; Gaps 0;	
OY	1 CAATATTGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGAAAGTCA	60	
DB	67 CAAAATGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGAGAGTCA	126	
OY	61 ATGACTTTCAGAGGGCCAGCTCAAGTGAATTAATCATGATGGTACCAGCAGAACCCAGA	120	
DB	127 ATGACTTTCAGAGGGCCAGCTCAAGTGAATTAATCATGATGGTACCAGCAGAACCCAGA	186	
OY	121 TCTCTCCCCCAACCTGTGATTTCTGCACATCAACCTGGCTTCGAGTCCCTGCTGC	180	
DB	187 TCTCTCCCCCAACCTGTGATTTATGCCACATCAACCTGGCTTCGAGTCCCTGCTGC	246	
OY	181 TTCAGTGGCAGAGGGGTCGAGGACCTTAACTCTCACAAATAGCAGAGTGAAGCTGA	240	
DB	247 TTCAGTGGCAGAGGGGTCGAGGACCTTAACTCTCACAAATAGCAGAGTGAAGCTGA	306	
OY	241 GATGCTGCCACTTATTACTGCCAGCAGTGAAGTGAATCAACCCAGCCTTCGAGAGGGGG	300	
DB	307 GATGCTGCCACTTATTACTGCCAGCAGTGAAGTGAATCAACCCAGCCTTCGAGAGGGGG	366	
OY	301 ACCATGCTGGAATTAAGA 318		
DB	367 ACCAAGCTGGAATCAAA 384		
RESULT 4			
AAV61793			
ID	AAV61793 standard; DNA; 19001 BP.		
AC	AAV61793;		
XX			

DT	07-JUN-1999	(first entry)
XX		
DE	Target plasmid	Molly containing anti-CD20 gene.
XX		
KW	Molly; target plasmid; gene integration; gene amplification;	
KW	homologous recombination; vector; neomycin phosphotransferase;	
KW	neo gene; selectable marker; immunoglobulin; CD20; C288; human; s	
XX		
OS	Chimeric - Mus sp.	
OS	Chimeric - Escherichia coli.	
OS	Chimeric - Baculovirus.	
OS	Chimeric - Cytomegalovirus.	
OS	Chimeric - Rhesus macaque polyoma virus.	
OS	Chimeric - Phebus sp.	
OS	Chimeric - Salmonella typhimurium.	
OS	Chimeric - Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	misc_feature	361..363
FT		/*tag=
FT		/note="
FT		a
FT		"these bases represent nucleotides missing
FT		from the sequence given in the
FT		specification. They are included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	721..722
FT		/*tag=
FT		/note="
FT		b
FT		"these bases represent nucleotides missing
FT		from the sequence given in the
FT		specification. They are included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	2942
FT		/*tag=
FT		/note="
FT		c
FT		"this base represents a nucleotide missing
FT		from the sequence given in the
FT		specification. It is included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	3301
FT		/*tag=
FT		/note="
FT		d
FT		"this base represents a nucleotide missing
FT		from the sequence given in the
FT		specification. It is included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	4261..4262
FT		/*tag=
FT		/note="
FT		e
FT		"these bases represent nucleotides missing
FT		from the sequence given in the
FT		specification. They are included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	4621..4622
FT		/*tag=
FT		/note="
FT		f
FT		"these bases represent nucleotides missing
FT		from the sequence given in the
FT		specification. They are included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	5581
FT		/*tag=
FT		/note="
FT		g
FT		"this base represents a nucleotide missing
FT		from the sequence given in the
FT		specification. It is included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"
FT	misc_feature	5941
FT		/*tag=
FT		/note="
FT		h
FT		"this base represents a nucleotide missing
FT		from the sequence given in the
FT		specification. It is included to
FT		maintain the nucleotide numbering in the
FT		specification for this sequence"

FT misc_feature 7201 specification for this sequence"
FT /*tag= 1
FT "this base represents a nucleotide missing
FT /note= from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 8161..8162
FT /*tag= j
FT "these bases represent nucleotides missing
FT /note= from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 8521..8522
FT /*tag= k
FT "these bases represent nucleotides missing
FT /note= from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 11101
FT /*tag= l
FT "this base represents a nucleotide missing
FT /note= from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 12061..12062
FT /*tag= m
FT "these bases represent nucleotides missing
FT /note= from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 12421..12422
FT /*tag= n
FT "these bases represent nucleotides missing
FT /note= from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 13381..13382
FT /*tag= o
FT "these bases represent nucleotides missing
FT /note= from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 15961..15962
FT /*tag= p
FT "these bases represent nucleotides missing
FT /note= from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 16321
FT /*tag= q
FT "this base represents a nucleotide missing
FT /note= from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 18541
FT /*tag= r
FT "this base represents a nucleotide missing
FT /note= from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 18901
FT /*tag= s

FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
PN W09841645-A1.
XX
XX
PD 24-SEP-1998.
XX
PF 09-MAR-1998; 98WO-US03935.
XX
PR 13-FEB-1998; 98US-0023715.
PR 14-MAR-1997; 97US-0819866.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Barnett RS, McLachlan KR, Refl ME;
XX WPI; 1998-521229/44.
DR
XX
XX
PT Site specific integration of DNA in mammals for expressing, e.g.
PT immunoglobulins - comprises homologous recombination using
PT selectable marker and target plasmids.
XX
XX
PS Example 1; Fig 8; 114pp: English.
XX
XX
CC This is the nucleotide sequence of novel target plasmid MollY.
CC The plasmid includes the murine dihydrofolate reductase (DHFR)
CC gene, the Escherichia coli beta-galactosidase gene, baculovirus
CC DNA, a cassette comprising the promoter and enhancer elements from
CC cytomegalovirus and SV40 virus, the E. coli beta-glucuronidase
CC (Gus) gene, firefly luciferase gene, salmonella typhimurium
CC histidinol dehydrogenase gene (HisD) and transposon Tn5 neomycin
CC phosphotransferase (neo) gene sequences, in a pBR-derived backbone,
CC and also an anti-B cell antigen CD20 chimeric antibody C288 gene.
CC The invention provides a novel method for integrating a desired
CC exogenous DNA at a target site within the genome of a mammalian
CC cell via homologous recombination. This involves transfecting the
CC cell with a 'marker plasmid' such as Desmond (see AAV61792), which
CC contains a unique sequence that is foreign to the mammalian cell
CC genome and which provides a substrate for homologous recombination,
CC followed by transfection with a 'target plasmid', such as MollY
CC or Mandy (see AAV61794), containing a sequence which provides for
CC homologous recombination with the unique sequences contained in
CC the marker plasmid, and further comprising a desired DNA that is
CC to be integrated into the mammalian cells, typically an
CC immunoglobulin or other secreted mammalian glycoprotein. The
CC homologous recombination system utilizes the neo gene as a
CC dominant selectable marker. The neo gene is split into 3 exons.

Query Match 93.8%; Score 298.4; DB 19; Length 19001;
Best local similarity 95.9%; Pred. No. 3,8e-76;
Matches 305; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGTCCTCAGCAATCTCTCTGTCATCTCCAGGCAAAAGTCACA 60
DB 8070 CAAATGTTCTCTCCAGTCCTCAGCAATCTCTCTGTCATCTCTCAGGCGAAGTCACA 8129
QY 61 ATGACTTGCGAGGGCCAGCTCAAGTGAATTACATGACAGCGAGCAGCAGAGCCAGGA 120
DB 8130 ATGACTTGCGAGGGCCAGCTCAAGTGAATTACATGACAGCGAGCAGCAGAGCCAGGA 8189
QY 121 TCCTCCCCCAAAACCTGGAATTTCTGCACATCCACCTGGCTTCTGAGTCCCTGCTCGC 180
DB 8190 TCCTCCCCCAAAACCTGGAATTTATGCACATCCACCTGGCTTCTGAGTCCCTGCTCGC 8249
QY 181 TTCAGTGGCAGTGCGTGTGGGACCTTACTCTCTCAATCAGCAGAGTGAGGCGTGA 240
DB 8250 TTCAGTGGCAGTGCGTGTGGGACCTTACTCTCTCAATCAGCAGAGTGAGGCGTGA 8309
QY 241 GATGTCGCCACTTATACGTCCAGCAGTGAGTAGTAACCCACCGTTCGAGGAGGGG 300
|||||

DB	8310	GATGCTGCCACTTATTACTGCGCAGCAGTGAGACTAGTAACCCACCCAGCTTCGGAGGGGG	8366
OY	301	ACCATGCTGGAAATAGAGA	318
DB	8370	ACCAAGCTGGAATCAAA	8387
RESULT 5			
AAAA3472			
ID	AAAA3472	standard; CDNA; 449 BP.	
XX			
AC	AAAA3472;		
XX			
DT	21-AUG-2000	(first entry)	
XX			
DE	Mouse secreted expressed sequence tag SEQ ID NO:47.		
KM	Human; mouse; chicken; rat; secreted expressed sequence tag; SESTR;		
KM	expressed sequence tag; EST; probe; chemotactic; proliferative;		
KM	immunomodulatory; hematopoietic; chemokine; analgesic; haemostatic;		
KM	thrombolytic; antiinflammatory; cytoskeletal; antibacterial; antifungal;		
KM	antiviral; antidiabetic; antisthmatic; vulnary; antiparkinsonian;		
KM	antitumor; osteopathic; neuroprotective; nocrotic; antiporiatic;		
KM	cerebroprotective; anticonvulsant; antidepressant; gene therapy;		
KM	vaccine; autoimmune disorder; multiple sclerosis; allergic condition;		
KM	insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;		
KM	lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;		
KM	central nervous system disorder; Alzheimer's disease; stroke;		
KM	Parkinson's disease; Huntington's disease; coagulation disorder;		
KM	haemophilia; thrombosis; inflammatory disorder; Crohn's disease;		
KM	tumour; infection; depression; psoriasis; ss.		
XX			
OS	Mus musculus.		
XX			
PN	WO20021991-A1.		
XX			
PD	20-APR-2000.		
XX			
PF	15-OCT-1999; 99WO-US24206.		
XX			
PR	15-OCT-1998; 98US-0104436.		
XX			
PA	(GEMV) GENETICS INST INC.		
XX			
PI	Jacobs K, McCoy JM, Lavallee ER, Collins-Racie LA, Evans C;		
PT	Merberg D, Treacy M, Bowman MR;		
DR	WPI: 2000-317938/27.		
XX			
PS	Claim 1; Page 214; 803pp; English.		
XX			
AAAA3426	to AAA45925	represent specifically claimed secreted expressed	
CC	sequence tags (SESTRs), isolated from human, mouse, chicken and rat		
CC	tissue sources. The SESTRs can have a range of activities depending on		
CC	the tissues they were isolated from. The activities include:		
CC	chemotactic; proliferative; immunomodulatory; hematopoietic;		
CC	chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory;		
CC	cytoskeletal; antibacterial; antifungal; antiviral; antidiabetic;		
CC	antisthmatic; vulnary; antitumor; osteopathic; neuroprotective;		
CC	nocrotic; antiparkinsonian; antiporiatic; cerebroprotective;		
CC	anticonvulsant; and antidepressant. The SESTRs can be used for gene		
CC	therapy and in vaccines. The SESTRs are useful as probes for the		
CC	identification and isolation of full-length cDNAs and genomic DNA		
CC	molecules which correspond to the SESTRs. Proteins encoded by the SESTRs		
CC	are useful in assays for determining biological activity and raising		
CC	antibodies. They may be useful for treatment of autoimmune disorders		
CC	(multiple sclerosis, insulin dependent diabetes), allergic conditions		
CC	(asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers		
CC	osteoporosis, osteoarthritis, central nervous system disorders		

CC	(Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (thrombophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAAA5926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.
CC	
CC	
XX	Sequence 449 BP; 110 A; 124 C; 107 G; 108 T; 0 other:
SO	
	Query Match 93.5%; Score 297.2; DB 21; Length 449;
	Best Local Similarity 95.9%; Pred. No. 3.1e-76;
	Matches 305; Conservative 0; Mismatches 13; Indels 0; Gaps 0
OY	1 CAATTTGTTCTTCTCCAGTGTCCACGAATTCGTCTGCATCTCCAGGGAAAGTCA 60
DB	
	90 CAAATTGTTCTTCTCCAGTGTCCACGAATTCGTCTGCATCTCCAGGGAGAGGTCA 149
OY	61 ATGACTTGACAGGGGCCACTCAAGTGTAAAATTACATGCATGTGTACCAGACAAGCCAGA 120
DB	
	150 ATGACTTGACAGGGGCCACTCAAGTGTAAAGTAGTACATGTGTGTACCAGACAAGCCAGA 209
OY	121 TCCTCCCCCAAACCGTGGATTTCTGCACATCCAAACCTGGCTTGTGAGTCCGTCTGC 180
DB	
	210 TCCTCCCCCAAACCGTGGATTTTAAGCACATCCAACCTGGCTTGTGAGTCCGTCTGC 269
OY	181 TTTCAGTGGCAGTGGGTGTGGGACCTCTTACTCTCTACAAATAGCAGAGTGAAGCTAA 240
DB	
	270 TTTCAGTGGCAGTGGGTGTGGGACCTCTTACTCTCTACAAATAGCAGAGTGAAGCTAA 329
OY	241 GATCGTGGCACTTTTACTCGCAGCAGTGGAGTAGTAACCCAGCCAGCTGGAGGGGG 300
DB	
	330 GATCGTGGCACTTTTACTCGCAGCAGTGGAGTAGTAACCCAGCTGGAGGGGG 389
OY	301 ACCATGCTGGAATAATPAGA 318
DB	
	390 ACCAAGCTGGAAATCAAA 407
RESULT 6	
AAAA63530	
ID	AAAA63530 standard; DNA; 708 BP.
XX	
AC	AAA63530;
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	DNA encoding a dimeric anti-CD20 light chain polypeptide.
XX	
KW	Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
KM	complement system; Fc gamma receptor; cytotoxic effector cell;
KW	host immune cell; programmed cell death; allergic disorder; cancer;
KM	autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;
KW	allergic bronchopulmonary aspergillosis; allergic rhinitis;
KM	Graefe's disease; food allergy; allergic contact dermatitis; cancer;
KW	B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;
KM	pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
KW	diabetes mellitus; candidiasis; aplastic anaemia; ss.
XX	
OS	Chimeric - Mus sp.
XX	Chimeric - Homo sapiens.
FH	
FH	Key Location/Qualifiers
FT	CDS 1..708
FT	/tag- a
FT	/product= "dimeric anti-CD20 light chain polypeptide"
FT	sig_peptide 1..66
FT	/tag- b
FT	misc_feature 67..384
FT	/tag- c
FT	/note= "encodes murine anti-human CD20 variable light chain"
FT	misc_feature 385..708
FT	/tag- d
FT	/note= "encodes human kappa light chain constant region"

XX WO20044788-A1.
 XX
 XX 03-AUG-2000.
 XX
 XX 28-JAN-2000; 2000WO-US01893.
 XX
 XX 28-JAN-1999; 99US-0238741.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Braslavsky GR, Hanna N, Harlharan K, Labarre MJ, Huynh TB;
 XX
 XX WPI: 2000-514811/46.
 XX
 XX P-PSDB: AAB08025.
 XX
 XX Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
 PT treatment of cancers, allergic disorders and autoimmune conditions -
 PS
 PS Example 1; Fig 1A-B; 65pp; English.

CC The present sequence encodes a dimeric anti-CD20 light chain
 CC polypeptide. The dimeric immunoglobulin is used in the method of the
 CC invention. The specification describes a method for producing an
 CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
 CC engineering a monoclonal antibody to introduce a cysteine molecule
 CC which inhibits formation of intramolecular disulphide bridges between
 CC sister heavy chains on the same antibody molecule. The dimer is a
 CC homodimer or heterodimer that is capable of activating components of the
 CC complement system, and has the ability to activate and kill cells via the
 CC complement cascade. The dimer is also capable of binding to Fcγamma
 CC receptors on cytotoxic effector cells and on host immune cells, and is
 CC capable of initiating programmed cell death. The IgG/IgG dimers may be
 CC used to treat allergic disorders, cancers and autoimmune diseases such
 CC as allergic asthma, allergic bronchopulmonary aspergillosis, allergic
 CC rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food
 CC allergies, allergic contact dermatitis, CLL cancers and/or B-cell
 CC lymphomas. They may also be used to treat a range of other diseases and
 CC disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,
 CC pigoen breeder's disease, hepatitis, leprosy, Lyme disease, diabetes
 CC mellitus, candidiasis and aplastic anaemia. They are also useful for
 CC inducing hyper-cross-linking of membrane antigens and for the
 CC preferential killing of selected cell populations.

CC Sequence 708 BP; 180 A; 196 C; 178 G; 154 T; 0 other;

Query Match 93.5%; Score 297.2; DB 21; Length 708;
 Best Local Similarity 95.9%; Pred. No. 3.5e-76;
 Matches 305; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGTCCACA 60
 DB 67 CAAATTTGTTCTCTCCAGTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGTCCACA 126
 OY 61 ATGACTTGGAGGGCCAGCTCACTGAATTAATTCATGCACTGGTACCAAGCAAGCAAGCA 120
 DB 127 ATGACTTGGAGGGCCAGCTCACTGAATTAATTCATGCACTGGTACCAAGCAAGCAAGCA 186
 OY 121 TCTTCCCCCAAAACCTGGATTTCTGCAATCCAACTGGCTTCTGGAGTCCCTGGTCCG 180
 DB 187 TCTTCCCCCAAAACCTGGATTTCTGCAATCCAACTGGCTTCTGGAGTCCCTGGTCCG 246
 OY 181 TTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCAATCAGCAGAGTGGAGGCTGAA 240
 DB 247 TTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCAATCAGCAGAGTGGAGGCTGAA 306
 OY 241 GATGCTGGCAGTATTATTCAGTCCAGCAGTGGAGTAAACCAACCACTTGGAGGGGG 300
 DB 307 GATGCTGGCAGTATTATTCAGTCCAGCAGTGGAGTAAACCAACCACTTGGAGGGGG 366
 OY 301 ACCATGCTGGAAATTAAGA 318
 DB 367 GCCAAGCTGGAAATTAAGA 384

RESULT 7
 AA065629
 ID AA065629 standard; DNA; 9208 BP.
 XX
 XX AA065629;
 AC
 XX 01-FEB-1995 (first entry)
 DT
 XX Vector contg. TCAE 8 DNA.
 DE
 XX B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 KW cell lysis; ss.
 KM
 XX Synthetic.
 OS
 XX WO9411026-A.
 PN
 XX 26-MAY-1994.
 PD
 XX 12-NOV-1993; 93WO-US10953.
 PF
 XX 13-NOV-1992; 92US-0978891.
 PR 03-NOV-1993; 93US-0149099.
 XX
 XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Leonard JE, Newman RA, Rustetter WH;
 PI Refine;
 PI
 XX WPI: 1994-183162/22.
 DR
 XX
 XX Treating B cell lymphoma with chimeric antibody - against CD20,
 PT causing rapid depletion of peripheral B cells, also new
 PT antibodies and hybridomas
 PS
 XX Disclosure; Fig 3; 101pp; English.

XX The sequence shows a vector contg. TCAE8, a gene encoding a chimeric
 CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
 CC contains 4 transcriptional cassettes; human Ig light and heavy chain
 CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
 CC and murine variable regions. The vector can be used to produce
 CC antibodies which cause depletion of peripheral blood B cells,
 CC including those associated with lymphoma. They mediate complement-
 CC dependent lysis and lyse target cells by antibody-dependent cellular
 CC cytotoxicity.
 CC See also AA065629-35.

CC Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T; 2 other;

Query Match 93.5%; Score 297.2; DB 15; Length 9208;
 Best Local Similarity 95.9%; Pred. No. 7e-76;
 Matches 305; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGTCCACA 60
 DB 1044 CAAATTTGTTCTCTCCAGTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGTCCACA 1103
 OY 61 ATGACTTGGAGGGCCAGCTCACTGAATTAATTCATGCACTGGTACCAAGCAAGCAAGCA 120
 DB 1104 ATGACTTGGAGGGCCAGCTCACTGAATTAATTCATGCACTGGTACCAAGCAAGCAAGCA 1163
 OY 121 TCTTCCCCCAAAACCTGGATTTCTGCAATCCAACTGGCTTCTGGAGTCCCTGGTCCG 180
 DB 1164 TCTTCCCCCAAAACCTGGATTTCTGCAATCCAACTGGCTTCTGGAGTCCCTGGTCCG 1223
 OY 181 TTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCAATCAGCAGAGTGGAGGCTGAA 240
 DB 1224 TTCAGTGGCAGTGGGTCTGGGACCTTCTACTCTCTCAATCAGCAGAGTGGAGGCTGAA 1283
 OY 241 GATGCTGGCAGTATTATTCAGTCCAGCAGTGGAGTAAACCAACCACTTGGAGGGGG 300

DB 1284 GATGCTGCCACTTATTACTGCGAGGTGACTAGTAACCAACCACTGTCGAGGGGGG 1343

OY 301 ACCATGCTGGAATAAGA 318

DB 1344 ACCAAGCTGGAATCAAA 1361

RESULT 8

AAT79900 standard; cDNA, 318 BP.

AC AAT79900;

DT 27-DEC-1997 (first entry)

DE Anti-Factor IX Mab chimeric light chain cDNA.

KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;

KW chimeric antibody; antibody engineering; light chain; ss.

OS Chimeric Mus musculus.

OS Chimeric Homo sapiens.

PN MO9726010-A1.

PD 24-JUL-1997.

PF 17-JAN-1997; 97WO-US00759.

PR 24-OCT-1996; 96US-0029119.

PR 17-JAN-1996; 96US-0010108.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

DR Blackburn MN, Church WR, Feuerstein GZ, Gross MS;

DR Nichols AJ, Padlan EA, Patel AH, Sylvester DR;

DR WPI; 1997-385117/35.

DR P-PSDB; AAW24532.

PT Inhibiting thrombosis with self-limiting antibody to coagulation

PT factor - avoids uncontrolled bleeding by providing only partial

PT inhibition

PS Example 7; Page 128; 150pp; English.

CC This cDNA sequence encodes a mouse-human chimeric antibody

CC light chain (AAW24532) in which the variable region is derived

CC from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see

CC AAT79899) and human sequences from the immunoglobulin Rf-TS3/CL

CC framework. It was obtained by PCR amplification (see AAT79897-98)

CC of BC2 cDNA and insertion of the PCR product into p9HHC 1-3 cDNA

CC (see AAT77374). Claimed anti-factor IX chimeric antibodies are

CC useful in the treatment of thrombosis.

SO Sequence 318 BP; 79 A; 91 C; 78 G; 70 T; 0 other;

Query Match 93.0%; Score 295.6; DB 18; Length 318;

Best Local Similarity 95.6%; Pred. No. 8.1e-76;

Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTGTGATCTCCAGGGGAAAGGTACA 60

DB 1 CAGATAGACTCTCCAGTCTCCAGCAATCTGTGATCTCCAGGGGAAAGGTACA 60

OY 61 ATGACTTGCAGGGCCAGCTCAGTGTAAATTACATGCACTGTACCAGAGAGCCAGA 120

DB 61 ATGACTTGCAGGGCCAGCTCAGTGTAAATTACATGCACTGTACCAGAGAGCCAGA 120

OY 121 TCCTCCCAACCCCTGATTTCTGCGACATCCACCTGCTTGGAGTCCCTGCTGC 180

DB 121 TCCTCCCAACCCCTGATTTATGCGACATCCACCTGCTTCTGAGTCCCTGCTGC 180

OY 181 TTCAGTGGCAGTGGTCTGCGACCTTCTCTACATCAGCAGTGGAGCTGAA 240

DB 181 TTCAGTGGCAGTGGTCTGCGACCTTCTCTACATCAGCAGTGGAGCTGAA 240

OY 241 GATGCTGCCACTTATTACTGCGAGGTGACTAGTAACCAACCACTGTCGAGGGGG 300

DB 241 GATGCTGCCACTTATTACTGCGAGGTGACTAGTAACCAACCACTGTCGAGGGGG 300

OY 301 ACCATGCTGGAATAAGA 318

DB 301 ACCAAGCTGGAATCAAA 318

RESULT 9

ABK24005 standard; cDNA, 318 BP.

AC ABK24005;

DT 09-APR-2002 (first entry)

DE Mouse-human light chain DNA.

KW Human; mouse; BC2; animal post-thromboembolic induced ischaemia;

KW thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss;

KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;

KW vasotropic; cardiatic; PCR primer; anti-respiratory syncytial virus;

KW heavy chain variable region; light chain variable region.

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

PN WO200187339-A1.

PD 22-NOV-2001.

PF 05-OCT-2000; 2000WO-US27438.

PR 15-MAY-2000; 2000US-0571434.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;

DR WPI; 2002-082944/11.

DR P-PSDB; AAU81002.

PT Treating post-thromboembolic induced ischaemia in an animal by

PT administering anti-factor IX antibody in combination with a plasminogen

PT activator

PS Example 7; Page 154-155; 163pp; English.

CC The invention relates to a method for treating an animal

CC post-thromboembolic induced ischaemia or reducing a required dose of a

CC thrombolytic agent in treatment of an animal post-thromboembolic induced

CC ischaemia, comprising administering an anti-factor IX antibody or its

CC fragment, optionally in combination with a plasminogen activator or

CC thrombolytic agent. The method is useful for treating thromboembolic

CC post-thromboembolic-induced ischaemia, for preventing thromboembolic

CC stroke in an animal, and for reducing a required dose of a thrombolytic

CC agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding

CC antibodies and PCR primers used in the method of the invention.

SO Sequence 318 BP; 79 A; 91 C; 78 G; 70 T; 0 other;

Query Match 93.0%; Score 295.6; DB 24; Length 318;

Best Local Similarity 95.6%; Pred. No. 8.1e-76;

Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy	1	CANAATGTTCTTCCTCCCAATCTCCAGCAATCTGCTGTGATCTCCAGGGGAAAGGTACA	60
Oy	1		
Db	1	CAGATAGTACTCTCCCACTCTCCAGCAATCTGTTGATCTCCAGGGGAAAGGTACA	60
Oy	61	ATGACTTTCAGAGGGCAGCTCAAGTGTAAATTACATGCACCTGGTACCAAGAACCCAGGA	120
Db	61	ATGACTTTCAGAGGGCAGCTCAAGTGTAAATTACATGCACCTGGTACCAAGAACCCAGGA	120
Oy	121	TCCTCCCCCAAAACCCTGGATTTCCTGTCACATCAACCTGGCTTGTGAGTCCCTGCTGC	180
Db	121	TCCTCCCCCAAAACCCTGGATTTCATGCCATCAACCTGGCTTGTGAGTCCCTGCTGC	180
Oy	181	TTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATACACAGAGGAGGCTGAA	240
Db	181	TTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATACACAGAGTGAAGGCTGAA	240
Oy	241	GATGCTGGCAGCTATTATTACTGGCAGCAGTGAAGTAAACCCAGCAGTTCGAGAGGGGG	300
Db	241	GATGCTGGCAGCTATTATTACTGGCAGCAGTGAAGTAAACCCAGAGGAGTTGGTGAAGGC	300
Oy	301	ACCATGCTGGAATTAAGA 318	
Db	301	ACCAAGCTGGAATTAACA 318	
RESULT 10			
AKT79899			
ID	AKT79899	standard; cDNA: 335 BP.	
AC	AAAT98899;		
XX			
DT	27-DEC-1997	(first entry)	
XX			
DE	Anti-Factor IX MAb BC2 light chain PCR product.		
XX			
KM	Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;		
XX	chimeric antibody; antibody engineering; light chain; ss.		
OS	Chimeric Mus musculus.		
OS	Chimeric synthetic.		
PN	W09726010-A1.		
PD	24-JUL-1997.		
XX			
PF	17-JAN-1997; 97WO-US00759.		
XX			
PR	24-OCT-1996; 96US-0029119.		
XX			
PR	17-JAN-1996; 96US-0010108.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
XX	(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.		
PI	Blackburn MN, Church WR, Feuerstein GZ, Gross MS;		
XX	Nichols AJ, Padian EA, Patel AH, Sylvester DR;		
DR	WPI: 1997-385117/35.		
XX	P-PSDB: AAW24531.		
PT	Inhibiting thrombosis with self-limiting antibody to coagulation		
XX	factor - avoids uncontrolled bleeding by providing only partial		
PT	inhibition		
XX			
PS	Example 7: Page 126; 150bp; English.		
XX			
CC	This cDNA sequence was obtained by PCR amplification (see AAT79897		
CC	and AAT79898) of the light chain variable region (see also AAT77377)		
CC	of mouse anti-human factor IX monoclonal antibody BC2 cDNA. The		
CC	amplification resulted in the addition of ScaI, NsiI ends to the		
CC	VL region. The PCR product was ligated into ScaI, NsiI-digested		
CC	Phi28HC 1-3 (see AAT77374) and digested with ScaI, NsiI to produce a		
CC	mouse-human chimeric light chain FcCHLC (see AAT79900, AAW24532).		
CC	Claimed anti-Factor IX chimeric antibodies are useful in the		

CC	treatment of thrombosis.
XX	
SQ	Sequence 335 BP; 80 A; 97 C; 85 G; 73 T; 0 other;
	93.0%; Score 295.6; DB 18; Length 335;
	Query Match Best Local Similarity 95.6%; Pred.No.8.2e-76;
	Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY	1 CAATATTGTCCTCACCAGTCTCCACCAATCGTGCTGCATTCACAGGGCAAAGGTACA 60
DB	1 CAGATAGTACTCTCCACGCTCCACCAATCCTGTCTGCATCTCCAGGGCAGAAGGTACA 60
OY	61 ATGACTTTGAGGGCCAGCGCATGTAAATTACATGCACTGGTAGCACAGAACAGGA 120
DB	61 ATGACTTTGAGGGCCAGCGCATGTAAATTACATGCACTGGTAGCACAGAACAGGA 120
OY	121 TCCTCCCCCAACCCCTGATTTCTGCCACATCCAACCTGGCTTCTGAGTCCCCTGCTGC 180
DB	121 TCCTCCCCCAACCCCTGATTTATGCGCATGTCCCAACCTGGCTTCTGAGTCCCCTGCTGC 180
OY	181 TTCAGTGGCAGTGGGTCTGGAGCCTTACTCTTCACATCAGCAGACTGGAGGCTGAA 240
DB	181 TTCAGTGGCAGTGGGTCTGGAGCCTTACTCTTCACATCAGCAGACTGGAGGCTGAA 240
OY	241 GATGCTGGCCACTTATTACGCCAGCAGAGTGTAGTAACCCACCCAGCTTGGAGGGGG 300
DB	241 GATGCTGGCCACTTATTACGCCAGCAGTGTAGTATTAACCCAGCAGCTTGGAGGGG 300
OY	301 ACCATCTGTGGAATAAAGA 318
DB	301 ACCAAGCTGGAATCAAA 318
RESULT 11	
ABK24004	
ID	ABK24004 standard; cDNA; 335 BP.
XX	
AC	ABK24004:
XX	
DT	09-APR-2002 (first entry)
XX	
DE	Murine BC2 light chain modified variable region DNA.
XX	
KM	Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
KW	thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss;
KM	thrombolitic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KW	vasotropic; cardiant; PCR primer; anti-respiratory syncytial virus;
XX	heavy chain variable region; light chain variable region.
OS	Mus sp.
OS	Synthetic.
XX	
PN	WO200187339-A1.
XX	
PD	22-NOV-2001.
XX	
PF	05-OCT-2000; 2000WO-US27438.
XX	
PR	15-MAY-2000; 2000US-0571434.
XX	
PA	(SMIK) SMITHLINE BEECHAM CORP.
PI	Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
XX	
DR	WPI; 2002-082944/11.
XX	
P	P-PsDB; AAU81001.
PT	Treating post-thromboembolic induced ischaemia in an animal by
XX	administering anti-factor IX antibody in combination with a plasminogen
PS	activator -
XX	
PS	Example 7; Page 152-153; 163pp; English.
XX	

CC The invention relates to a method for treating an animal
 CC post-thromboembolic induced ischaemia or reducing a required dose of a
 CC thrombolytic agent in treatment of an animal post-thromboembolic induced
 CC ischaemia, comprising administering an anti-factor IX antibody or its
 CC fragment, optionally in combination with a plasminogen activator or
 CC thrombolytic agent. The method is useful for treating
 CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
 CC stroke in an animal, and for reducing a required dose of a thrombolytic
 CC agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding
 CC antibodies and PCR primers used in the method of the invention.
 XX

SQ Sequence 335 BP; 80 A; 97 C; 85 G; 73 T; 0 other;

Query Match 93.0%; Score 295.6; DB 24; Length 335;
 Best Local Similarity 95.6%; Pred. No. 8.2e-76;
 Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTGTGATCTCCAGGGGAAAGTTCACA 60
 |||||
 Db 1 CAGATGTAAGTCTCCAGTCTCCAGCAATCTGTGATCTCCAGGGGAAAGTTCACA 60
 OY 61 ATGACTTGCAGGGCCAGCTCAAGTGAATATACATGCTGACCAAGAGCCAGGA 120
 |||||
 Db 61 ATGACTTGCAGGGCCAGCTCAAGTGAATATACATGCTGACCAAGAGCCAGGA 120
 OY 121 TCCTCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTGGAGTCCCTGCTCG 180
 |||||
 Db 121 TCCTCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTGGAGTCCCTGCTCG 180
 OY 181 TTCAGTGGCAGTGGTCTGTGGACCTTCTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 240
 |||||
 Db 181 TTCAGTGGCAGTGGTCTGTGGACCTTCTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 240
 OY 241 GATGCTGCCACTTATTACTGCCAGCAGTGAAGTAAACCCACGTTTGGAGGGGG 300
 |||||
 Db 241 GATGCTGCCACTTATTACTGCCAGCAGTGAAGTAAACCCACGTTTGGAGGGGG 300
 OY 301 ACCATCTGGAATAAGA 318
 |||||
 Db 301 ACCATCTGGAATAAGA 318

RESULT 12

AAAT0972
 ID AAAT0972 standard; cDNA: 403 BP.

AC AAAT0972;

DT 03-OCT-2002 (updated)
 DT 09-APR-1991 (first entry)

XX 2H7 VL sequence in which the VK gene contains JK5 sequences.

XX Chimeric antibody; Anti-cancer antibody; ss.

OS Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX

XX key Location/Qualifiers

XX CDS /tag= a

XX CDS /label=leader peptide

XX CDS /tag= b

XX CDS /label=FR1

XX CDS /tag= c

XX CDS /label=CDR1

XX CDS /tag= d

XX CDS /label=FR2

XX CDS /tag= e

FT /label-CDR2
 FT 232..327
 FT /tag= f
 FT /label=FR3
 FT 328..354
 FT /tag= g
 FT /label=CDR3
 FT 355..403
 FT /tag= h
 FT /label=FR4
 FT 349..403
 FT /tag= i
 FT /label=JK5

PN MO8702671-A.

PD 07-MAY-1987.

PF 27-OCT-1986; 86WO-US02269.

PR 01-NOV-1985; 85US-0793980.

PA (ITGE-) INT GENETIC ENG INC.

PA (ROBI/) ROBINSON R. R.

PI Robinson RR, Liu AY, Horvitz AH, Wall R;

DR WPI; 1987-136004/19.

DR P-PSDB; AAP70628.

PT Prodn. of immunoglobulin chains and molecules - is by recombinant

PT DNA procedures, with chimeric antibodies etc. related to cancer

PT specific antigens.

PS Example; Fig 22; 126bp; English.

CC The patentors claim a chimeric antibody molecule comprising 2 light

CC chains and 2 heavy chains, each comprising a constant human region

CC and a variable non-human region. Coding sequences for the Ig chains

CC are also claimed. The invention provides consensus sequences of

CC light and heavy chain J regions useful in the design of

CC oligonucleotides (UIGs) for use as primers or probes for cloning

CC immunoglobulin light or heavy chain mRNAs or genes. Depending on the

CC nature of design of a particular UIG, it may be capable of

CC hybridizing to all Ig mRNAs or genes containing a single specific J

CC sequence. UIG denotes universal immunoglobulin gene.

CC (updated on 03-OCT-2002 to add missing OS field.)

XX

XX Sequence 403 BP; 100 A; 112 C; 93 G; 98 T; 0 other;

XX

XX

XX

XX

XX

Query Match 93.0%; Score 295.6; DB 8; Length 403;
 Best Local Similarity 95.6%; Pred. No. 8.7e-76;
 Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTGTGATCTCCAGGGGAAAGTTCACA 60
 |||||
 Db 86 CAAATGTTCTCTCCAGTCTCCAGCAATCTGTGATCTCCAGGGGAAAGTTCACA 145
 OY 61 ATGACTTGCAGGGCCAGCTCAAGTGAATATACATGCTGACCAAGAGCCAGGA 120
 |||||
 Db 146 ATGACTTGCAGGGCCAGCTCAAGTGAATATACATGCTGACCAAGAGCCAGGA 205
 OY 121 TCCTCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTGGAGTCCCTGCTCG 180
 |||||
 Db 206 TCCTCCCAAAACCTGGATTTCTGCCACATCCAACTGGCTTGGAGTCCCTGCTCG 265
 OY 181 TTCAGTGGCAGTGGTCTGTGGACCTTCTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 240
 |||||
 Db 266 TTCAGTGGCAGTGGTCTGTGGACCTTCTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 325
 OY 241 GATGCTGCCACTTATTACTGCCAGCAGTGAAGTAAACCCACGTTTGGAGGGGG 300
 |||||
 Db 326 GATGCTGCCACTTATTACTGCCAGCAGTGAAGTAAACCCACGTTTGGAGGGGG 385


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QY 1 CAAATGTTCTCTCCAGAGTCTCAGCAATCCTGTCTGCATCTCCAGGGGAAAGTCA 60
  |||
Db 87 CAAATGTTCTCTCCAGAGTCTCAGCAATCCTGTCTGCATCTCCAGGGGAAAGTCA 146
QY 61 ATGACTTGCAAGGGCCAGCTCAAGTGAATTAATGATGACAGTGGACAGCAAGCCAGGA 120
  |||
Db 147 ATGACTTGCAAGGGCCAGCTCAAGTGAATTAATGATGACAGTGGACAGCAAGCCAGGA 206
QY 121 TCCGCCCCCAAAACCTGGATTTCTGCCACATCCCAACCTGGTCTGGAGTCCCTGCTGC 180
  |||
Db 207 TCCGCCCCCAAAACCTGGATTTATGCCCCCAACCTGGTCTGGAGTCCCTGCTGC 266
QY 181 TTCAGTGGCAGTGGTCTGGAGCTCTTACTCTCTCAACAATCAGACAGTGGAGCTGAA 240
  |||
Db 267 TTCAGTGGCAGTGGTCTGGAGCTCTTACTCTCTCAACAATCAGACAGTGGAGCTGAA 326
QY 241 GATGCTGCCACTTATTAATCTGCGACAGTGGAGTGAACCCAGCTTCCGAGGGGG 300
  |||
Db 327 GATGCTGCCACTTATTAATCTGCGACAGTGGAGTGAACCCAGCTTCCGAGGGGG 386
QY 301 ACCATGCTGGAATTAAGA 318
  |||
Db 387 ACCAAGCTGGAGCTGAAA 404
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RESULT 15

AAH22071 standard; DNA; 404 BP.

AAH22071:

17-AUG-2001 (first entry)

2H7 light chain variable region gene sequence.

Human; mouse; chimeric immunoglobulin; chimeric antibody;

genetic engineering; primer; ss.

Homo sapiens.

Mus sp.

US6204023-B1.

20-MAR-2001.

06-JUN-1995; 95US-0472691.

18-AUG-1994; 94US-0299085.

29-MAR-1990; 90US-0501092.

08-DEC-1992; 92US-0987555.

25-MAY-1995; 95US-0450731.

01-NOV-1985; 85US-0793980.

27-OCT-1986; 86MO-US02269.

24-JUL-1987; 87US-0077528.

(XOMA) XOMA LTD.

Robinson RR, Liu AY, Horwitz AH, Better M, Wall R, Lei S;

Wilcox GL;

WPI; 2001-289514/30.

P-PsDB; AAB98093.

The present invention describes a method for preparing an immunoglobulin

that is capable of binding antigen involves modular assembly of

antibodies through gene cloning and expression of light and heavy

chains. The cloned immunoglobulin gene can be produced by expression in

CC genetically engineered organisms. The method comprises: (a) expressing, in a bacterial cell, of a first nucleic acid that encodes a bacterial signal sequence operably linked to either the heavy chain or heavy chain fragment, and a second nucleic acid that encodes a bacterial signal sequence operably linked to either the light chain or light chain fragment, and obtaining the immunoglobulin from the periplasmic space or culture medium; or (b) operably linking a nucleic acid encoding a bacterial signal sequence to a nucleic acid encoding the heavy chain variable region or the light chain variable region or both of the variable regions, and obtaining the immunoglobulin from the periplasmic space or culture medium. The bacterial signal sequences bring about the transport of the heavy chain or heavy chain fragment, and the light chain or light chain fragment, or the variable regions through the cytoplasmic membrane of a bacterial cell. The immunoglobulin comprises: (a) a heavy chain or heavy chain variable region and a light chain or light chain fragment; or (b) a heavy chain variable region and a light chain variable region. The method is useful for producing genetically engineered antibodies of desired variable region specificity and constant region properties. The method is also useful for large scale production of human antibodies. The AAH21985 to AAH22082 and AAB98085 to AAB98097 represent sequences used in the exemplification of the present invention.

Sequence 404 BP; 100 A; 113 C; 93 G; 98 T; 0 other;

Query Match 93.0%; Score 295.6; DB 22; Length 404;
Best Local Similarity 95.6%; Pred. No. 8.7e-76;
Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 1 CAAATGTTCTCTCCAGAGTCTCAGCAATCCTGTCTGCATCTCCAGGGGAAAGTCA 60
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Db 87 CAAATGTTCTCTCCAGAGTCTCAGCAATCCTGTCTGCATCTCCAGGGGAAAGTCA 146
QY 61 ATGACTTGCAAGGGCCAGCTCAAGTGAATTAATGATGACAGTGGACAGCAAGCCAGGA 120
  |||
Db 147 ATGACTTGCAAGGGCCAGCTCAAGTGAATTAATGATGACAGTGGACAGCAAGCCAGGA 206
QY 121 TCCGCCCCCAAAACCTGGATTTCTGCCACATCCCAACCTGGTCTGGAGTCCCTGCTGC 180
  |||
Db 207 TCCGCCCCCAAAACCTGGATTTATGCCCCCAACCTGGTCTGGAGTCCCTGCTGC 266
QY 181 TTCAGTGGCAGTGGTCTGGAGCTCTTACTCTCTCAACAATCAGACAGTGGAGCTGAA 240
  |||
Db 267 TTCAGTGGCAGTGGTCTGGAGCTCTTACTCTCTCAACAATCAGACAGTGGAGCTGAA 326
QY 241 GATGCTGCCACTTATTAATCTGCGACAGTGGAGTGAACCCAGCTTCCGAGGGGG 300
  |||
Db 327 GATGCTGCCACTTATTAATCTGCGACAGTGGAGTGAACCCAGCTTCCGAGGGGG 386
QY 301 ACCATGCTGGAATTAAGA 318
  |||
Db 387 ACCAAGCTGGAGCTGAAA 404
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Search completed: November 27, 2002, 03:53:51
Job time : 187.766 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:45:51 ; Search time 1318.29 Seconds
(without alignments)
3906.706 Million cell updates/sec

Title: US-09-893-615-88

Sequence: 1 CAAATGTTCTCTCCAGTC.....GGACCACTCGGAATAGA 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estb1:*
- 2: em_estb2:*
- 3: em_estb3:*
- 4: em_estb4:*
- 5: em_estb5:*
- 6: em_estb6:*
- 7: em_estb7:*
- 8: em_estb8:*
- 9: em_estb9:*
- 10: em_estb10:*
- 11: em_estb11:*
- 12: em_estb12:*
- 13: em_estb13:*
- 14: em_estb14:*
- 15: em_estb15:*
- 16: em_estb16:*
- 17: em_estb17:*
- 18: em_estb18:*
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- 21: em_estb21:*
- 22: em_estb22:*
- 23: em_estb23:*
- 24: em_estb24:*
- 25: em_estb25:*
- 26: em_estb26:*
- 27: em_estb27:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	286.8	90.2	639	13	BG968615 602836416
2	276.4	86.9	959	14	BG939046 AGENCOURT
3	274.8	86.4	532	13	B1104783 602891329
4	274.4	86.3	798	13	BG968518 602835104
5	273.2	85.9	755	13	B1150509 602915167
6	273.2	85.9	918	14	BQ946795 AGENCOURT

7	272.2	85.6	312	12	BG090240 uc58e10.y
8	271.2	85.3	413	10	BE624609 uc24c05.y
9	267.2	84.0	396	9	AA691311 vs14f01.t
10	266.8	83.9	871	12	BF165585 601777486
11	266.6	83.8	865	13	BG964349 602831966
12	266.4	83.8	960	12	BE581607 602099949
13	263.6	82.9	728	13	BG962985 602827980
14	263.2	82.8	639	12	BF583310 602101781
15	262.2	82.5	743	13	B1106381 602892928
16	260.4	81.9	472	10	BE289692 601088922
17	260.4	81.9	862	13	BG962582 602829965
18	259.4	81.6	975	13	BG961850 602826515
19	257.8	81.1	948	12	BF139176 601783324
20	256.2	80.6	876	12	BF141750 601787615
21	256	80.5	807	17	BH035104 RPT1-24-2
22	253	79.6	1532	12	BF133688 601778590
23	251.4	79.1	918	12	BF142385 601786637
24	250.8	78.9	641	12	BF134573 601784982
25	246.8	77.6	569	13	BG964957 602829274
26	246.6	77.5	401	12	BF015569 uc23c09.y
27	246.6	77.5	854	14	BQ947692 AGENCOURT
28	245.8	77.3	722	12	BF140170 601786735
29	245.8	77.3	1000	14	BQ937284 AGENCOURT
30	245.6	77.2	953	12	BE583869 602096867
31	245	77.0	403	14	BQ375976 RC3-TN009
32	245	77.0	407	14	BQ328151 MR4-RT004
33	245	77.0	409	12	BF822649 CM2-RT000
34	245	77.0	410	12	BF768589 QVA-IT000
35	245	77.0	416	13	B1025870 I10-MT036
36	245	77.0	419	14	BQ321312 RC0-CT047
37	245	77.0	424	14	BQ376239 MR4-TN010
38	245	77.0	425	13	B1063029 I13-UT011
39	245	77.0	427	12	BF752315 RC3-BN042
40	245	77.0	432	17	AQ580097 T135654b
41	245	77.0	433	12	BF843458 MR1-HT113
42	245	77.0	437	14	BQ321307 RC0-CT047
43	245	77.0	439	14	BQ321297 QV1-CT041
44	245	77.0	444	12	BF894856 QV1-MT016
45	245	77.0	444	12	BF894857 QV1-MT016

ALIGNMENTS

RESULT 1
LOCUS 602836416P1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4991067 5',
DEFINITION BG968615 639 bp mRNA linear EST 12-JUN-2001
ACCESSION BG968615
VERSION BG968615.1 GI:14356252
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 639)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgrpbbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNL11007 row: O column: 04
High quality sequence stop: 639.
Location/Qualifiers
1. 639

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pcwv-sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 172 a 173 c 151 g 143 t

ORIGIN

Query Match 90.2%; Score 286.8; DB 13; Length 639;
Best Local Similarity 95.9%; Pred. No. 2.5e-75;
Matches 305; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 CAATTTGTTCTTCCAGTCTCCAGCAATCCCTGTGCAATCTCCAGGGGAAAGGTAC 60
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Db 76 CAATTTGTTCTTCCAGTCTCCAGCAATCCCTGTGCAATCTCCAGGGGAAAGGTAC 134
QY 61 ATGACTTGCGAGGGCCAGCTCAAGTGAATTAATGACACTGTGACAGCAGAACCCAGGA 120
|||||
Db 135 ATGACTTGCGAGGGCCAGCTCAAGTGAATTAATGACACTGTGACAGCAGAACCCAGGA 194
QY 121 TCCTCCCCCAACCCCTGGATTTCTGCGACATCCAGCTGCTTCTGGAGTCCCTGCTCGC 180
|||||
Db 195 TCCTCCCCCAACCCCTGGATTTATGCCATGCCAACCTGCTTCTGGAGTCCCTGCTCGC 254
QY 181 TTGAGTGGCGAGTGGGTCTGGGACCTCTTACTCTCTCAGCATCAGCAGAGAGAGGTGAA 240
|||||
Db 255 TTGAGTGGCGAGTGGGTCTGGGACCTCTTACTCTCTCAGCATCAGCAGAGAGAGGTGAA 314
QY 241 GATGCTGCCACTTATTACTCCAGCAGTGGAGTGAATACCACCCAGCTTCGAGAGGGGG 300
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Db 315 GATGCTGCCACTTATTACTCCAGCAGTGGAGTGAATACCACCCAGCTTCGAGAGGGGG 374
QY 301 ACCATGCTGGAATTAAGA 318
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Db 375 ACCAAGCTGGAATTAAGA 392

RESULT 2 959 bp mRNA linear EST 21-AUG-2002
B0939046
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B0939046 959 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8946838 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6395050 5', mRNA sequence.
B0939046 B0939046.1 GI:22354524
EST.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 959)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM13889 row: b column: 11
High quality sequence stop: 517.
Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"

FEATURES
source

/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pcwv-sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 267 a 256 c 214 g 222 t

ORIGIN

Query Match 86.9%; Score 276.4; DB 14; Length 959;
Best Local Similarity 91.8%; Pred. No. 4.2e-72;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 CAATTTGTTCTTCCAGTCTCCAGCAATCCCTGTGCAATCTCCAGGGGAAAGGTAC 60
|||||
Db 70 CAATTTGTTCTTCCAGTCTCCAGCAATCCCTGTGCAATCTCCAGGGGAAAGGTAC 129
QY 61 ATGACTTGCGAGGGCCAGCTCAAGTGAATTAATGACACTGTGACAGCAGAACCCAGGA 120
|||||
Db 130 ATGACTTGCGAGGGCCAGCTCAAGTGAATTAATGACACTGTGACAGCAGAACCCAGGA 189
QY 121 TCCTCCCCCAACCCCTGGATTTCTGCGACATCCAGCTGCTTCTGGAGTCCCTGCTCGC 180
|||||
Db 190 ACCTCCCCCAACCCCTGGATTTATGCCATGCCAACCTGCTTCTGGAGTCCCTGCTCGC 249
QY 181 TTGAGTGGCGAGTGGGTCTGGGACCTCTTACTCTCTCAGCATCAGCAGAGAGAGGTGAA 240
|||||
Db 250 TTGAGTGGCGAGTGGGTCTGGGACCTCTTACTCTCTCAGCATCAGAGAGAGGTGAA 309
QY 241 GATGCTGCCACTTATTACTCCAGCAGTGGAGTGAATACCACCCAGCTTCGAGAGGGGG 300
|||||
Db 310 GATGCTGCCACTTATTACTCCAGCAGTGGAGTGAATACCACCCAGCTTCGAGAGGGGG 369
QY 301 ACCATGCTGGAATTAAGA 318
|||||
Db 370 ACCAAGCTGGAATTAAGA 387

RESULT 3 532 bp mRNA linear EST 26-JUN-2001
B1104783
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B1104783 532 bp mRNA linear EST 26-JUN-2001
602891329F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036622 5',
mRNA sequence.
B1104783 B1104783.1 GI:14555676
EST.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 532)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM11101 row: 1 column: 07
High quality sequence stop: 532.
Location/Qualifiers
1..532
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5036622"

FEATURES
source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5036622"

/clone.lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin
/lab_host="DH10B"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 139 a 148 c 113 g 132 t
ORIGIN

Query Match 86.4%; Score 274.8; DB 13; Length 532;
Best Local Similarity 91.5%; Pred. No. 9.3e-72;
Matches 291; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAGTCCACA 60
Db 102 CAAATTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAGTCCACC 161
Qy 61 ATGACTTGAGGGGCGAGCTCAAGTGTAAATTCATGCACTGTACAGCAGAGAGCCAGCA 120
Db 162 ATGACCTCGAGTGCAGCTCAAGTGTAAATTCATGCACTGTACAGCAGAGAGCCAGCA 221
Qy 121 TCCCTCCCAAAACCTGGATTCTGCGACATCCAACTGGCTTGTGAGTCCCTGCTGCG 180
Db 222 TCCCTCCCAAAACCTGGATTCTGCGACATCCAACTGGCTTGTGAGTCCCTGCTGCG 281
Qy 181 TTCACTGCGAGTGGTCTGGGACCTTCTACTCTCTCACAATCAGACAGAGTGGAGCTGAA 240
Db 282 TTCACTGCGAGTGGTCTGGGACCTTCTACTCTCTCACAATCAGAGCTGTGAGCTGAAA 341
Qy 241 GATGTGCGCACTTATTACTGCGCAGCAGTGTAGTAAACCCAGCCAGCTGGAGGGGGG 300
Db 342 GATGTGCGCACTTATTACTGCGCAGCAGTGTATCATAGTACCCTATATACGTTCCGATCGGGG 401
Qy 301 ACCATGCTGGAAATAGA 318
Db 402 ACCAAGCTGGAATATAA 419

RESULT 4
BC968518 798 bp mRNA linear EST 12-JUN-2001
LOCUS 602835104F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4989720 5',
DEFINITION mRNA sequence.
ACCESSION BC968518
VERSION BC968518.1 GI:14356142
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 798)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1004 row: g column: 01
High quality sequence stop: 797.
Location/Qualifiers
1..798
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAG:4989720"

FEATURES
source

/clone.lib="NCI_CGAP_C024"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."

BASE COUNT 225 a 222 c 179 g 172 t
ORIGIN

Query Match 86.3%; Score 274.4; DB 13; Length 798;
Best Local Similarity 91.8%; Pred. No. 1.5e-71;
Matches 290; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 3 AATTGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAGTCCACT 62
Db 86 AATGTTCTCACCAGCTCCAGCAATCTGTCTGCATCTCCAGGGGAAAGTCCACT 145
Qy 63 GACTTGACAGGGGCGAGCTCAAGTGTAAATTCATGCACTGTACAGCAGAGAGCCAGATC 122
Db 146 GACCTGCACTGCGCACTCAAGTGTAAATTCATGCACTGTACAGCAGAGAGCCAGATC 205
Qy 123 CTCGCCCAAAACCTGGATTCTGCGACATCCAACTGGCTTGTGAGTCCCTGCTGCTT 182
Db 206 CTCGCCCAAAATGATGATTATGACACATCCAACTGCTTGTGAGTCCCTGCTGCTT 265
Qy 183 CAGTGGCACTGGGCTGGGACCTTCTACTCTCTCACAATCAGAGAGTGGAGCTGAA 242
Db 266 CAGTGGCACTGGGCTGGGACCTTCTACTCTCTCACAATCAGAGAGTGGAGCTGAA 325
Qy 243 TCTGCGCACTTATTACTGCGCAGCAGTGTAGTAAACCCAGCCAGCTGGAGGGGGGAC 302
Db 326 TCTGCGCACTTATTACTGCGCAGCAGTGTAGTAAATTCATGCACTGTACAGAGTGGAGG 385
Qy 303 CATGCTGGAATAGA 318
Db 386 CAAGCTGGAATATAA 401

RESULT 5
B1150509 755 bp mRNA linear EST 05-JUL-2001
LOCUS 602915167F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5065720 5',
DEFINITION mRNA sequence.
ACCESSION B1150509
VERSION B1150509.1 GI:14610510
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 755)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1177 row: e column: 17
High quality sequence stop: 738.
Location/Qualifiers
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/strain="CZECH IT"
/db_xref="taxon:10090"
/clone="IMAG:5065720"
/clone.lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."

FEATURES
source


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"organism"="Mus musculus"
"db_xref"="taxon:10090"
"clone_1"="IMAGE:3372872"
"clone_1b"="Soares-mammary_gland_MMLNG"
"sex"="female (lactating)"
"tissue_type"="mammary gland"
"lab_host"="Dh10b"
"note"="Vector: pT73D-Pac (pharmacia) with a modified

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FEATURES
source
Seq primer: -28m13 rev2 ET from AmerSham.
Location/Qualifiers
1. .396

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:1138201"
/clone_1lb="Barstead mouse irradiated colon MFLB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/ab_vector: pr773D-Pac (Pharmacia) with a modified
polylinker. Site.1: EcoRI. Site.2: NotI. Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
[5'TGTACGATCTGAAAGCGGAGCGCCCTTTTTTTTTTTTTTTTTTTT
T 3']: double-stranded cDNA was ligated to Eco RI
adaptors [AATTCGATCCCTTG], digested with Not I and cloned
into the Not I and Eco RI sites of the modified pr773
vector. Library constructed by Bob Barstead. "

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Query Match	84.0%:	Score 267.2:	DB 9:	Length 396:
Best Local Similarity	92.4%:	Pred. No. 1.5e-69:		
Matches 281:	Conservative 0:	Mismatches 23:	Indels 0:	Gaps 0:
OY	1	CAAAATGTTCTCTCCAGACTCTCCAGACAAATCCTGTCTGCATCTCCAGGGGAAAAGTCA	60	
Db	92	CAAAATTTCTTTCACCCAGCTCTCCAGACAAATCATGTCTGCATCTCCAGGGGAGAAGTCA	151	
OY	61	ATGACTTTCAGGGCCAGCTCAAGTCTAAATTAATCATGACACTGGTACCAGACAGGACAGA	120	
Db	152	ATGACCTCAGAGGCGAGCTCAAGTCTAATTAATTAATCATGACACTGGTACCAGACAGGAC	211	
OY	121	TCTCTCCCCCAACCCCTGGAGTTTCTGCAATCCAACTGGCTTCTGAGATCCCTCTGC	180	
Db	212	ACCTCCCAAGAAAGATGATTTATATACACATCCAAACAGCGCTTCTGAGATCCCTCTGC	271	
OY	181	TTCACTGCGAGTGGGTCTGGGACCTTACTCTCTCACAAATCAGCAGAGTGGAGGCTGAA	240	
Db	272	TTCACTGCGAGTGGGTCTGGGACCTTACTCTCTCACAAATCAGCAGAGTGGAGGCTGAA	331	
OY	241	GATGCTGCGACTTATTACTGCGACGACAGTGGAGTATTAACCAACCCAGCTGGAGGGGG	300	
Db	332	GATGCTGCGACTTATTACTGCGACGACAGTGGAGTATTAACCCAGCTGGAGGGGG	391	
OY	301	ACCA 304		
Db	392	ACCA 395		
RESULT 10				
LOCUS	BF165585	871 bp	mRNA	linear EST 30-OCT-2000
DEFINITION	6017747486p1	NCI_GMAP_Lu29	Mus musculus	cdna clone IMAGE:4019109 5',
ACCESION	BF165585			
VERSION	BF165585.1	GI:11045937		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 871)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-r@mail.nih.gov			
	Tissue Procurement: Gilbert Smith, Ph.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LMNL at:			

BASE COUNT	ORIGIN	FEATURES	SOURCE					
226	a	240	c	201	g	204	t	<p>http://image.jhmi.gov</p> <p>Plate: ULM9270 row: 1 column: 22</p> <p>High quality sequence stop: 714.</p> <p>Location/Qualifiers</p> <p>1. .871</p> <p>/organism="Mus musculus"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="IMAGE:4019109"</p> <p>/clone_id="NCI-CGAP.Lu29"</p> <p>/tissue_type="spontaneous tumor, metastatic to mammary.</p> <p>Stem cell origin.</p> <p>/lab_host="DH10B"</p> <p>/note="Organ: lung; Vector: pCMV-SF006; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"</p>

Query Match	83.9%	Score 266.8	DB 12	Length 871
Best Local Similarity	89.9%	Pred. No. 3e-69		
Matches 286	Conservative 0	Mismatches 32	Indels 0	Gaps 0
QY	1	CAAAATGTTCTCTCCAGCTCTCCAGCAATCTGTCTGATCTCCAGGGGAAAAGTCACA	60	
DB	90	CAAAATTTCTTCTCCACCAGCTCTCCAGCAATCAATGCTGTCTCCAGGGGAAAAGTCACC	149	
QY	61	ATGACTTGCAGGGCCAGCTCAGTGTAATTTACATGCACTGGTTACCAGAGAAGCCAGGA	120	
DB	150	ATGACCTGTGAGTGCAGCTCAAGTGAATTTCTATGCACTGGTATTCAGAGAGCCAGGA	209	
QY	121	TCTCTCCCCCAAAACCTGTGATTTCTGTGCACATCCAACTGGCTTGTGGAGTCCCTGCTCCG	180	
DB	210	TCTCTCCCCCAAAACCTGTGATTTCTGTGCACATCCAACTGGCTTGTGTGAGTCCCTGCTCCG	269	
QY	181	TTTCAGTGCAGTGGGTCTGGGACCTTTACTCTCTCACAATACAGCAGATGGAGCTGAA	240	
DB	270	TTTCAGTGGCAGTGGGACTGGGACCTTTACTCTCTCACAATACAGCAGATGGAGCTGAA	329	
QY	241	GATGTGTCACACTTATTTATTCAGCAGAGCTGAGAGTGAATGACCCACCCGCTTCGAGAGGGG	300	
DB	330	GATGTGTCACACTTATTTATTCAGCAGAGCTGAGAGTGAATGATGTTACCCACGACGCTTCGAGAGGG	389	
QY	301	ACCATGCTGGAAATAGA	318	
DB	390	ACCAAGCTGGAATACAA	407	
RESULT 11				
LOCUS	BG964349	865 bp	mRNA	linear EST 12-JUN-2001
DEFINITION	602831966F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:498568 5'			
ACCESSION	BG964349			
VERSION	BG964349.1			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	NIH-MGC http://mgc.nci.nih.gov/			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgabbs-remail.nih.gov			
	Tissue Procurement: Jeffrey E. Green, M.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			

/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="Spontaneous tumor, metastatic to mammary.
Stem cell origin"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site:1; Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 197 a 214 c 168 g 164 t
ORIGIN

Query Match 82.5%; Score 262.2; DB 13; Length 743;
Best Local Similarity 89.5%; Pred. No. 6.7e-68;
Matches 282; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
OY 4 ATTGTTCTCTCCAGTCTCCAGCAATCCGTCTGCATCTCCAGGGAAAGGTCACAAATG 63
DB 25 ATTCTTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGAGAGAGAGGTCACCAATG 84
OY 64 ACTTCAGAGGCCAGCTCAAGTGAATTAATGACATGCACTGGTACCAAGAGCCAGAGATCC 123
DB 85 ACCTGCAGTGCAGCTCAAGTGAATTAATTCATGCACTGGTATCAGCAGAGAGCCAGATCC 144
OY 124 TCCCCCAACCTGGATTTCTGCCACATCCAGACTGGCTTCTGGAGTCCCTGCTGCTTC 183
DB 145 TCCCCCAAGCCCTGGATTTCTGTACATCCGACCTGGCTTCTGGAGTCCCTGCTGCTTC 204
OY 184 AGTGCAGTGGGTCTGGAGCTCTTACTCTCTCACAATCAGCAGAGTGGAGCTGAAGAT 243
DB 205 AGTGCAGTGGAGCTGGAGCTCTTACTCTCTCACAATCAGCAGATGAGAGCTGAAGAT 264
OY 244 GCTGCCACTTATTACTGCCAGAGTGGAGTAGTAACCCACCGTTCGAGGGGGGAGCC 303
DB 265 GCTGCCACTTATTACTGCCAGAGTGGAGTAGTAACCCACCGAGAGTTCGAGGGAGCC 324
OY 304 ATGCTGAAATAGA 318
DB 325 AAGCTGAAATCAAA 339

Search completed: November 27, 2002, 05:29:45
Job time : 1336.29 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:35:53 ; Search time 35.6419 Seconds
(Without alignments)
2736.194 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318

Sequence: 1 CAATGTCTCTCCAGTC.....GACCATCGTGAATAGA 318

Scoring table: IDENTITY_NUC

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents.NA:*

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- 2: /cgn2_6/p/locdata/1/lna/5B_COMB.seq:*
- 3: /cgn2_6/p/locdata/1/lna/6A_COMB.seq:*
- 4: /cgn2_6/p/locdata/1/lna/6B_COMB.seq:*
- 5: /cgn2_6/p/locdata/1/lna/PCrTUS_COMB.seq:*
- 6: /cgn2_6/p/locdata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300.4	94.5	321	3	US-08-783-853A-6
2	300.4	94.5	321	4	US-09-344-050-6
3	300.4	94.5	384	1	US-08-149-099C-6
4	300.4	94.5	384	2	US-08-478-967A-6
5	300.4	94.5	384	4	US-08-475-815B-6
6	300.4	94.5	9209	1	US-08-149-099C-3
7	300.4	94.5	9209	2	US-08-478-967A-3
8	300.4	94.5	9209	4	US-08-475-815B-3
9	300.4	94.5	18986	2	US-08-819-866-2
10	300.4	94.5	18986	2	US-09-023-715-2
11	300.4	94.5	18986	4	US-09-343-485A-2
12	282.8	94.0	384	1	US-08-476-275-3
13	287.2	93.5	9209	1	US-08-476-275-2
14	295.6	93.0	318	3	US-08-783-853A-104
15	295.6	93.0	318	4	US-09-344-050-104
16	295.6	93.0	335	3	US-08-783-853A-102
17	295.6	93.0	335	4	US-09-344-050-102
18	282.4	91.9	387	2	US-08-449-287-1
19	290.8	91.4	732	2	US-08-860-882A-26
20	290.8	91.4	732	4	US-09-423-439-57
21	290.8	91.4	732	4	US-09-011-769A-22
22	287.6	90.4	705	4	US-09-423-439-17
23	287.6	90.4	3217	1	US-09-423-439-52
24	285.8	89.9	315	1	US-08-459-310-3
25	281.8	88.6	321	1	US-08-211-202-4
26	281.8	88.6	711	1	US-08-061-092A-1
27	281.2	88.4	758	3	US-08-279-772A-5

28	281.2	88.4	759	3	US-08-902-486-8
29	280.2	88.1	711	2	US-08-468-252-4
30	280.2	88.1	711	3	US-08-668-706B-4
31	280.2	88.1	711	5	PCT-US95-10740-4
32	273.4	86.0	292	2	US-08-308-494A-12
33	273.2	85.9	384	2	US-08-656-586-1
34	273.2	85.9	393	2	US-08-116-778E-39
35	273.2	85.9	393	2	US-08-438-562-39
36	273.2	85.9	393	2	US-08-483-528B-2
37	273.2	85.9	393	3	US-08-673-799C-2
38	273.2	85.9	393	4	US-09-393-385B-2
39	271.8	85.5	292	2	US-09-280-028-3
40	271.4	85.3	331	3	US-08-836-561-32
41	270	84.9	669	2	US-08-190-199A-66
42	270	84.9	708	2	US-08-190-199A-60
43	268.4	84.4	390	1	US-08-482-882-79
44	268.4	84.4	390	1	US-08-483-389-79
45	268.4	84.4	390	2	US-08-487-113D-79

ALIGNMENTS

RESULT 1
US-08-783-853A-6
Sequence 6, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-783-853A-6

Query Match 94.5%; Score 300.4; DB 3; Length 321;
Best Local Similarity 96.5%; Pred. No. 9e-86;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTCCACA 60
DB 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTCCACA 60
QY 61 ATGACTTGACAGGGCCAGCTCAAGTGAATTAATACATGACAGTGGACAGCAGAGCCAGGA 120
DB 61 ATGACTTGACAGGGCCAGCTCAAGTGAATTAATACATGACAGTGGACAGCAGAGCCAGGA 120
QY 121 TCCTCCCCCAAAACCCGTGATTTCTGCGACATCCCAACCTGCTTCTGAGTCCCTGCTCGC 180
DB 121 TCCTCCCCCAAAACCCGTGATTTCTGCGACATCCCAACCTGCTTCTGAGTCCCTGCTCGC 180
QY 181 TTCAGTGGCAGTGGGTCTGGGACCTTCTCTCTCTCAATCAGCAGAGTGGAGCTGAA 240
DB 181 TTCAGTGGCAGTGGGTCTGGGACCTTCTCTCTCTCAATCAGCAGAGTGGAGCTGAA 240
QY 241 GATGCTGCACATTATTACTGCGCAGCAGTGGAGTAAACCCAGCAGTTCGAGAGGGGG 300
DB 241 GATGCTGCACATTATTACTGCGCAGCAGTGGAGTAAACCCAGCAGTTCGAGAGGGGG 300
QY 301 ACCAGCTGGAAATTAAGA 318
DB 301 ACCAGCTGGAAATTAAGA 318

RESULT 2
US-09-344-050-6

Sequence 6, Application US/09344050
Patent No. 6391299
GENERAL INFORMATION:

APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
TITLE OF INVENTION: ANTICOGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344, 050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-09-344-050-6

Query Match 94.5%; Score 300.4; DB 4; Length 321;
Best Local Similarity 96.5%; Pred. No. 9e-86;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTCCACA 60
DB 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTCCACA 60
QY 61 ATGACTTGACAGGGCCAGCTCAAGTGAATTAATACATGACAGTGGACAGCAGAGCCAGGA 120
DB 61 ATGACTTGACAGGGCCAGCTCAAGTGAATTAATACATGACAGTGGACAGCAGAGCCAGGA 120
QY 121 TCCTCCCCCAAAACCCGTGATTTCTGCGACATCCCAACCTGCTTCTGAGTCCCTGCTCGC 180
DB 121 TCCTCCCCCAAAACCCGTGATTTCTGCGACATCCCAACCTGCTTCTGAGTCCCTGCTCGC 180
QY 181 TTCAGTGGCAGTGGGTCTGGGACCTTCTCTCTCTCAATCAGCAGAGTGGAGCTGAA 240
DB 181 TTCAGTGGCAGTGGGTCTGGGACCTTCTCTCTCTCAATCAGCAGAGTGGAGCTGAA 240
QY 241 GATGCTGCACATTATTACTGCGCAGCAGTGGAGTAAACCCAGCAGTTCGAGAGGGGG 300
DB 241 GATGCTGCACATTATTACTGCGCAGCAGTGGAGTAAACCCAGCAGTTCGAGAGGGGG 300
QY 301 ACCAGCTGGAAATTAAGA 318
DB 301 ACCAGCTGGAAATTAAGA 318

RESULT 3
US-08-149-099C-6

Sequence 6, Application US/08149099C
Patent No. 5736137
GENERAL INFORMATION:

APPLICANT: ANDERSON, Darrell R.
APPLICANT: HANNA, Nabil
APPLICANT: LEONARD, John E.
APPLICANT: NEWMAN, Roland A.
APPLICANT: REFF, Mitchell E.
TITLE OF INVENTION: THERAPEUTIC ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P O Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,099C
FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..384
NAME/KEY: mat-peptide
LOCATION: 67..384
US-08-149-099C-6

Query Match 94.5%; Score 300.4; DB 1; Length 384;
Best Local Similarity 96.5%; Pred. No. 9.7e-86;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 CAAATTGTTCTCTCCAGCTCCAGCAATCCGTGTCATCTCCAGGGGAAAGGTGACA 60
DB 67 CAAATTGTTCTCTCCAGCTCCAGCAATCCGTGTCATCTCCAGGGGAAAGGTGACA 126
OY 61 ATGACTTGAGGGCCAGCTCAAGTGAATTACATGCATGCTGACGAGGAGGAGGAGA 120
DB 127 ATGACTTGAGGGCCAGCTCAAGTGAATTACATGCATGCTGACGAGGAGGAGGAGA 186
OY 121 TCCTCCCCCAACCTGGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTGC 180
DB 187 TCCTCCCCCAACCTGGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTGC 246
OY 181 TTCAGTGGAGTGGGCTGGGACCTCTTACTCTCACAATCAGACAGAGTGGAGGCTGAA 240
DB 247 TTCAGTGGAGTGGGCTGGGACCTCTTACTCTCACAATCAGACAGAGTGGAGGCTGAA 306
OY 241 GATGCTGCCACTTATTACTGCGACAGAGTGAAGTAAACCCACGCTTGGAGGGGG 300
DB 307 GATGCTGCCACTTATTACTGCGACAGAGTGAAGTAAACCCACGCTTGGAGGGGG 366
OY 301 ACCATGCTGGAATAAGA 318
DB 367 ACCAAGCTGGAATCAAA 384

RESULT 4
US-08-478-967A-6
Sequence 6, Application US/08478967A
Patent No. 5843439
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
APPLICANT: HANNA, Nabil
APPLICANT: LEONARD, John E.
APPLICANT: NEWMAN, Roland A.
APPLICANT: REFF, Mitchell E.
APPLICANT: RASTETTER, William H.

TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
LYMPHOMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,967A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..384
NAME/KEY: mat-peptide
LOCATION: 67..384
US-08-478-967A-6

Query Match 94.5%; Score 300.4; DB 2; Length 384;
Best Local Similarity 96.5%; Pred. No. 9.7e-86;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 CAAATTGTTCTCTCCAGCTCCAGCAATCCGTGTCATCTCCAGGGGAAAGGTGACA 60
DB 67 CAAATTGTTCTCTCCAGCTCCAGCAATCCGTGTCATCTCCAGGGGAAAGGTGACA 126
OY 61 ATGACTTGAGGGCCAGCTCAAGTGAATTACATGCATGCTGACGAGGAGGAGGAGA 120
DB 127 ATGACTTGAGGGCCAGCTCAAGTGAATTACATGCATGCTGACGAGGAGGAGGAGA 186
OY 121 TCCTCCCCCAACCTGGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTGC 180
DB 187 TCCTCCCCCAACCTGGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTGC 246
OY 181 TTCAGTGGAGTGGGCTGGGACCTCTTACTCTCACAATCAGACAGAGTGGAGGCTGAA 240
DB 247 TTCAGTGGAGTGGGCTGGGACCTCTTACTCTCACAATCAGACAGAGTGGAGGCTGAA 306
OY 241 GATGCTGCCACTTATTACTGCGACAGAGTGAAGTAAACCCACGCTTGGAGGGGG 300
DB 307 GATGCTGCCACTTATTACTGCGACAGAGTGAAGTAAACCCACGCTTGGAGGGGG 366

Best Local Similarity 96.5%; Pred. No. 3.2e-85;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCCACTTCACCAATCTCTGTGCATCTCCAGGGGAAAAGTGCACA 60
Db 1045 CAAATGTTCTCTCCCACTTCACCAATCTCTGTGCATCTCCAGGGGAAAAGTGCACA 1104
QY 61 ATGACTTCAGAGGCGAGCTCAAGTGTAAATTACATGCAGTGTACACAGAGGAGGAGG 120
Db 1105 ATGACTTCAGAGGCGAGCTCAAGTGTAAATTACATGCAGTGTACACAGAGGAGGAGG 1164
QY 121 TCTCTCCCAAAACCTGGATTTCTGCGACATCAACCTGGCTTCTGAGTCCCTGCTGC 180
Db 1165 TCTCTCCCAAAACCTGGATTTATGCGACATCAACCTGGCTTCTGAGTCCCTGCTGC 1224
QY 181 TTCAGTGGCAGTGGGTGGGAGCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
Db 1225 TTCAGTGGCAGTGGGTGGGAGCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 1284
QY 241 GATGCTGCCACTTATTACTGCCAGAGTGGAGTAACTAACCCACGCTTGGAGGGGG 300
Db 1285 GATGCTGCCACTTATTACTGCCAGAGTGGAGTAACTAACCCACGCTTGGAGGGGG 1344
QY 301 ACCATGCTGGAATTAAGA 318
Db 1345 ACCAAGCTGGAATTAAGA 1362

RESULT 7
US-08-478-967A-3
Sequence 3, Application US/08478967A
Patent No. 5843439

GENERAL INFORMATION:

APPLICANT: ANDERSON, Darrell R.
APPLICANT: HANNA, Nabill
APPLICANT: LEONARD, John E.
APPLICANT: NEWMAN, Roland A.
APPLICANT: REFF, Mitchell E.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478, 967A

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149, 099

FILING DATE: 03-NOV-1993

APPLICATION NUMBER: US 07/978, 891

FILING DATE: 12-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35, 030

REFERENCE/DOCKET NUMBER: 012712-014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 9209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-478-967A-3

Query Match 94.5%; Score 300.4; DB 2; Length 9209;
Best Local Similarity 96.5%; Pred. No. 3.2e-85;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCCACTTCACCAATCTCTGTGCATCTCCAGGGGAAAAGTGCACA 60
Db 1045 CAAATGTTCTCTCCCACTTCACCAATCTCTGTGCATCTCCAGGGGAAAAGTGCACA 1104
QY 61 ATGACTTCAGAGGCGAGCTCAAGTGTAAATTACATGCAGTGTACACAGAGGAGGAGG 120
Db 1105 ATGACTTCAGAGGCGAGCTCAAGTGTAAATTACATGCAGTGTACACAGAGGAGGAGG 1164
QY 121 TCTCTCCCAAAACCTGGATTTCTGCGACATCAACCTGGCTTCTGAGTCCCTGCTGC 180
Db 1165 TCTCTCCCAAAACCTGGATTTATGCGACATCAACCTGGCTTCTGAGTCCCTGCTGC 1224
QY 181 TTCAGTGGCAGTGGGTGGGAGCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
Db 1225 TTCAGTGGCAGTGGGTGGGAGCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 1284
QY 241 GATGCTGCCACTTATTACTGCCAGAGTGGAGTAACTAACCCACGCTTGGAGGGGG 300
Db 1285 GATGCTGCCACTTATTACTGCCAGAGTGGAGTAACTAACCCACGCTTGGAGGGGG 1344
QY 301 ACCATGCTGGAATTAAGA 318
Db 1345 ACCAAGCTGGAATTAAGA 1362

RESULT 8
US-08-475-815B-3
Sequence 3, Application US/08475815B
Patent No. 639061

GENERAL INFORMATION:

APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABILL
APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: REFF, MITCHELL E.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475, 815B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/149, 099

FILED DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-473-815B-3

Query Match 94.5%; Score 300.4; DB 4; Length 9209;
Best Local Similarity 96.5%; Pred. No. 3.2e-85;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGGTCACA 60
DB 1045 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGGTCACA 1104
QY 61 ATGACTTGCGAGGCGCAGCTCAAGTGAATTAATGATGACGAGTGAAGGAGCCAGGA 120
DB 1105 ATGACTTGCGAGGCGCAGCTCAAGTGAATTAATGATGACGAGTGAAGGAGCCAGGA 1164
QY 121 TCCTCCGCCAAACCTGGATTTCTGCGACATGCCACCTGCTTCTGGAGTCCCTGCTCGC 180
DB 1165 TCCTCCGCCAAACCTGGATTTCTGCGACATGCCACCTGCTTCTGGAGTCCCTGCTCGC 1224
QY 181 TTCAAGTGGCAGTGGGTCTGGAGCCTCTTACTCTCTCAATCAGCAGAGTGGAGCTGAA 240
DB 1225 TTCAAGTGGCAGTGGGTCTGGAGCCTCTTACTCTCTCAATCAGCAGAGTGGAGCTGAA 1284
QY 241 GATGCTGCGCACTTAATTAAGTCCAGCAGTGAAGTAAAGCCAGCCAGTGGAGGGGG 300
DB 1285 GATGCTGCGCACTTAATTAAGTCCAGCAGTGAAGTAAAGCCAGCCAGTGGAGGGGG 1344
QY 301 ACCATGCTGGAATTAAGA 318
DB 1345 ACCATGCTGGAATTAAGA 1362

RESULT 9
US-08-819-866-2
Sequence 2, Application US/08819866
Patent No. 5830698

GENERAL INFORMATION:
APPLICANT: REEF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Rella
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
City: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,866
FILING DATE: 14-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-352
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-819-866-2

Query Match 94.5%; Score 300.4; DB 2; Length 18986;
Best Local Similarity 96.5%; Pred. No. 4.2e-85;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGGTCACA 60
DB 8077 CAAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGGTCACA 8136
QY 61 ATGACTTGCGAGGCGCAGCTCAAGTGAATTAATGATGACGAGTGAAGGAGCCAGGA 120
DB 8137 ATGACTTGCGAGGCGCAGCTCAAGTGAATTAATGATGACGAGTGAAGGAGCCAGGA 8196
QY 121 TCCTCCGCCAAACCTGGATTTCTGCGACATGCCACCTGCTTCTGGAGTCCCTGCTCGC 180
DB 8197 TCCTCCGCCAAACCTGGATTTCTGCGACATGCCACCTGCTTCTGGAGTCCCTGCTCGC 8256
QY 181 TTCAAGTGGCAGTGGGTCTGGAGCCTCTTACTCTCTCAATCAGCAGAGTGGAGCTGAA 240
DB 8257 TTCAAGTGGCAGTGGGTCTGGAGCCTCTTACTCTCTCAATCAGCAGAGTGGAGCTGAA 8316
QY 241 GATGCTGCGCACTTAATTAAGTCCAGCAGTGAAGTAAAGCCAGCCAGTGGAGGGGG 300
DB 8317 GATGCTGCGCACTTAATTAAGTCCAGCAGTGAAGTAAAGCCAGCCAGTGGAGGGGG 8376
QY 301 ACCATGCTGGAATTAAGA 318
DB 8377 ACCATGCTGGAATTAAGA 8394

RESULT 10
US-09-023-715-2
Sequence 2, Application US/09023715
Patent No. 5998144

GENERAL INFORMATION:
APPLICANT: REEF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Rella
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
City: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/819,866
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-352
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-715-2

Query Match 94.5%; Score 300.4; DB 2; Length 18986;
Best Local Similarity 96.5%; Pred. No. 4,2e-85;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGAAGGTGACA 60
DB 8077 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGAAGGTGACA 8136
QY 61 ATGACTTGACAGGCGCAGCTCAAGTAAATACATGACCTGTGACAGCAGACAGCA 120
DB 8137 ATGACTTGACAGGCGCAGCTCAAGTAAATACATGACCTGTGACAGCAGACAGCA 8196
QY 121 TCTTCCCCCAAACTGGATTCTGACACATCAACCTGGCTTGGAGTCCCTGCTGC 180
DB 8197 TCTTCCCCCAAACTGGATTCTGACACATCAACCTGGCTTGGAGTCCCTGCTGC 8256
QY 181 TTCAGTGGACAGTGGGTCTGGAGCTCTTACTCTCTCACAATCAGACAGAGTGA 240
DB 8257 TTCAGTGGACAGTGGGTCTGGAGCTCTTACTCTCTCACAATCAGACAGAGTGA 8316
QY 241 GATCTGCGACATTATTAAGTCCAGCAGTGAAGTAAACCCAGCTTGGAGGGGG 300
DB 8317 GATCTGCGACATTATTAAGTCCAGCAGTGAAGTAAACCCAGCTTGGAGGGGG 8376
QY 301 ACCATGCTGGAATTAAGA 318
DB 8377 ACCAAGCTGGAATTAAGA 8394

RESULT 11
US-09-343-485A-2
Sequence 2, Application US/09343485A
Patent No. 6413777
GENERAL INFORMATION:
APPLICANT: REE, MITCHELL R.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MCILACHLAN, KAREN R.
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
FILE REFERENCE: 037003-0275807
CURRENT APPLICATION NUMBER: US/09/343,485A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/023,715
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 08/819,866
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

LENGTH: 18986
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
OTHER INFORMATION: referred to as "Molly"
US-09-343-485A-2

Query Match 94.5%; Score 300.4; DB 4; Length 18986;
Best Local Similarity 96.5%; Pred. No. 4,2e-85;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGAAGGTGACA 60
DB 8077 CAAATGTTCTCTCCAGCTCCAGCAATCTGTCTGCATCTCCAGGGAAGGTGACA 8136
QY 61 ATGACTTGACAGGCGCAGCTCAAGTAAATACATGACCTGTGACAGCAGACAGCA 120
DB 8137 ATGACTTGACAGGCGCAGCTCAAGTAAATACATGACCTGTGACAGCAGACAGCA 8196
QY 121 TCTTCCCCCAAACTGGATTCTGACACATCAACCTGGCTTGGAGTCCCTGCTGC 180
DB 8197 TCTTCCCCCAAACTGGATTCTGACACATCAACCTGGCTTGGAGTCCCTGCTGC 8256
QY 181 TTCAGTGGACAGTGGGTCTGGAGCTCTTACTCTCTCACAATCAGACAGTGA 240
DB 8257 TTCAGTGGACAGTGGGTCTGGAGCTCTTACTCTCTCACAATCAGACAGTGA 8316
QY 241 GATCTGCGACATTATTAAGTCCAGCAGTGAAGTAAACCCAGCTTGGAGGGGG 300
DB 8317 GATCTGCGACATTATTAAGTCCAGCAGTGAAGTAAACCCAGCTTGGAGGGGG 8376
QY 301 ACCATGCTGGAATTAAGA 318
DB 8377 ACCAAGCTGGAATTAAGA 8394

RESULT 12
US-08-476-275-3
Sequence 3, Application US/08476275
Patent No. 5776456
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reiff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-cell
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: murine variable region light chain
FEATURE:
NAME/KEY: CDS
LOCATION: 1..384
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 67..384
US-08-476-275-3

Query Match 94.0%; Score 298.8; DB 1: Length 384;
Best Local Similarity 96.2%; Pred. No. 3.1e-85;
Matches 306; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CAAATTGTTCTCTCCAGTCCTCCAGCAATCTGTGATCTCCAGGGGAAAGTCCACA 60
DB 67 CAAATTGTTCTCTCCAGTCCTCCAGCAATCTGTGATCTCCAGGGGAAAGTCCACA 126
QY 61 ATGACTTGACGGGCGGCTCAAGTGAATTAATTAATGACACTGGTACACAGAGAGCCAGGA 120
DB 127 ATGACTTGACGGGCGGCTCAAGTGAATTAATTAATGACACTGGTACACAGAGAGCCAGGA 186
QY 121 TCCTCCCGCCAAACCTGGATTTCTGCGACATCCAACTGGCTTCTGAGAGTCCCTGCTCG 180
DB 187 TCCTCCCGCCAAACCTGGATTTCTGCGACATCCAACTGGCTTCTGAGAGTCCCTGCTCG 246
QY 181 TTCAGTGGCAGTGGGTCTGGAGACCTTTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 240
DB 247 TTCAGTGGCAGTGGGTCTGGAGACCTTTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 306
QY 241 GATGCTGCCACTTATTAAGTCCAGCAGTGGAGTAAACCCAGCTTCGAGAGGGGG 300
DB 307 GATGCTGCCACTTATTAAGTCCAGCAGTGGAGTAAACCCAGCTTCGAGAGGGGG 366
QY 301 ACCAGCTGGAAATAGA 318
DB 367 ACCAGCTGGAAATAGA 384

RESULT 13

US-08-476-275-2
Sequence 2, Application US/08476275
Patent No. 5776456
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
TITLE OF INVENTION: Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
POSITION IN GENOME:
CHROMOSOME/SEGMENT: anti-CD20 in TCAE 8
US-08-476-275-2

Query Match 93.5%; Score 297.2; DB 1: Length 9209;
Best Local Similarity 95.9%; Pred. No. 3.3e-84;
Matches 905; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 CAAATTGTTCTCTCCAGTCCTCCAGCAATCTGTGATCTCCAGGGGAAAGTCCACA 60
DB 1045 CAAATTGTTCTCTCCAGTCCTCCAGCAATCTGTGATCTCCAGGGGAAAGTCCACA 1104
QY 61 ATGACTTGACGGGCGGCTCAAGTGAATTAATTAATGACACTGGTACACAGAGAGCCAGGA 120
DB 1105 ATGACTTGACGGGCGGCTCAAGTGAATTAATTAATGACACTGGTACACAGAGAGCCAGGA 1164
QY 121 TCCTCCCGCCAAACCTGGATTTCTGCGACATCCAACTGGCTTCTGAGAGTCCCTGCTCG 180
DB 1165 TCCTCCCGCCAAACCTGGATTTCTGCGACATCCAACTGGCTTCTGAGAGTCCCTGCTCG 1224
QY 181 TTCAGTGGCAGTGGGTCTGGAGACCTTTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 240
DB 1225 TTCAGTGGCAGTGGGTCTGGAGACCTTTACTCTCTCACAATCAGCAGAGTGGAGCTGAA 1284
QY 241 GATGCTGCCACTTATTAAGTCCAGCAGTGGAGTAAACCCAGCTTCGAGAGGGGG 300
DB 1285 GATGCTGCCACTTATTAAGTCCAGCAGTGGAGTAAACCCAGCTTCGAGAGGGGG 1344
QY 301 ACCAGCTGGAAATAGA 318
DB 1345 ACCAGCTGGAAATAGA 1362

RESULT 14

US-08-783-853A-104
Sequence 104, Application US/08783853A
Patent No. 6005091

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..318
OTHER INFORMATION:
US-08-783-853A-104

Query Match 93.0%; Score 295.6; DB 3; Length 318;
Best Local Similarity 95.6%; Pred.No.2.9e-84;
Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCTGTCATCTCCAGGAGAAAGTGCACA 60
DB 1 CAGATAGTACTCTCCAGTCTCCAGCAATCTGTCATCTCCAGGAGAAAGTGCACA 60
QY 61 ATGACTTGCAGGCGCAGCTCAAGTGTAAATTAATGACGACTGTACCCAGAGAGCAGAGA 120
DB 61 ATGACTTGCAGGCGCAGCTCAAGTGTAAATTAATGACGACTGTACCCAGAGAGCAGAGA 120
QY 121 TCCTCCCGCCAAACCCGATTTCTGCGACATCCCAACTGGCTTTGAGATCCCTGCTCGC 180
DB 121 TCCTCCCGCCAAACCCGATTTCTGCGACATCCCAACTGGCTTTGAGATCCCTGCTCGC 180
QY 181 TTCAGTGCAGTGGTCTGTGGACCTCTTACTCTCTCACAATGAGAGTGAAGCTGAA 240

|||||
DB 181 TTCAGTGCAGTGGTCTGTGGACCTCTTACTCTCTCACAATGAGAGTGAAGCTGAA 240
QY 241 GATGCTGCCACTTATTACTGCCAGAGTGGAGTAGTACCACCCACGTTGGAGGGGG 300
DB 241 GATGCTGCCACTTATTACTGCCAGAGTGGAGTAGTACCACCCACGTTGGAGGGGG 300
QY 301 ACCATGCTGGAATAAGA 318
DB 301 ACCATGCTGGAATAAGA 318

RESULT 15
US-09-344-050-104
Sequence 104, Application US/09344050
Patent No. 6391289

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..318
OTHER INFORMATION:
US-09-344-050-104

Query Match 93.0%; Score 295.6; DB 4; Length 318;

Best Local Similarity 95.6%; Pred. No. 2.9e-84;
Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 1 CAAATGTTCTCTCCAGTCTCCAGCAATCCTGCTGTGATCTCCAGGGGAAAAAGTCACA 60
    || || || || || || || || || || || || || || || || || || || || ||
Db 1 CAGATAGTACTCTCCAGTCTCCAGCAATCCTGCTGTGATCTCCAGGGGAGAGGTCACA 60
    || || || || || || || || || || || || || || || || || || || || ||
QY 61 ATGACTTGACAGGGCCAGCTCAAGTAAATACATGCACCTGGTACACAGACAGCCAGGA 120
    || || || || || || || || || || || || || || || || || || || || ||
Db 61 ATGACTTGACAGGGCCAGCTCAAGTAAATACATGCACCTGGTACACAGACAGCCAGGA 120
    || || || || || || || || || || || || || || || || || || || || ||
QY 121 TCTTCCCCCAAAACCCTGGATTTCGCCACATCAACCTGGCTTCGAGTCCCTGCTGC 180
    || || || || || || || || || || || || || || || || || || || || ||
Db 121 TCTTCCCCCAAAACCCTGGATTTCGCCACATCAACCTGGCTTCGAGTCCCTGCTGC 180
    || || || || || || || || || || || || || || || || || || || || ||
QY 181 TTCAGTGGCAAGTGGGTCTGGGACCTTCTACTCTCTCACAAATCAGCAGAGTGGAGCTGAA 240
    || || || || || || || || || || || || || || || || || || || || ||
Db 181 TTCAGTGGCAAGTGGGTCTGGGACCTTCTACTCTCTCACAAATCAGCAGAGTGGAGCTGAA 240
    || || || || || || || || || || || || || || || || || || || || ||
QY 241 GATGCTGCACCTTATTTACTGCCAGCAGTGGAGTAGTAACCCACGCTTGGAGGGGG 300
    || || || || || || || || || || || || || || || || || || || || ||
Db 241 GATGCTGCACCTTATTTACTGCCAGCAGTGGAGTAGTAACCCACGACGTTGGTGGAGGC 300
    || || || || || || || || || || || || || || || || || || || || ||
QY 301 ACCATGCTGGAATTAAGA 318
    || || || || || || || || || || || || || || || || || || || || ||
Db 301 ACCAAGCTGGAATCAAA 318
    || || || || || || || || || || || || || || || || || || || || ||
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Search completed: November 27, 2002, 03:55:49
Job time : 72.1419 secs

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: November 27, 2002, 05:38:32 : Search time 58.5251 Seconds
(without alignments)
241.342 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 556

Sequence: 1 QIVLSQSPAILASPGKVT.....CQWSSNPFGGTMLEIR 106

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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3: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
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22: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	526	94.6	106	AAW24532	Anti-Factor IX Mab
2	526	94.6	106	AAU61002	Mouse-human light
3	526	94.6	107	AAW24520	Mouse anti-human F
4	526	94.6	107	AAU60976	Murine BC2 light c
5	526	94.6	112	AAW24531	Anti-Factor IX Mab
6	526	94.6	112	AAU61001	Murine BC2 light c
7	521	93.7	128	AAW55214	Murine variable re
8	517	93.0	412	AAW30694	A fusion of anti-C
9	517	93.0	423	AAW30695	A fusion of anti-C
10	516	92.8	128	AAW70628	Sequence encoded b

11	516	92.8	128	10	AAW94781
12	516	92.8	128	18	AAW10589
13	516	92.8	128	18	AAW16344
14	516	92.8	128	18	AAW10243
15	516	92.8	128	19	AAW47521
16	516	92.8	128	19	AAW41071
17	516	92.8	128	19	AAW47514
18	516	92.8	128	20	AAW69541
19	516	92.8	128	22	AAW68093
20	514	92.4	633	21	AAW84965
21	507	91.2	129	13	AAW20789
22	507	91.2	129	13	AAW30430
23	507	91.2	235	17	AAW06178
24	507	91.2	235	20	AAW82746
25	507	91.2	235	20	AAW82746
26	507	91.2	235	21	AAW08025
27	504	90.6	145	12	AAW15323
28	504	90.6	145	14	AAW32127
29	503	90.5	106	23	AAW72834
30	501	90.1	105	18	AAW19914
31	491	88.3	108	16	AAW79883
32	489	87.9	236	15	AAW45442
33	489	87.9	237	17	AAW94020
34	489	87.9	237	18	AAW15185
35	486	87.4	107	14	AAW34263
36	486	87.4	246	15	AAW60522
37	484	87.1	252	21	AAW12562
38	484	87.1	252	22	AAW36825
39	482	86.7	107	13	AAW79059
40	478	86.0	107	13	AAW24723
41	475	85.4	97	11	AAW07317
42	475	85.4	97	17	AAW14485
43	475	85.4	97	17	AAW98874
44	475	85.4	97	20	AAW33426
45	475	85.4	97	21	AAW51369

ALIGNMENTS

RESULT 1
AAW24532
AAW24532 standard; Protein; 106 AA.
AAW24532;
27-DEC-1997 (first entry)
Anti-Factor IX Mab chimeric light chain.
Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
Chimeric antibody; antibody engineering; light chain.
Chimeric Mus musculus.
Chimeric Homo sapiens.
Chimeric synthetic.
W09726010-A1.
24-JUL-1997.
17-JAN-1997; 97WO-US00759.
24-OCT-1996; 96US-0029119.
17-JAN-1996; 96US-0010108.
(SMK) SMITHKLINE BEECHAM CORP.
(UYVE) UNIV VERMONT & STATE AGRIC COLLEGE.
Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
Nichols AJ, Padlan EA, Patel AH, Sylvester CR;
WPI, 1997-385117/35.

2 H7 VL gene. Syn
2H7 antibody light
2H7 light chain va
Light chain variab
Mouse 2H7 antibody
Mouse 2H7 antibody
Mouse 2H7 antibody
Mouse antibody 2H7
2H7 light chain va
Amino acid sequenc
Unprocessed variab
ASB7 antibody light
Murine ASB7 light
Plasmid pNC3/ASB7
A dimeric anti-CD2
IL-2 chimeric anti
Anti-IL2R-alpha an
Anti-IL2R2 hybrido
Kappa light chain
Anti-EGFR antibody
Sequence of the si
Anti-erbB2 scfv.
Single-chain anti-
Mab32 V-gene heavy
Anti-TNF antibody D
Chimeric L6 anti-C
I6 scv protein. U
Amino acid sequenc
Sequence encoded b
VK domain of antib
Monoclonal antibod
Monoclonal antibody
Mouse monoclonal a

DR N-PSDB; AAT79900.
 XX Inhibiting thrombosis with self-limiting antibody to coagulation
 PT factor - avoids uncontrolled bleeding by providing only partial
 PT inhibition
 XX Example 7; Page 128; 150pp; English.
 PS
 CC This polypeptide comprises a mouse-human chimeric antibody
 CC light chain in which the variable region is derived from mouse
 CC anti-human factor IX monoclonal antibody BC2 (see AAW24531) and
 CC human sequences from the immunoglobulin RF-7S3/CL framework.
 CC It can be expressed in transfected mammalian cells utilizing a
 CC cDNA construct (see AAT79900) obtained by PCR amplification (see
 CC AAT79897-98) of BC2 cDNA and insertion of the PCR product into
 CC F9H2HC 1-3 cDNA (see AAT77374). Claimed anti-Factor IX chimeric
 CC antibodies are useful in the treatment of thrombosis.
 XX
 SO Sequence 106 AA:
 Query Match 94.6%; Score 526; DB 18; Length 106;
 Best Local Similarity 95.3%; Pred. No. 1.8e-30;
 Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QIVLSQSPALLSAPGKRYMTTCRASSSVYMHYQOKPSSSPKWTLSATSNLASGVPAR 60
 DB 1 QIVLSQSPALLSAPGKRYMTTCRASSSVYMHYQOKPSSSPKWTLSATSNLASGVPAR 60
 QY 61 FSGSGSGTSTSTSRVEAEDAATYYCQWSSNPPFGCGTMLEIR 106
 DB 61 FSGSGSGTSTSTSRVEAEDAATYYCQWSSNPPFGCGTMLEIR 106
 RESULT 2
 ID AAW81002 standard; Protein; 106 AA.
 AC AAW81002;
 DT 09-APR-2002 (first entry)
 DE Mouse-human light chain polypeptide.
 KW Human: mouse; BC2; animal post-thromboembolic induced ischaemia;
 KW thrombolytic agent; anti-factor IX antibody; plasminogen activator;
 KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
 KW vasotropic; cardiant; anti-respiratory syncytial virus;
 KW heavy chain variable region; light chain variable region.
 XX Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN WO200187339-A1.
 PD 22-NOV-2001.
 PF 05-OCT-2000; 2000MO-US27438.
 PR 15-MAY-2000; 2000US-0571434.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR,
 DR WPI; 2002-082944/11.
 DR N-PSDB; ABR24005.
 XX Treating post-thromboembolic induced ischaemia in an animal by
 PT administering anti-factor IX antibody in combination with a plasminogen
 PT activator
 XX Example 7; Page 155-156; 163pp; English.
 PS

CC The invention relates to a method for treating an animal
 CC post-thromboembolic induced ischaemia or reducing a required dose of a
 CC thrombolytic agent in treatment of an animal post-thromboembolic induced
 CC ischaemia, comprising administering an anti-factor IX antibody or its
 CC fragment, optionally in combination with a plasminogen activator or
 CC thrombolytic agent. The method is useful for treating thromboembolic
 CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
 CC stroke in an animal, and for reducing a required dose of a thrombolytic
 CC agent. Sequences AAW80972-AAW81004 represent antibodies and vector
 CC polypeptides used in the method of the invention.
 XX
 SO Sequence 106 AA:
 Query Match 94.6%; Score 526; DB 23; Length 106;
 Best Local Similarity 95.3%; Pred. No. 1.8e-30;
 Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QIVLSQSPALLSAPGKRYMTTCRASSSVYMHYQOKPSSSPKWTLSATSNLASGVPAR 60
 DB 1 QIVLSQSPALLSAPGKRYMTTCRASSSVYMHYQOKPSSSPKWTLSATSNLASGVPAR 60
 QY 61 FSGSGSGTSTSTSRVEAEDAATYYCQWSSNPPFGCGTMLEIR 106
 DB 61 FSGSGSGTSTSTSRVEAEDAATYYCQWSSNPPFGCGTMLEIR 106
 RESULT 3
 ID AAW24520 standard; Protein; 107 AA.
 AC AAW24520;
 DT 26-DEC-1997 (first entry)
 DE Mouse anti-human Factor IX antibody BC2 light chain variable region.
 KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
 KW humanised antibody; antibody engineering; light chain; CDR;
 KW complementarity determining region; myocardial infarction;
 KW angina; atrial fibrillation; stroke; kidney damage;
 KW pulmonary embolism; deep vein thrombosis; coronary angioplasty;
 KW disseminated intravascular coagulation; artificial organ; sepsis;
 KW shunt; prosthesis.
 XX Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT Region 24..33
 FT /label= CDR1
 FT /note= "(Claim 23)"
 FT Region 49..55
 FT /label= CDR2
 FT /note= "(Claim 23)"
 FT Region 88..96
 FT /label= CDR3
 FT /note= "(Claim 23)"
 PN WO9726010-A1.
 PD 24-JUL-1997.
 PF 17-JAN-1997; 97MO-US00759.
 PR 24-OCT-1996; 96US-0029119.
 PR 17-JAN-1996; 96US-0010108.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 DR Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
 PI Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
 DR WPI; 1997-385117/35.
 PS

DR N-PSDB: AAT77377.
 XX Inhibiting thrombosis with self-limiting antibody to coagulation
 PT factor - avoids uncontrolled bleeding by providing only partial
 PT inhibition
 XX
 PS Example 5; Page 66-67; 150pp; English.
 XX
 CC This sequence comprises the light chain variable region of mouse
 CC anti-human factor IX monoclonal antibody BC2. Claimed humanised
 CC antibodies (see AAM24510-18) contain CDRs (see AAM24504-09) of BC2
 CC heavy and light chain variable regions inserted into framework
 CC regions of selected human antibody sequences. They have self-
 CC limiting neutralising activity, and are useful as anticoagulant
 CC agents in treatment of thrombosis associated with myocardial
 CC infarction, unstable angina, atrial fibrillation, stroke, renal
 CC damage, pulmonary embolism, deep vein thrombosis, percutaneous
 CC transluminal coronary angioplasty, disseminated intravascular
 CC coagulation, sepsis, or artificial organs, shunts or prostheses
 CC (claimed). Also claimed are chimeric antibodies (see AAM24532), and
 CC Fab and F(ab')₂ fragments. The claimed antibodies do not cause
 CC uncontrolled bleeding (contrast heparin and warfarin) since they
 CC provide only partial inhibition of coagulation.
 XX
 SQ Sequence 107 AA:
 Query Match 94.6%; Score 526; DB 18; Length 107;
 Best Local Similarity 95.3%; Pred. No. 1.8e-30;
 Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 OY 1 QIVLSGSPAILLSAPGKVTMTCRASSSVNMYHWYQOKRGSSPKPWISATSNLASGVPAR 60
 DB 1 QIVLSGSPAILLSAPGKVTMTCRASSSVNMYHWYQOKRGSSPKPWIVATSNLASGVPAR 60
 OY 61 FSGSGSGTSYSLTISRVEAEDATYYCOQWSSNPFFGGGTMLEIR 106
 DB 61 FSGSGSGTSYSLTISRVEAEDATYYCOQWSSNPFFGGGTMLEIR 106
 RESULT 4
 AAU80976
 ID AAU80976 standard; Protein: 107 AA.
 XX
 AC AAU80976;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Murine BC2 light chain variable region.
 XX
 KM Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
 KM thrombolytic agent; anti-factor IX antibody; plasminogen activator;
 KM thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
 KM vasotropic; cardiant; anti-respiratory syncytial virus;
 KM heavy chain variable region; light chain variable region.
 XX
 OS Mus sp.
 XX
 PN WO200187339-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27438.
 XX
 PR 15-MAY-2000; 2000US-0571434.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
 XX
 DR WPI: 2002-082944/11.
 XX
 DR N-PSDB: ABR23937.
 XX
 PT Treating post-thromboembolic induced ischaemia in an animal by

PT administering anti-factor IX antibody in combination with a plasminogen
 PT activator
 XX
 PS Example 5; Page 97; 163pp; English.
 XX
 CC The invention relates to a method for treating an animal
 CC post-thromboembolic induced ischaemia or reducing a required dose of a
 CC thrombolytic agent in treatment of an animal post-thromboembolic induced
 CC ischaemia, comprising administering an anti-factor IX antibody or its
 CC fragment, optionally in combination with a plasminogen activator or
 CC thrombolytic agent. The method is useful for treating
 CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
 CC stroke in an animal, and for reducing a required dose of a thrombolytic
 CC agent. Sequences AAU80972-AAU81004 represent antibodies and vector
 CC polypeptides used in the method of the invention.
 XX
 SQ Sequence 107 AA:
 Query Match 94.6%; Score 526; DB 23; Length 107;
 Best Local Similarity 95.3%; Pred. No. 1.8e-30;
 Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 OY 1 QIVLSGSPAILLSAPGKVTMTCRASSSVNMYHWYQOKRGSSPKPWISATSNLASGVPAR 60
 DB 1 QIVLSGSPAILLSAPGKVTMTCRASSSVNMYHWYQOKRGSSPKPWIVATSNLASGVPAR 60
 OY 61 FSGSGSGTSYSLTISRVEAEDATYYCOQWSSNPFFGGGTMLEIR 106
 DB 61 FSGSGSGTSYSLTISRVEAEDATYYCOQWSSNPFFGGGTMLEIR 106
 RESULT 5
 AAM24531
 ID AAM24531 standard; Protein: 112 AA.
 XX
 AC AAM24531;
 XX
 DT 27-DEC-1997 (first entry)
 XX
 DE Anti-Factor IX Mab BC2 modified light chain.
 XX
 KM Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
 KM chimeric antibody; antibody engineering; light chain.
 XX
 OS Chimeric Mus musculus.
 XX
 OS Chimeric synthetic.
 XX
 PN WO9726010-A1.
 XX
 PD 24-JUL-1997.
 XX
 PF 17-JAN-1997; 97WO-US00759.
 XX
 PR 24-OCT-1996; 96US-0029119.
 XX
 PR 17-JAN-1996; 96US-0010108.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX
 PI Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
 XX
 PI Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
 XX
 DR WPI: 1997-385117/35.
 XX
 DR N-PSDB: AAT79899.
 XX
 PT Inhibiting thrombosis with self-limiting antibody to coagulation
 PT factor - avoids uncontrolled bleeding by providing only partial
 PT inhibition
 XX
 PS Example 7; Page 126; 150pp; English.
 XX
 CC This polypeptide sequence comprises a modified light chain variable
 CC region (see also AAM24520) of mouse anti-human factor IX monoclonal

CC antibody BC2. It is encoded by a DNA fragment (see AAT79899)
CC produced by PCR amplification of BC2 cDNA. The modified BC2 VL
CC region is incorporated into novel mouse-human chimeric light chain
CC FgHC (see AAW24532). Claimed anti-Factor IX chimeric antibodies
CC are useful in the treatment of thrombosis.

XX Sequence 112 AA:

Query Match 94.6%; Score 526; DB 18; Length 112;
Best Local Similarity 95.3%; Pred. No. 1.9e-30;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 QIVLSQSPAILASAPGKVTMTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

DB 1 QIVLSQSPAILASAPGKVTMTCRASSSVNYMHYQOKPGSSPKPWIVATSNLASGVPAR 60

OY 61 FSGSGSGTYSLTISRVEADATYYCQOWSNPPTFGGTMLEIR 106
DB 61 FSGSGSGTYSLTISRVEADATYYCQOWSNPPTFGGTMLEIR 106

RESULT 6

AAU81001 standard; Protein: 112 AA.

AC AAU81001;

DT 09-APR-2002 (first entry)

DE Murine BC2 light chain modified variable region.

XX Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
XX thrombolytic agent; anti-factor IX antibody; plasminogen activator;
XX thromboembolic stroke; cerebroprotective; anticoagulant; thrombolytic;
XX vasotropic; cardiac; anti-respiratory syncytial virus;
XX heavy chain variable region; light chain variable region.

OS Mus sp.
OS Synthetic.

PN WO200187339-A1.

PD 22-NOV-2001.

XX 05-OCT-2000; 2000WO-US27438.

XX 15-MAY-2000; 2000US-0571434.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;

DR WPI: 2002-082944/11.

DR N-PSDB; ABK24004.

PT Treating post-thromboembolic induced ischaemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator

XX Example 7; Page 153-154; 163pp; English.

XX The invention relates to a method for treating an animal
XX post-thromboembolic induced ischaemia or reducing a required dose of a
XX thrombolytic agent in treatment of an animal post-thromboembolic induced
XX ischaemia, comprising administering an anti-factor IX antibody or its
XX fragment, optionally in combination with a plasminogen activator or
XX thrombolytic agent. The method is useful for treating thromboembolic
XX post-thromboembolic-induced ischaemia, for preventing thromboembolic
XX stroke in an animal, and for reducing a required dose of a thrombolytic
XX agent. Sequences AAU80972-AAU81004 represent antibodies and vector
XX polypeptides used in the method of the invention.

Sequence 112 AA;

Query Match 94.6%; Score 526; DB 23; Length 112;
Best Local Similarity 95.3%; Pred. No. 1.9e-30;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 QIVLSQSPAILASAPGKVTMTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

DB 1 QIVLSQSPAILASAPGKVTMTCRASSSVNYMHYQOKPGSSPKPWIVATSNLASGVPAR 60

OY 61 FSGSGSGTYSLTISRVEADATYYCQOWSNPPTFGGTMLEIR 106
DB 61 FSGSGSGTYSLTISRVEADATYYCQOWSNPPTFGGTMLEIR 106

RESULT 7

AAU55214 standard; Protein: 128 AA.

AC AAU55214;

DT 01-FEB-1995 (first entry)

DE Murine variable region light chain from 2B5.

XX B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
XX cell lysis.

XX Mus musculus.

PN WO9411026-A.

PD 26-MAY-1994.

XX 12-NOV-1993; 93WO-US10953.

XX 13-NOV-1992; 92US-0978891.

XX 03-NOV-1993; 93US-0149099.

XX (IDEC-) IDEC PHARM CORP.

PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rustletter WH;

PI RefTime;

DR WPI: 1994-183162/22.

DR N-PSDB; Q65630.

PT Treating B cell lymphoma with chimeric antibody - against CD20,
PT causing rapid depletion of peripheral B cells, also new
PT antibodies and hybridomas

XX Disclosure; Fig 4; 101pp; English.

XX The sequence is the murine variable region light chain derived from
XX murine anti-CD20 monoclonal antibody 2B5.

XX See also AAQ65629-35.

XX Sequence 128 AA;

Query Match 93.7%; Score 521; DB 15; Length 128;
Best Local Similarity 92.5%; Pred. No. 4.8e-30;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 QIVLSQSPAILASAPGKVTMTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

DB 23 QIVLSQSPAILASAPGKVTMTCRASSSVNYMHYQOKPGSSPKPWIVATSNLASGVPAR 82

OY 61 FSGSGSGTYSLTISRVEADATYYCQOWSNPPTFGGTMLEIR 106
DB 83 FSGSGSGTYSLTISRVEADATYYCQOWSNPPTFGGTMLEIR 128

RESULT 8

AAU30694

ID AAB30694 standard; Protein: 412 AA.
 AC AAB30694;
 XX
 XX 02-APR-2001 (first entry)
 DT
 XX
 DE A fusion of anti-CD20 single chain antibody/streptavidin.
 XX
 XX Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; B9E9.
 XX
 XX Synthetic.
 OS Streptomyces avidinii.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Protein 1..108
 FT /note= "VL chain"
 FT Peptide 109..126
 FT /note= "linker"
 FT Protein 127..248
 FT /note= "VH chain"
 FT Peptide 249..253
 FT /note= "linker"
 FT Protein 254..412
 FT /note= "streptavidin"
 XX
 XX WO200075333-A1.
 FN
 XX
 XX 14-DEC-2000.
 PD
 XX
 XX 05-JUN-2000; 2000WO-US15595.
 PF
 XX 07-JUN-1999; 99US-0137900.
 PR
 PR 03-DEC-1999; 99US-0168976.
 XX
 XX (NEOR-) NEORX CORP.
 PA
 XX
 XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 PI
 XX MPI: 2001-091213/10.
 DR
 DR N-PSDB; AAC86563.
 XX
 XX New vector constructs for expressing genomic streptavidin fusion
 PT proteins which are useful for targeting tumour cells associated with
 FT cancer; e.g. adenocarcinomas -
 XX
 XX Example 2; Fig 11B; 100pp; English.
 PS
 XX
 XX The present sequence represents a fusion of an anti-CD20 single chain
 CC antibody (B9E9) streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 CC nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second
 CC nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic
 CC acid sequence. Alternatively, the vector construct comprises a nucleic
 CC acid, operatively linked to a promoter, encoding a polypeptide to be
 CC fused with streptavidin, and a cloning site for insertion of a second
 CC nucleic acid encoding at least 129 amino acids of streptavidin or its
 CC functional variant. The fusion proteins are useful for targeting tumour
 CC cells, particularly tumour cells associated with cancer,
 CC e.g. adenocarcinomas or hematological malignancies. The vector construct
 CC is useful for expressing of streptavidin fusion proteins. In particular,
 CC these are useful as tools for medical diagnostics and therapeutic
 CC purposes, e.g. for detecting the presence or absence of, or treating, a
 CC target site within a mammalian host.
 CC
 XX
 XX Sequence 412 AA;
 S0
 Query Match 93.0%; Score 517; DB 22; Length 412;
 Best Local Similarity 93.3%; Pred. NO. 2.8e-29;

Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 2 IVLSQSPAILLSAPGEKVTMTCRASSVYVMHWYQOKPCSSPKPWLSATSNLASGVPARF 61
 DB 2 IVLSQSPAILLSAPGEKVTMTCRASSVYVMHWYQOKPCSSPKPWIVTSNLASGVPARF 61
 OY 62 SSGSGSTSYSLTISRVEADATYTCQOMSSNPFFGGTWTLEIK 106
 DB 62 SSGSGSTSYSLTISRVEADATYTCQOMSSNPFFGGTWTLEIK 106
 RESULT 9
 ID AAB30695 standard; Protein: 423 AA.
 AC AAB30695;
 XX
 XX 02-APR-2001 (first entry)
 DT
 XX
 DE A fusion of anti-CD20 single chain antibody/streptavidin.
 XX
 XX Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; B9E9.
 XX
 XX Synthetic.
 OS Streptomyces avidinii.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Protein 1..126
 FT /note= "VH chain"
 FT Peptide 127..150
 FT /note= "linker"
 FT Protein 151..259
 FT /note= "VL chain"
 FT Peptide 260..264
 FT /note= "linker"
 FT Protein 265..423
 FT /note= "streptavidin"
 XX
 XX WO200075333-A1.
 FN
 XX
 XX 14-DEC-2000.
 PD
 XX
 XX 05-JUN-2000; 2000WO-US15595.
 PF
 XX 07-JUN-1999; 99US-0137900.
 PR
 PR 03-DEC-1999; 99US-0168976.
 XX
 XX (NEOR-) NEORX CORP.
 PA
 XX
 XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
 PI
 XX MPI: 2001-091213/10.
 DR
 DR N-PSDB; AAC86564.
 XX
 XX New vector constructs for expressing genomic streptavidin fusion
 PT proteins which are useful for targeting tumour cells associated with
 FT cancer; e.g. adenocarcinomas -
 XX
 XX Example 2; Fig 11C; 100pp; English.
 PS
 XX
 XX The present sequence represents a fusion of an anti-CD20 single chain
 CC antibody (B9E9) streptavidin. The fusion protein is expressed using
 CC vectors of the invention. The specification describes vector constructs
 CC for expressing streptavidin fusion proteins. The vector comprises a
 CC nucleic acid encoding streptavidin or its functional variant operatively
 CC linked to a promoter, and a cloning site for insertion of a second
 CC nucleic acid sequence encoding a polypeptide to be fused with
 CC streptavidin, interposed between the promoter and the first nucleic
 CC acid sequence. Alternatively, the vector construct comprises a nucleic
 CC acid, operatively linked to a promoter, encoding a polypeptide to be
 CC fused with streptavidin, and a cloning site for insertion of a second

	CC	nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, vector construct e.g. adenocarcinoma or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
XX	CC	
CC	SQ	Sequence 423 AA:
		: : :
	Query Match	93.0%; Score 517; DB 22; Length 423;
	Best Local Similarity	93.3%; Pred. No. 2.9e-29;
	Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
OY	2	IYLSSPAILASSPEEKYTMTCRASSVNYMHMYOOKPSSSKPPMISATSNLASGVPARF 61 DB 153 IYLSOSPAILASSPEEKYMTCTCRASSSVSYMWYOOKPSSKPMIYATSNLASGVPARF 212
OY	62	SGSGSSTSYSLTISRVEAEDAAITYYCQQWSSNPFPGGTMLEIR 106 ::: Db 213 SGSGSSTSYSLTISRVEAEDAAITYYCQQWISSNPFFGAETKRLKK 257
RESULT 10		
AAP70628	ID	AAP70628 standard; protein; 128 AA.
XX	AC	AAP70628;
XX	DT	03-Oct-2002 (updated)
DT	DT	09-Apr-1991 (first entry)
XX	DE	Sequence encoded by the 2H7 VL sequence in which the Vk gene contains JK5 sequences.
DE	xx	
KX	Chimeric antibody; Anti-cancer antibody.	
OS	Chimeric - Homo sapiens.	
OS	Chimeric - Mus sp.	
XX	Key	Location/Qualifiers
FH	FT Region	1..23 /tag= a
FT		/label=leader peptide
FT	Region	24..47 /tag= b
FT		/label=FRL
FT	Region	48..56 /tag= c
FT		/label=CDR1
FT	Region	57..71 /tag= d
FT		/label=FR2
FT	Region	72..78 /tag= e
FT		/label=CDR2
FT	Region	79..110 /tag= f
FT		/label=FR3
FT	Region	111..119 /tag= g
FT		/label=CDR3
FT	Region	118..128 /tag= h
FT		/label=JK5
FT	Region	120..128 /tag= i
FT		/label=FR4
XX		
PX		WO8702671-A.
XX		
DD		07-MAY-1987.

[illegible]


```

FT Domain 110..118
FT /label=CDR3.
FT Domain 119..128
FT /label=FR4.
XX
XX WO8900999-A.
XX
XX 09-FEB-1989.
XX
XX 25-JUL-1988; 86WO-US02514.
XX
XX 24-JUL-1987; 87US-0077528.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX
XX Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;
XX
XX WPI; 1989-061144/08.
XX
XX N-PSDB; AAN91147.
XX
XX Polynucleotide(s) encoding immunoglobulin molecules -
XX used for efficient produ. of chimeric human or non-human or
XX class switched antibodies.
XX
XX Disclosure; 7pp; English.
XX
XX Sequence carries the variable region of the chimeric immunoglobulin
XX sequence. The antibodies are useful in passive immunisation avoiding
XX negative immune reactions. They are also useful in assaying and in vitro
XX imaging.
XX
XX Sequence 128 AA;
XX
XX Query Match 92.8%; Score 516; DB 10; Length 128;
XX Best Local Similarity 92.5%; Pred. No. 1.1e-29;
XX Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

OY 1 QIVLSOSPAILLSASPEKXTMTCRASSSYNMHWYQOKFGSSPKPWISATSNLASGVPAR 60
DB 23 QIVLSOSPAILLSASPEKXTMTCRASSSYNMHWYQOKFGSSPKPWISATSNLASGVPAR 82
OY 61 FSGSGSGTSTSLTISRVEADATYCCQWSSNPPTFGGTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEADATYCCQWSSNPPTFGGTMLEIR 128

RESULT 12
AAM10589
ID AAM10589 standard; Protein: 128 AA.
XX
XX AAM10589;
XX
XX 21-OCT-1997 (first entry)
XX
XX 2H7 antibody light chain variable region.
XX
XX Immunoglobulin G; IgG; light chain; recombinant production;
XX antibody; passive immunisation; serum sickness; anaphylactic shock;
XX immunosassay; imaging; reagent; complement mediated lysis;
XX therapy; variable; region; complementarity determining; CDR;
XX framework.
XX
XX Mus spp.
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX /label= sig_peptide
XX Peptide 23..128
XX /label= mat_peptide
XX Region 23..46
XX /label= framework_1
XX Region 47..55
XX /label= CDR_1

```

```

FT Region 56..70
FT /label= framework_2
FT Region 71..77
FT /label= CDR_2
FT Region 78..109
FT /label= framework_3
FT Region 110..118
FT /label= CDR_3
FT Region 119..128
FT /label= framework_4
XX
XX US5595898-A.
XX
XX 21-JAN-1997.
XX
XX 01-NOV-1985; 85US-0793980.
XX
XX 29-MAR-1990; 90US-0501092.
XX
XX 01-NOV-1985; 85US-0793980.
XX
XX 27-OCT-1986; 86WO-US02269.
XX
XX 24-JUL-1987; 87US-0077528.
XX
XX 11-JAN-1988; 88US-0142039.
XX
XX 08-DEC-1992; 92US-0987555.
XX
XX 18-AUG-1994; 94US-0299085.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
XX Wall R, Wilcox GL;
XX
XX WPI; 1997-107579/10.
XX
XX N-PSDB; AAT36317.
XX
XX Nucleic acid encoding immunoglobulin fragment - comprising
XX dicistronic transcription unit with pectate lyase signal sequences
XX
XX Example; Fig 22; 95pp; English.
XX
XX The present sequence is the light chain variable region of
XX the 2H7 antibody. The 2H7 cDNA was used in the preparation of
XX a novel polynucleotide molecule encoding an Ig fragment. The DNA
XX molecule comprises 2 DNA sequences encoding 2 pectate lyase
XX secretion signal sequences respectively linked to a DNA sequence
XX encoding an Ig Fd molecule or Ig light chain, operably linked to a
XX single prokaryotic promoter so as to form a dicistronic
XX transcription unit, provided that the Ig fragment can bind an
XX antigen and is produced and secreted by an E. coli host cell when
XX the nucleic acid molecule is expressed in the host cell.
XX The polynucleotide molecule is used for the production of
XX recombinant antibodies, which can be used for passive immunisation
XX without negative immune reactions (e.g. serum sickness and
XX anaphylactic shock), in labelled forms as immunoassay or imaging
XX reagents, in complement mediated lysis and for therapeutic
XX purposes when coupled to a toxin or other therapeutic agent.
XX
XX Sequence 128 AA;
XX
XX Query Match 92.8%; Score 516; DB 18; Length 128;
XX Best Local Similarity 92.5%; Pred. No. 1.1e-29;
XX Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

OY 1 QIVLSOSPAILLSASPEKXTMTCRASSSYNMHWYQOKFGSSPKPWISATSNLASGVPAR 60
DB 23 QIVLSOSPAILLSASPEKXTMTCRASSSYNMHWYQOKFGSSPKPWISATSNLASGVPAR 82
OY 61 FSGSGSGTSTSLTISRVEADATYCCQWSSNPPTFGGTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEADATYCCQWSSNPPTFGGTMLEIR 128

RESULT 13
AAM16344
ID AAM16344 standard; Protein: 128 AA.

```

```

XX AC AAW16344:
XX
XX 04-SEP-1997 (first entry)
XX DE 2H7 light chain variable sequence.
XX
XX Antibody engineering: heavy chain: chimaeric antibody;
XX passive immunisation; diagnosis; hybridoma; monoclonal antibody;
XX 2H7; B-cell antigen; Bp35.
XX
XX Mus sp.
XX
XX Key location/Qualifiers
XX FH 1..22
XX FT Peptide /label= Sig-peptide
XX FT 23..46
XX FT Region /label= FRL
XX FT /note= "framework region 1"
XX FT 47..55
XX FT Region /label= CDRI
XX FT /note= "complementarity determining region 1"
XX FT 56..70
XX FT Region /label= FR2
XX FT /note= "framework region 2"
XX FT 71..77
XX FT Region /label= CDR2
XX FT /note= "complementarity determining region 2"
XX FT 78..109
XX FT Region /label= FR3
XX FT /note= "framework region 3"
XX FT 110..118
XX FT Region /label= CDR3
XX FT /note= "complementarity determining region 3"
XX FT 119..128
XX FT /label= FR4
XX FT /note= "framework region 4"
XX
XX US5618920-A.
XX
XX 08-APR-1997.
XX
XX 01-NOV-1985; 85US-0793980.
XX
XX 29-MAR-1990; 90US-0501092.
XX 01-NOV-1985; 85US-0793980.
XX 27-OCT-1986; 86WO-US02269.
XX 24-JUL-1987; 87US-0077528.
XX 11-JAN-1988; 88US-0142039.
XX 17-APR-1992; 92US-0870404.
XX 29-APR-1994; 94US-0235225.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
XX Wall R, Wilcox GL;
XX
XX WPI; 1997-225473/20.
XX
XX N-PSDB; AAT70869.
XX
XX Secretable immunoglobulin heavy and light chain fragments - capable
XX of assembling into chimeric antibodies, useful for e.g. passive
XX immunisation, diagnosis, etc
XX
XX Example 4; Fig 22; 96pp; English.
XX
XX A polypeptide (AAW16344) comprises the light chain variable region of
XX mouse monoclonal antibody 2H7, which recognises human B-cell surface
XX antigen Bp35. It is encoded by a cDNA clone (AAT70869) obtd. from a
XX 2H7 cDNA library by PCR amplification. The 2H7 heavy chain variable
XX sequence (AAW16343) is also provided. A novel human-mouse chimaeric
XX antibody with specificity for the human B-cell antigen has been
XX constructed.

```

```

XX SQ Sequence 128 AA:
XX
XX Query Match 92.8%; Score 516; DB 18; Length 128;
XX Best Local Similarly 92.5%; Pred. No: 1; Le-29;
XX Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 QIVTSGSPALISASPGKVTMTCTCRASSSVYMMHYOQKPGSSPKRWTATSNLASGVPAR 60
XX 23 QIVTSGSPALISASPGKVTMTCTCRASSSVYMMHYOQKPGSSPKRWTATSNLASGVPAR 82
XX
XX 61 FSGSGSGTSTSLTISRVEAEDATYYCOQSSNPTEFGGTMLEIR 106
XX 83 FSGSGSGTSTSLTISRVEAEDATYYCOQSSNPTEFGGTMLEIR 128
XX
XX RESULT 14
XX ID AAW10243 standard; Protein: 128 AA.
XX
XX AC AAW10243:
XX
XX 06-AUG-1997 (first entry)
XX
XX Light chain variable sequence of 2H7.
XX
XX Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
XX protein production; human; constant region; passive immunisation; toxin;
XX serum sickness; anaphylaxis; sweetener; thrombatin; cytoplasm; periplasm;
XX antibody; Ig; light-chain; hepatitis; mouse; lung carcinoma; cancer;
XX myeloma cell.
XX
XX Mus musculus.
XX
XX
XX Key location/Qualifiers
XX FH 1..22
XX FT Peptide /note= "leader peptide"
XX FT 23..46
XX FT Region /note= "framework region 1"
XX FT 47..55
XX FT Region /note= "complementarity determining region 1"
XX FT 56..70
XX FT Region /note= "framework region 2"
XX FT 71..77
XX FT Region /note= "complementarity determining region 2"
XX FT 78..109
XX FT Region /note= "framework region 3"
XX FT 110..118
XX FT Region /note= "complementarity determining region 3"
XX FT 119..128
XX FT /note= "framework region 4"
XX
XX US5576195-A.
XX
XX 19-NOV-1996.
XX
XX 01-NOV-1985; 85US-0793980.
XX
XX 29-MAR-1990; 90US-0501092.
XX 01-NOV-1985; 85US-0793980.
XX 27-OCT-1986; 86WO-US02269.
XX 24-JUL-1987; 87US-0077528.
XX 11-JAN-1988; 88US-0142039.
XX 08-DEC-1992; 92US-0987555.
XX 22-FEB-1993; 93US-0020671.
XX 09-DEC-1994; 94US-0357234.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better M, Lei S, Robinson RR, Wilcox GL;
XX
XX WPI; 1997-011254/01.
XX
XX N-PSDB; AAT51043.

```

```

XX Improved prodn. of protein in Gram -ve bacteria using signal
PT sequence - from pectate lyase to ensure transport of protein from
PT the cytoplasm, esp. for prodn. of antibodies
XX
XX Example 4; Fig 22; 86pp; English.
XX
CC This sequence represents the light chain variable region of the 2H7
CC mouse monoclonal antibody. The 2H7 antibody recognises the human B-cell
CC surface antigen Bp35, which plays a role in B-cell activation. This
CC sequence was used in a human-mouse chimeric antibody with human B-cell
CC antigen specificity, that was produced using the method of the invention.
CC The method of the invention is for the production of a protein in a
CC Gram-negative bacterium. The method improves on current techniques, by
CC using a vector including DNA encoding the pectate lyase signal sequence
CC (see AAT51034), attached to the sequence encoding the protein for
CC production. The method is especially used to make immunoglobulins (Ig),
CC particularly those with a human constant region, suitable for passive
CC immunisation (without risk of serum sickness or anaphylaxis) or for in
CC vivo/in vitro diagnosis and imaging. The Ig may also be used
CC therapeutically, optionally coupled to toxins, etc. Alternatively the
CC protein to be produced is the sweetener thaumatin. The presence of this
CC signal sequence means that the protein is exported from the cytoplasm
CC and can be recovered from the culture medium or periplasm, in active and
CC correctly folded form. The method allows the class of any antibody to be
CC switched, e.g. most human-human Ig are of M class, easily reduced and
CC aggregated, and these can now be changed to G, A or E classes.
XX
SQ Sequence 128 AA:
Query Match 92.8%; Score 516; DB 18; Length 128;
Best Local Similarity 92.5%; Pred. No. 1.1e-29;
Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 QIVLSOSPAILASPGKVTMTCRASSSVNMYHWYQOKFGSSPKPWISATSNLASGVPAR 60
DB 23 QIVLSOSPAILASPGKVTMTCRASSSVNMYHWYQOKFGSSPKPWIVAPSNLASGVPAR 82
OY 61 FSGSGSGTSTSLTISRVEADAATYYCQOWSSNPFFGGCTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEADAATYYCQOWSSNPFFGGCTMLEIR 128
RESULT 15
AAM47521
ID AAM47521 standard: Protein; 128 AA.
XX
AC AAM47521;
XX
DT 05-JUN-1998 (first entry)
XX
DE Mouse 2H7 antibody light chain variable region.
XX
KM Mouse; murine; light chain; variable region;
KM Immunoglobulin fragment production; Ig fragment production;
KM monoclonal antibody 2H7; human B-cell surface antigen.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 1..22 /label= sig_peptide
FT 23..128 /label= mat_peptide
FT Peptide
XX
PN US5698417-A.
XX
PD 16-DEC-1997.
XX
PF 06-JUN-1995; 95US-0466203.
XX
PR 29-MAR-1990; 90US-0501092.
PR 01-NOV-1985; 85US-0793980.

```

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PR 27-OCT-1986; 86WO-US02269.
PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0987555.
PR 18-AUG-1994; 94US-0299085.
PR 25-MAY-1995; 95US-0450731.
PR 06-JUN-1995; 95US-0466203.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX
DR WPI: 1998-051487/05.
DR N-PSDB: AAV18594.
XX
PT Production of recombinant immunoglobulin fragment - comprising Fd
PT molecule and light chain
XX
PS Example IV, Fig 22; 98pp; English.
XX
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
XX
SQ Sequence 128 AA:
Query Match 92.8%; Score 516; DB 19; Length 128;
Best Local Similarity 92.5%; Pred. No. 1.1e-29;
Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 QIVLSOSPAILASPGKVTMTCRASSSVNMYHWYQOKFGSSPKPWISATSNLASGVPAR 60
DB 23 QIVLSOSPAILASPGKVTMTCRASSSVNMYHWYQOKFGSSPKPWIVAPSNLASGVPAR 82
OY 61 FSGSGSGTSTSLTISRVEADAATYYCQOWSSNPFFGGCTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEADAATYYCQOWSSNPFFGGCTMLEIR 128

```

Search completed: November 27, 2002, 07:17:57
 Job time : 62.5251 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:15:05 ; Search time 29.0579 Seconds
(without alignments) 350.688 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 556

Sequence: 1 QIVLSQSPALISAPGEKVT.....CQKMSNPPTFGGCTMLEIR 106

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: plr1:.*
2: plr2:.*
3: plr3:.*
4: plr4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	94.1	106	2	PL0082
2	492	88.5	107	2	A42848
3	480	86.3	107	2	PC4405
4	474	85.3	107	2	A30362
5	469	84.4	107	2	S26338
6	465.5	83.9	108	2	B30562
7	465.5	83.7	108	2	G30560
8	462	83.1	140	2	S38720
9	459	82.6	106	2	PL0013
10	458	82.4	104	2	PS0071
11	458	82.4	107	2	B49049
12	458	82.4	107	2	PD0011
13	457	82.2	130	1	JL0079
14	457	82.2	103	2	S29591
15	454	81.7	100	2	S29580
16	454	81.7	107	2	PT0406
17	452	81.3	97	2	S26341
18	446	80.2	106	2	B54378
19	445	80.0	235	2	S25058
20	444	79.9	107	2	S11118
21	442.5	79.6	104	2	TC6076
22	442	79.5	107	2	S11119
23	440	79.1	130	2	A32513
24	437	78.6	97	2	PH1084
25	434	78.1	107	2	S11121
26	433	77.9	107	2	S11121
27	433	77.9	130	2	B32456
28	433	77.9	130	2	S04573
29	430	77.3	99	2	S29585

30	429	77.2	106	2	G27887	Ig kappa chain V r
31	427	76.8	97	2	PH1085	Ig light chain V r
32	426	76.6	94	2	S26340	Ig light chain V r
33	426	76.6	99	2	D38601	Ig kappa chain V r
34	425	76.4	109	2	PT0405	Ig light chain V r
35	423	76.1	95	2	D33730	Ig kappa chain V r
36	423	76.1	107	2	S11112	Ig kappa chain V r
37	423	76.1	107	2	S11113	Ig kappa chain V r
38	423	76.1	108	2	S29581	Ig kappa chain V r
39	421	75.7	108	2	PL0278	Ig kappa chain V r
40	420	75.5	109	2	PT0404	Ig light chain V r
41	420	75.5	132	2	S05268	Ig kappa chain pre
42	419	75.4	106	2	PS0070	Ig kappa chain V r
43	418	75.2	107	1	KYMSX4	Ig kappa chain V r
44	417	75.0	108	2	PL0276	Ig kappa chain V r
45	417	75.0	108	2	PL0277	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PL0082

Ig kappa chain V region (2D3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000

C:Accession: PL0082

R:Meek, K.; Hasemann, C.; Pollok, B.; Alken, S.S.; Bratt, M.; Slouli, M.; Urbain, J.;

J. Exp. Med. 169, 519-533, 1989

A:Title: Structural characterization of antidiabetic antibodies; evidence that Ab2s

A:Reference number: PL0080; MUID:89094248; PMID:2492056

A:Accession: PL0082

A:Molecule type: mRNA

A:Residues: 1-106 <ME>

A:Experimental source: Strain BALB/c

A>Note: the sequence shown here is from the V kappa region of an antidiabetic monoclonal

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:16-89/Domain: Immunoglobulin homology <IM>

Query Match

Best Local Similarity 94.1%; Score 523; DB 2; Length 106;

Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 OIVLSQSPALISAPGEKVTTCRASSSVYHWQKPGSSPKPMISVTSNLASGVAPR 60

Db 1 OIVLSQSPALISAPGEKVTTCRASSSVYHWQKPGSSPKPMISVTSNLASGVAPR 60

Oy 61 FSGSGSGTSTLTISRVEADATATTCQWSSNPPTFGGCTMLEIR 106

Db 61 FSGSGSGTSTLTISRVEADATATTCQWSSNPPTFGGCTMLEIR 106

RESULT 2

A42848

Ig light chain V region - mouse (fragment)

N:Alternate names: I6 anti-tumor antibody

C:Species: Mus musculus (house mouse)

C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: A42848; S33902

R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsitch, L.; Schlieden, G.L.; Marken, J.S.; Aru

J. Biol. Chem. 267, 15552-15558, 1992

A:Title: Chimeric I6 anti-tumor antibody. Genomic construction, expression, and chara

A:Reference number: A42848; MUID:92348410; PMID:1639794

A:Accession: A42848

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-107 <FE>

A:Cross-references: EMBL:M90690

A>Note: sequence extracted from NCBI backbone (NCBI:109958, NCBI:109959)

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: Immunoglobulin

F:16-89/Domain: Immunoglobulin homology <IM>

Query Match	88.5%	Score 492;	DB 2;	Length 107;
Best Local Similarity	-87.7%	Pred. No. 3.9e-35;		
Matches	93;	Conservative	7;	Mismatches 6;
			Indels	0;
			Gaps	0;

Oy 1 QIVLSQSPALISASPGENVITMICRASSVNYMHVIYQKPGSSPKPMIATSNLNSGVPAR 600
||||| : ||||| |||||
Db 1 QIVLSQSPALISASPGENVITLTICRASSVSFMMNYYQKPGSSPKPMIATSNLNSGVPAR 600

```
QY      61 FSGSGSGTSLTISRVEAEATYYCQQWSSNPPTFGGGTMELEIR 106
        |||||
        61 FSGSGSGTSLAISRVEAEATYYCQQWSSNPPLTFGAGTKLELK 106
```

RESULT 3

Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1997 #Accession: 20010101

F:16-89/Domain: Immunoglobulin homology <IMM>

Query Match 81.7%; Score 454; DB 2; Length 100;
 Best Local Similarity 87.0%; Pred. No. 6.1e-32;
 Matches 87; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 QIVLSQSPAILASAPGEKVTMTCRASSSVNWMYQOKPGSSPKPWISATSNLASGVPAR 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 QIVLTQSPAIMSAPGEKVTMTCSASSSVYWMYQOKSGTSPKRWIYDTSKLAGVPPAR 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 FSGSGSGTSTSLTISRVAEDATYYCOQWSSNPPTFGGG 100
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 FSGSGSGTSTSLTISMEAEADATYYCOQWSSNPWTFGGG 100
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 27, 2002, 07:24:16
 Job time : 30.0579 secs

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GenCore version 5.1.3
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OM protein: - protein search, using sw model

Run on: November 27, 2002, 05:39:34 : Search time 15.1429 Seconds
(without alignments)
290.334 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 556
Sequence: 1 QIVLSQSPALISASPEKVT.....COQSSNPPTFGGTMLEIR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwisssProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	451	81.1	107	1	P04940 mus musculu
2	446	80.2	107	1	KV6F_MOUSE
3	445	80.0	107	1	P04942 mus musculu
4	442	79.5	107	1	KV6H_MOUSE
5	441	79.3	107	1	P04941 mus musculu
6	435	78.2	108	1	KV6J_MOUSE
7	419	75.4	107	1	KV6K_MOUSE
8	418	75.2	107	1	KV6D_MOUSE
9	413	74.3	107	1	KV6A_MOUSE
10	411	73.9	107	1	P01676 mus musculu
11	405	72.8	129	1	KV4A_MOUSE
12	396	71.2	107	1	KV6E_MOUSE
13	349.5	62.9	111	1	KV3J_MOUSE
14	349.5	62.9	111	1	KV3T_MOUSE
15	348.5	62.7	111	1	KV3L_MOUSE
16	348.5	62.7	111	1	KV3I_MOUSE
17	346.5	62.3	111	1	KV3H_MOUSE
18	344.5	62.0	111	1	KV3Q_MOUSE
19	342.5	61.6	111	1	KV3R_MOUSE
20	341.5	61.4	111	1	KV3M_MOUSE
21	340.5	61.2	111	1	KV3N_MOUSE
22	340.5	61.2	111	1	KV3L_MOUSE
23	340	61.2	129	1	KV3D_HUMAN
24	338	60.8	109	1	KV3D_HUMAN
25	338	60.8	109	1	KV3E_HUMAN
26	337.5	60.7	111	1	KV3O_MOUSE
27	337	60.6	109	1	KV3B_HUMAN
28	336	60.4	129	1	KV3H_HUMAN
29	335.5	60.3	111	1	KV3M_MOUSE
30	335	60.3	129	1	KV3L_MOUSE
31	330.5	59.4	129	1	KV1M_HUMAN
32	330	59.4	109	1	KV3E_HUMAN
33	329	59.2	109	1	KV3G_HUMAN

34	329	59.2	110	1	KV3P_MOUSE	P01668 mus musculu
35	326.5	58.7	108	1	KV1E_HUMAN	P01597 homo sapien
36	326	58.6	108	1	KV3A_HUMAN	P01619 homo sapien
37	325.5	58.5	111	1	KV3U_MOUSE	P01673 mus musculu
38	324.5	58.4	108	1	KV1V_HUMAN	P01643 homo sapien
39	324.5	58.4	108	1	KV5J_MOUSE	P01643 mus musculu
40	324.5	58.4	108	1	KV5K_MOUSE	P01644 mus musculu
41	324	58.3	109	1	KV1T_MOUSE	P01612 mus sapien
42	323.5	58.2	108	1	KV1H_HUMAN	P01600 homo sapien
43	323.5	58.2	108	1	KV1M_HUMAN	P01605 homo sapien
44	323.5	58.2	108	1	KV1Y_HUMAN	P01602 homo sapien
45	322.5	58.0	108	1	KV1O_HUMAN	P01607 homo sapien

ALIGNMENTS

RESULT 1

ID	KV6F_MOUSE	STANDARD:	PRT:	107 AA.
AC	P04940:			
DR	13-AUG-1987 (Rel. 05, Created)			
DR	13-AUG-1987 (Rel. 05, Last sequence update)			
DR	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-VI region NQ2-17.4.1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83271467; PubMed=6877353;			
RA	Kaattinen M., Griffiths G.M., Markham A.F., Milstein C.;			
RT	"mRNA sequences define an unusually restricted IgG response to 2-			
RT	phenylloxazalone and its early diversification."			
RC	Nature 304:320-324(1983).			
CC	-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.			

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DR EMBL: K00735; AAA8680.1; -
DR HSSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 34 43
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68B6 CRC64;

Query Match Best Local Similarity 81.1%; Score 451; DB 1; Length 107;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Oy 1 QIVLSQSPALISASPEKVTCTCRASSSYNYHHWQQRGSSPKWISATSMASGVPAR 60
Db 1 QIVLSQSPALISASPEKVTCTCRASSSYNYHHWQQRGSSPKWISATSMASGVPAR 60
Oy 61 FGSQSSGTSYSLTISRVEADATYCCQWSSNPPTFGGTMLEIR 106

```

Db      61  FSGSGSATSYSLTITSMQAEADATATYYCOOWSSNPPLTFAGTKLEIK 106
      ||||| ||||| :::||||| ||||| ||| ||| :
      FSGSGSATSYSLTITSMQAEADATATYYCOOWSSNPPLTFAGTKLEIK 106

RESULT 2
KV6I_MOUSE STANDARD: PRT: 107 AA.
ID KV6I_MOUSE
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NO6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nucleic Acids Res. 1983; 11:320-324.
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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DR EMBL; K00740; AAA8685.1; -.
DR HSSP; P01679; 2EBJ.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
KW Immunoglobulin V region; HydrIdoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6f694824ecf0c8e6 CnC64;

Query Match 80.2%; Score,446; DB 1; Length 107;
Best Local Similarity 79.2%; Pred.No.1,2e-35;
Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0.

OY 1 OIVLQSPALISASGEKYTMTCRASSSYVNMHWYQOKRPSGSPKPMISATSNLASGVPAR 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QIVLQSPAIMKASPGQKQYTMTCSSASSSYVNMHWYQOKRPSGSPKPMIYDTSLASGXPAR 60
OY 61 FSGSGSATSYSLTITRVEAEDATATYYCOOWSSNPPLTFGGTGLEIR 106
      ||||| ||||| :::||||| ||||| ||| ||| :
Db 61 FSGSGSATSYSLTITSMQAEADATATYYCOOWSSNPPLTFAGTKLEIK 106

RESULT 3
KV6H_MOUSE STANDARD: PRT: 107 AA.
ID KV6H_MOUSE
AC P04942;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NO5-6.1.1.2.
OS Mus musculus (Mouse).

```

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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-----
CC
CC EMBL; K00739; AAA38684.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.1.
DR SMART; SM00406; Igv.1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11605 MW; CA6C4284FCFB550 CRC64;
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Query Match 80.0%; Score 445; DB 1; Length 107;
Best Local Similarity 79.2%; Pred. NO. 1.5e-35;
Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
OY 1 OIVLSQSPALISAGEVYTMCRASSSVNVMHWYQOKPGSSPKFMISATSMASGVPAR 60
DB 1 QIVLTQSPALMSASPGQAVYTMTCSSSSSYVHMWYQOKSGTSPKRMVITDTSRLDSGVPAR 60
OY 61 FSGSGSGTYSLTISRVEAEDATYYCOOWSSNPPTFGGTMLEIR 106
DB 61 FSGSGSATSYSLTISMQAEDATYYCOOWSSNPPTFGAGTKLEIK 106
-----
RESULT 4
KV6G_MOUSE STANDARD; PRT; 107 AA.
P04941.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 kappa chain V-VI region M02-48.2.2.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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DR EMBL: K00737: AAA38682.1; -
DR HSSP: P01679: 2FBJ.
DR InterPro: IPR003006: Ig_MHC.
DR Pfam: PF00047: Ig_V.
DR SMART: SM00406: Igy_1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA: 11556 MW: 72488DA9EF354934 CRC64;

Query Match
Best Local Similarity 79.5%; Score 442; DB 1; Length 107;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 QIVLSQSPALISAPGKVTMTCTCRASSSVYMHVYQOKPSSPKPMVTSATSLASGVAP 60
1 QILTQSPALMSAPGKVTMTCTCRASSSVYMHVYQOKSGSPRMVYDTSKLASGVAP 60
Db 1 QILTQSPALMSAPGKVTMTCTCRASSSVYMHVYQOKSGSPRMVYDTSKLASGVAP 60
QY 61 FSSGSGTSTSLTSRYEADATYYCOQWSSNPPTFGGTMLEIR 106
61 FSSGSGTSTSLTSRYEADATYYCOQWSSNPPTFGGTMLEIR 106
Db 61 FSSGSGTSTSLTSRYEADATYYCOQWSSNPPTFGGTMLEIR 106
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-83271467; PubMed-6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RT phenylloxazone and its early diversification."
RL Nature 304:320-324(1983).
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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DR EMBL: K00744: AAA38689.1; -
DR HSSP: P01679: 2FBJ.
DR InterPro: IPR003006: Ig_MHC.
DR Pfam: PF00047: Igy_1.
DR SMART: SM00406: Igy_1.

KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA: 11611 MW: A38290781F3C30D3 CRC64;

Query Match
Best Local Similarity 79.3%; Score 441; DB 1; Length 107;
Matches 83; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 QIVLSQSPALISAPGKVTMTCTCRASSSVYMHVYQOKPSSPKPMVTSATSLASGVAP 60
1 QILTQSPALMSAPGKVTMTCTCRASSSVYMHVYQOKSGSPRMVYDTSKLASGVAP 60
Db 1 QILTQSPALMSAPGKVTMTCTCRASSSVYMHVYQOKSGSPRMVYDTSKLASGVAP 60
QY 61 FSSGSGTSTSLTSRYEADATYYCOQWSSNPPTFGGTMLEIR 106
61 FSSGSGTSTSLTSRYEADATYYCOQWSSNPPTFGGTMLEIR 106
Db 61 FSSGSGTSTSLTSRYEADATYYCOQWSSNPPTFGGTMLEIR 106
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-83271467; PubMed-6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RT phenylloxazone and its early diversification."
RL Nature 304:320-324(1983).
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DR EMBL: K00746: AAA38691.1; -
DR HSSP: P01679: 2FBJ.
DR InterPro: IPR003006: Ig_MHC.
DR Pfam: PF00047: Igy_1.
DR SMART: SM00406: Igy_1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 98
FT DOMAIN 99 108
FT DISULFID 23 87
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11713 MW: DABF235CD9680AC6 CRC64;

Query Match
Best Local Similarity 78.2%; Score 435; DB 1; Length 108;
Matches 83; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

```

Matches 84; Conservative 12; Mismatches 10; Indels 2; Gaps 1;
QY 1 QIVLSQSPAILLSASGEVYMTCRASSSVYNNHHYQOKPGSSPKRWISATSLASGVPAR 60
Db 1 QILQLSPAIMSASPGQVYMTCSASSSVYNNHHYQOKPGSSPKRWISATSLASGVPAR 60
QY 61 FSGSGSGTSTLTISRVEAEDATATYCCQWSSNP--FFGGTMTLEIR 106
Db 61 FSGSGSGTSTLTITRMOAEDATATYCCQWSSNPPLITFGAGTKLEK 108

RESULT 7
KV6D_MOUSE STANDARD: PRT: 107 AA.
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region SAC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glandemann C.P.J., Potter M.;
RT "Kappa Chain Joining segments and structural diversity of antibody
RT combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTIN.
DR PIR: A01941; KVM5X4.
DR HSSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CnC64;

Query Match 75.4%; Score 419; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 4; 3e-33;
Matches 81; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 1 QIVLSQSPAILLSASGEVYMTCRASSSVYNNHHYQOKPGSSPKRWISATSLASGVPAR 60
Db 1 EIVLQSPAIMSASPGQVYMTCSASSSVYNNHHYQOKPGSSPKRWISATSLASGVPAR 60
QY 61 FSGSGSGTSTLTISRVEAEDATATYCCQWSSNPFFGGTMTLEIR 106
Db 61 FSGSGSGTSTLTITRMOAEDATATYCCQWSSNPPLITFGAGTKLEK 106

RESULT 8
KV6A_MOUSE STANDARD: PRT: 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_TaxId=10090;	
RN	[1]	
RP	SEQUENCE:	
RX	MEDLINE=79082830; PubMed=103573;	
RA	Rao D.N., Rudikoff S., Potter M.;	
RT	"k Chain variable regions from three galactan binding myeloma proteins.";	
RL	Biochemistry 17:5555-5559(1978).	
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.	
DR	HSSP; P01679; 2FBJ.	
DR	IInterPro; IPR003306; Ig_MHC.	
DR	IInterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IgV; 1.	
KW	Immunoglobulin V region.	
FT	DOMAIN 1 23 FRAMEWORK-1.	
FT	24 33 COMPLEMENTARITY-DETERMINING-1.	
FT	DOMAIN 34 48 FRAMEWORK-2.	
FT	49 55 COMPLEMENTARITY-DETERMINING-2.	
FT	DOMAIN 56 87 FRAMEWORK-3.	
FT	88 96 COMPLEMENTARITY-DETERMINING-3.	
FT	DOMAIN 97 106 FRAMEWORK-4.	
FT	DISULFD 23 87 BY SIMILARITY.	
FT	NON_TER 107 107	
SQ	SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;	
 Query Match 75.2%; Score 418; DB 1; Length 107; Best Local Similarity 76.4%; Pred. No. 5.4e-33;		
Matches 81; Conservative 10; Mismatches 15; Indels 0; Gaps 0;		
OY	1 QIVLSQSPTALIASPGKGVMTTCRASSVSNVMHWIOOKPGSGSPKMISATSLMAGVPAR 60 : ::: : : : : : Db 1 ELVLGSPALTAAASLGQRVTITCSASSSYWMHWIQAKSGTSPKWIEISSLASGVPAR 60 TTTTTTSTTSRVPAEDAATYYCOOWSNSPPTEGGCTMLEIR 106 TTTTTTSTTSRVEDAATAIYYCOWNPPLTFEGGTLETK 106 OY 61 FSGSGSSTSYSLTITSRVPAEDAATYYCOOWSNSPPTEGGCTMLEIR 106 DB 61 FSGSGSSTSYSLTITSMEAEIDAIIYYCOWNPPLTFEGGTLETK 106 RESULT 9 KV6B_MOUSE STANDARD; PROT; 107 AA. ID KV6B_MOUSE P01676; AC P01676; DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE 1g kappa chain V-VI region XRPC 24. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxId=10090; RN [1] RP SEQUENCE: RX MEDLINE=79082830; PubMed=103573; RA Rao D.N., Rudikoff S., Potter M.;	
RT	"k Chain variable regions from three galactan binding myeloma proteins.";	
RL	Biochemistry 17:5555-5559(1978).	
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.	
DR	HSSP; P01679; 2FBJ.	
DR	IInterPro; IPR003306; Ig_MHC.	
DR	IInterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IgV; 1.	
KW	Immunoglobulin V region.	
FT	DOMAIN 1 23 FRAMEWORK-1.	
FT	24 33 COMPLEMENTARITY-DETERMINING-1.	
FT	DOMAIN 34 48 FRAMEWORK-2.	

FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 56 87 FRAMEWORK-3.
 FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 97 106 FRAMEWORK-4.
 FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA: 11584 MW: 366D022A5EC34D7 CRC64:

Query Match 74.3%; Score 413; DB 1; Length 107;
 Best Local Similarity 75.5%; Pred. No. 1.6e-32;
 Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Oy 1 QVLSQSPALISASPEKVTMTCRASSSVNYMHVQOKPGSSPKPMISATSNLASGVPAR 60
 Db 1 EIVLQSPALISASLGQKVTITCSASSSVSYMHVQOKSGTSPKPIYIISKLASGVPAR 60
 Oy 61 FSGSGGTSYSLTISRVEADATYYCOQWSSNPFTGGTMLEIR 106
 Db 61 FSGSGGTSYSLTISRVEADATYYCOQWSSNPFTGGTMLEIR 106

RESULT 10
 KV6C_MOUSE STANDARD: PRT; 107 AA.
 ID KV6C_MOUSE
 AC P01677;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region TEPC 601/TEPC 191.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX MEDLINE=79082830; PubMed=103573;
 RA Rao D.N., Rudkoff S., Potter M.;
 RT "k Chain variable regions from three galactan binding myeloma
 RT proteins";
 RL Biochemistry 17:555-5559(1978).
 RN [2]

RP SEQUENCE (TEPC 601).
 RX MEDLINE=81054757; PubMed=6776525;
 RA Rudkoff S., Rao D.N., Glandens C.P.J., Potter M.;
 RT "kappa Chain joining segments and structural diversity of antibody
 RT combining sites";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
 CC -1- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
 CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
 CC THAT BIND GALACTAN.
 PIR: A01941; KVMX4.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 34 48 FRAMEWORK-2.
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 56 87 FRAMEWORK-3.
 FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 87 FRAMEWORK-4.
 FT NON_TER 107 107 BY SIMILARITY.
 SQ SEQUENCE 107 AA: 11568 MW: 203CDV52A5EC34D7 CRC64:

Query Match 73.9%; Score 411; DB 1; Length 107;
 Best Local Similarity 74.5%; Pred. No. 2.5e-32;
 Matches 79; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Oy 1 QVLSQSPALISASPEKVTMTCRASSSVNYMHVQOKPGSSPKPMISATSNLASGVPAR 60

Db 1 EIVLQSPALISASLGQKVTITCSASSSVSYMHVQOKSGTSPKPIYIISKLASGVPAR 60
 Oy 61 FSGSGGTSYSLTISRVEADATYYCOQWSSNPFTGGTMLEIR 106
 Db 61 FSGSGGTSYSLTISRVEADATYYCOQWSSNPFTGGTMLEIR 106

RESULT 11
 KV4A_MOUSE STANDARD: PRT; 129 AA.
 ID KV4A_MOUSE
 AC P01680;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region S107B precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX MEDLINE=82113500; PubMed=6799208;
 RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharif M.D.;
 RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
 RL Cell 26:57-66(1981).
 CC -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
 CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
 CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
 CC NORMAL KAPPA CHAIN S107.

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DR EMBL: J00577; AAA8780.1;
 DR EMBL: V00780; CAA24157.1;
 DR PIR: A01943; KVM57B.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
 FT DOMAIN 23 45 FRAMEWORK-1.
 FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 58 72 FRAMEWORK-2.
 FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 80 111 FRAMEWORK-3.
 FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 128 FRAMEWORK-4.
 FT DISULFID 45 111 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA: 13833 MW: E4B873072DC6BE4 CRC64:

Query Match 72.8%; Score 405; DB 1; Length 129;
 Best Local Similarity 77.4%; Pred. No. 1.1e-31;
 Matches 82; Conservative 8; Mismatches 12; Indels 4; Gaps 2;

Oy 3 VLSQSPALISASPEKVTMTCRASSSV--NYMHVQOKPGSSPKPMISATSNLASGVPAR 60
 Db 25 VLTQSPALISASLGQKVTITCSASSSVSYLHMVQOKSGASPKPIYIISKLASGVPAR 84
 Oy 61 FSGSGGTSYSLTISRVEADATYYCOQWSSNPFTGGTMLEIR 106
 Db 85 FSGSGGTSYSLTISRVEADATYYCOQWSSNPFTGGTMLEIR 128

RESULT 12
KV3E_MOUSE STANDARD: PRT; 107 AA.
ID KV3E_MOUSE
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappa chain V-VI region J539.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Gaudemans C.P.J., Potter M.;
RT "Kappa Chain Joining segments and structural diversity of antibody
RT combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; PubMed=3449853;
RA Sun S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01942; KYMSU5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 48 FRAMEWORK-2.
FT DOMAIN 4 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87
FT STRAND 4 7
FT TURN 10 14
FT STRAND 15 16
FT TURN 19 25
FT STRAND 31 37
FT TURN 39 40
FT STRAND 44 48
FT TURN 51 51
FT STRAND 52 53
FT TURN 55 56
FT TURN 59 60
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 74
FT HELIX 79 81
FT STRAND 83 91
FT TURN 92 93
FT STRAND 94 97
FT STRAND 101 106
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;

Query Match 71.2%; Score 396; DB 1; Length 107;
Best Local Similarity 71.7%; Pred. No. 6, 4e-31;
Matches 76; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

OY 1 QIVSOSPALISASPGKVMTCRASSSVNMHYOQKPCSSPKPMISATSNLASGVPAR 60
:|||||:|:|:|||||:|||||:|||||:|||||:|

Db 1 EIVLTOSPALISASPGKVTITCSASSVSSLHWYQKSGTSPKPMIYEISKLASGVPAR 60
OY 61 FSGSGSTSYSLTISRVEADATYCCOQSSNPFGGSTMLEIR 106
:|||||:|:|:|||||:|||||:|||||:|
Db 61 FSGSGSTSYSLTISRVEADATYCCOQNTYPLITFGAGTKLEIK 106

RESULT 13
KV3J_MOUSE STANDARD: PRT; 111 AA.
ID KV3J_MOUSE
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Garmalan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KYMSM6.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 62.9%; Score 349.5; DB 1; Length 111;
Best Local Similarity 63.6%; Pred. No. 1, 6e-26;
Matches 70; Conservative 14; Mismatches 21; Indels 5; Gaps 1;

OY 2 IIVSOSPALISASPGKVTMTCRASSSV-----NYMHYQKPCSSPKPMISATSNLASG 56
:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|
Db 2 IIVLTOSPALISASPGKVTITCSASSVSSLSHWYQKSGTSPKPMIYEISKLASGVPAR 61

OY 57 VPARFSGSGSTSYSLTISRVEADATYCCOQSSNPFGGSTMLEIR 106
:|||||:|:|:|||||:|||||:|||||:|
Db 62 VPARFSGSGSTSYSLTISRVEADATYCCOQNNEDPYFGGSTMLEIR 111

RESULT 14
KV3T_MOUSE STANDARD: PRT; 111 AA.
ID KV3T_MOUSE
AC P01672;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappa chain V-III region PC 7940.

Query Match	62.98;	Score 349.5;	DB 1;	Length 111;
Best Local Similarity	63.68;	Pred. No. 1.6e-26;		
Matches 70; Conservative	10;	Mismatches 25;	Indels 5;	Gaps 1.

RESULT 15
KV31 MOUSE

ID	KEYID.MOUSE	STANDARD:	PRT;	111 AA.
AD	KV01664:			
AC				
DT	21-JUL-1986 (Rel. 01,	Created)		
DT	21-JUL-1986 (Rel. 01,	Last sequence update)		
DT	15-JUL-1999 (Rel. 38,	Last annotation update)		
DE	Ig kappa chain V-II region	CBCP 101.		
DE	Mus musculus (Mouse).			
.OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheraia; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
OK	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79012520; Pubmed=99744;			
RA	McKean D.J., Bell M., Potter M.;			
RT	"Mechanisms of antibody diversity: multiple genes encode structurally			
RT	related mouse kappa variable regions."			
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).			
CC	-I- MYCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.			
DR	PIR: A01936; KVMSC1.			
DR	HSSP: P80362; IWTL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART: SM00406; IGV; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN	1	23	FRAMEWORK-1.
FT	DOMAIN	24	38	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	39	53	FRAMEWORK-2.
FT	DOMAIN	54	60	COMPLEMENTARITY-DETERMINING-2.

Query Match	62.7%	Score 348.5;	DB 1;	Length 111;
Best Local Similarity	62.7%	Pred. No. 2e-26;		
Matches 69;	Conservative 15;	Mismatches 21;	Indels 5;	Gaps 1;

Search completed: November 27, 2002, 07:18:57
Job time : 16.1429 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 06:27:07 ; Search time 58.934 Seconds
(without alignments)
370.599 Million cell updates/sec

Title: US-09-893-615-89
Perfect score: 556
Sequence: 1 QIVLSQSPAILSASPEKVT.....CQWSSNPPTFGGTMLEIR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: . 671580
```

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

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Database :
SPTRMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vetlebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriopl.*
17: sp_archaeopl.*
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pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	455.5	81.9	97	11	Q9J176	Q9J176 mus musculu
2	453	81.5	134	11	Q8VD00	Q8VD00 mus musculu
3	441	79.3	235	11	Q91W12	Q91W12 mus musculu
4	427	76.8	106	5	Q9U410	Q9U410 schistosoma
5	368.5	66.3	101	11	Q9J178	Q9J178 mus musculu
6	352	63.3	109	4	Q9UL78	Q9UL78 homo sapien
7	343.5	61.8	111	11	Q920E9	Q920E9 mus musculu
8	341.5	61.4	108	4	Q9UL70	Q9UL70 homo sapien
9	339.5	61.1	108	4	Q9UL79	Q9UL79 homo sapien
10	331	59.5	107	4	Q96SA9	Q96SA9 homo sapien
11	327	58.8	107	4	Q9UL81	Q9UL81 homo sapien
12	323.5	58.2	108	4	Q9UL77	Q9UL77 homo sapien
13	323	58.1	109	4	Q9UL85	Q9UL85 homo sapien
14	319	57.4	109	4	Q9UL86	Q9UL86 homo sapien
15	317.5	57.1	109	11	Q920E6	Q920E6 mus musculu
16	317.5	57.1	234	11	Q8U062	Q8U062 mus musculu

17	317.5	56.7	1	298	11	Q9VFE0	Q9VFE0	mus	musculus
18	313.5	56.4	123	108	4	Q9ULB3	Q9ULB3	homo	sapient
19	315.5	55.7	203	11	Q91WS9	Q91WS9	mus	musculus	
20	309.5	55.7	214	11	Q9RIA5	Q9RIA5	mus	musculus	
21	309	55.6	238	11	Q8VC16	Q8VC16	mus	musculus	
22	307.5	55.3	127	11	Q925S9	Q925S9	mus	musculus	
23	307.5	55.3	234	11	Q91W88	Q91W88	mus	musculus	
24	306.5	55.1	108	11	Q8VJ10	Q8VJ10	mus	musculus	
25	299.5	53.9	107	11	Q9JL84	Q9JL84	mus	musculus	
26	296.5	53.3	103	11	Q9JL80	Q9JL80	mus	musculus	
27	293.5	52.8	234	11	Q8VC00	Q8VC00	mus	musculus	
28	292	52.5	238	11	Q9JW37	Q9JW37	mus	musculus	
29	285.5	51.3	99	11	Q9JL74	Q9JL74	mus	musculus	
30	281.5	50.6	107	11	Q9ER9	Q9ER9	mus	musculus	
31	280.5	50.4	116	4	Q96PF6	Q96PF6	homo	sapient	
32	280	50.4	104	11	Q9JL82	Q9JL82	mus	musculus	
33	280	50.4	239	11	Q8VC55	Q8VC55	mus	musculus	
34	280	50.4	241	11	Q921A6	Q921A6	mus	musculus	
35	277	49.8	239	4	Q8RC00	Q8RC00	homo	sapient	
36	270.5	48.7	114	4	Q9UL80	Q9UL80	homo	sapient	
37	265.5	47.8	109	6	Q9N0W5	Q9N0W5	homo	sapient	
38	264	47.1	237	4	Q8WU4	Q8WU4	homo	sapient	
39	262	47.1	237	4	Q8WU6	Q8WU6	homo	sapient	
40	261.5	47.0	234	11	Q8R028	Q8R028	mus	musculus	
41	245.5	43.6	236	4	Q96E51	Q96E51	homo	sapient	
42	232.5	42.4	129	11	Q8VDE2	Q8VDE2	mus	musculus	
43	235	42.3	108	4	Q9S6B0	Q9S6B0	homo	sapient	
44	235	42.3	110	4	Q8RE63	Q8RE63	homo	sapient	
45	234.5	42.2	112	4	Q96J11	Q96J11	homo	sapient	

ALIGNMENTS

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
11	81.9%	Score 455.5; DB 11; Length 97;				
1	91.8%	Pred. NO. 1,1e-38;	2;	5;	1;	1;
LSASGCEVYTMICRASSSVSYMHVQQRKSGSPKRWISATSNLASCIVPAREFGSGSGCTSY 70						
LSASGCEVYTMICRASSSVSYMHVQQRKSGSPKRWIATSNLASCIVPAREFGSGSGCTSY 60						

QY 71 SLTISRVEADATYYCCQWSSN-PPYFGGTMLEIR 106
 DB 61 SLTISRVEADATYYCCQWSSKMYTFGGTKLEIK 97

RESULT 2
 ID 08VDD0 PRELIMINARY: PRT: 134 AA.
 AC 08VDD0:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Anti-MOG Z12 variable light chain (Fragment).
 GN ANTI-MOG KAPPA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Cheraiovsky Y.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Sempd P.;
 RT "Targeting T cells to the CNS.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AA416331; CAC94866.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00406; IGV_1.
 DR NON_TER 134
 SQ SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;

Query Match 81.5%; Score 453; DB 11; Length 134;
 Best Local Similarity 83.0%; Pred. No. 3e-38; 11; Indels 0; Gaps 0;
 Matches 88; Conservative 7; Mismatches 11;

QY 1 QIVLSOSPALISAPGEKVTMTCRASSSVNMYOHQOKPGSSPKPWISATSNLASGVPAR 60
 DB 23 QIVLTOSPALMSAPGEKVTMTCSASSISYMHMYOQKPTSPKRWLYDTSKLASGVPAR 82

QY 61 FSGSGGTSYSLTISRVEADATYYCCQWSSNPPYFGGTMLEIR 106
 DB 83 FSGSGGTSYSLTISRVEADATYYCQWSSYPPTFGGTMLEIK 128

RESULT 3
 ID 091W12 PRELIMINARY: PRT: 235 AA.
 AC 091W12:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Unknown (protein for MGC:65382).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC006643; AAH06643.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.

DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 79.3%; Score 441; DB 11; Length 235;
 Best Local Similarity 78.3%; Pred. No. 9.5e-37;
 Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 QIVLSOSPALISAPGEKVTMTCRASSSVNMYOHQOKPGSSPKPWISATSNLASGVPAR 60
 DB 23 QIVLTOSPALMSAPGEKVTMTCSASSISYMHMYOQKPTSPKRWLYDTSKLASGVPAR 82

QY 61 FSGSGGTSYSLTISRVEADATYYCCQWSSNPPYFGGTMLEIR 106
 DB 83 FSGSGGTSYSLTISRVEADATYYCQWSSNPPYFGGTMLEIK 128

RESULT 4
 ID 09U410 PRELIMINARY: PRT: 106 AA.
 AC 09U410:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Monoclonal anti-Idiotypic antibody NP30 immunoglobulin light chain
 DE variable region (Fragment).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiidae;
 OC Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the light chain
 RT variable region gene of monoclonal anti-Idiotypic antibody NP30 of
 RT Schistosoma japonicum.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF207620; AAJ19434.1; -
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV_1.
 DR NON_TER 106
 FT NON_TER 106
 SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 76.8%; Score 427; DB 5; Length 106;
 Best Local Similarity 78.8%; Pred. No. 9.5e-36;
 Matches 82; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 3 VLSQSPALISAPGEKVTMTCRASSSVNMYOHQOKPGSSPKPWISATSNLASGVPAR 62
 DB 3 LITQSPALMSAPGEKVTMTCSASSISYVYWLQKPGSSPRLLIYDTSNLAGVPRFS 62

QY 63 GSGSGGTSYSLTISRVEADATYYCCQWSSNPPYFGGTMLEIR 106
 DB 63 GSGSGGTSYSLTISRVEADATYYCQWSSYPPTFGGTMLEIK 106

RESULT 5
 ID 09JL78 PRELIMINARY: PRT: 101 AA.
 AC 09JL78:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)

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RP SEQUENCE FROM N.A.
RC STRAIN-A.CA.
RX MEDLINE-20448942; PubMed-10992488;
RA Makiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF060628; AAF69326.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 10778 MW; 0AF65E6A7E6F14D CRC64;

Query Match
Best Local Similarity 66.3%; Score 368.5; DB 11; Length 101;
Matches 74; Conservative 8; Mismatches 14; Indels 3; Gaps 2;

OY 11 LSASPEKVTMTCRASSV--NYMHYQOKPGSSPKWISATSNLASGVAPRFGSGSGT 68
Db 3 MAASPEKITITCSASSISSNLYHWYQOKPGSPKLLIRTSNLSAGVPTFRSGSGST 62
OY 69 SYSLTISRVEADATATYTCQWSSNPP-TFGGSTMLEIR 106
Db 63 SYSLTIGTMEADATATYTCQWSSNPP-TFGGSTMLEIR 101

RESULT 6
OY 09UL78 PRELIMINARY: PRT; 109 AA.
AC 09UL78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match
Best Local Similarity 63.3%; Score 352; DB 4; Length 109;
Matches 66; Conservative 19; Mismatches 21; Indels 2; Gaps 1;

OY 1 QVILSOPAILASPEKVTMTCRASSV--NYMHYQOKPGSSPKWISATSNLASGV 58
Db 1 EYLTSPGTLSPERATLSCRASQSSSTLYANQOKPGAPPLLYIGASRATGIP 60
OY 59 ARFSGSGSTSYSLTISRVEADATATYTCQWSSNPP-TFGGSTMLEIR 106
Db 61 DRFSGSGSTDTLTISRLEPEDCAVYTCQWSSNPP-TFGGSTMLEIR 108
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RESULT 7
OY 0920E9 PRELIMINARY: PRT; 111 AA.
AC 0920E9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotypic kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Jape A., Jennings I.G., Horvath O., Cotton R.G.H.;
RT "Definition of the idiotype of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079335; AAL09419.1; -.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988A6858526 CRC64;

Query Match
Best Local Similarity 61.8%; Score 343.5; DB 11; Length 111;
Matches 70; Conservative 10; Mismatches 25; Indels 5; Gaps 1;

OY 2 IVLSOPAILASPEKVTMTCRASSV-----NYMHYQOKPGSSPKWISATSNLASG 56
Db 2 IVLTSPASLAVSLGORATISCRASKSVSTSGYMHYQOKGPGPKLLIYANLASG 61
OY 57 VPARFSGSGSTSYSLTISRVEADATATYTCQWSSNPP-TFGGSTMLEIR 106
Db 62 VPARFSGSGSTDTLTISRLEPEDCAVYTCQWSSNPP-TFGGSTMLEIR 111

RESULT 8
OY 09UL70 PRELIMINARY: PRT; 108 AA.
AC 09UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; 1REL.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match
Best Local Similarity 61.4%; Score 341.5; DB 4; Length 108;
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[illegible]

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RT      "Molecular analysis of polyclonal monoclonal antibodies from  
RT      rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RT      antibody V region genes.";  
RL      J. Immunol. 161:2020-2031(1998).  
DR      EMBL; U96396; AAB68785.1; -  
DR      InterPro: IPR003006; IG_MHC.  
PI      Pfam: PF00047; 1g; 1.  
FT      NON_TER  
FT      NON_TER  
SO      SEQUENCE    107 AA; 107 MW; 4BB43E9C5B577F16 CMC64;  
  
Query Match          59.5%; Score 331; DB 4; Length 107;  
Best Local Similarity 62.3%; Pred. No. 4.7e-26;  
Matches   66; Conservative 20; Mismatches 18; Indels 2; Gaps 2;  
  
QY      2 IVLSGSPALISAPGEKYTMTCRASSV-NVMHWQOKRGSSPKPWISATSNLASGVPAR 60  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
DB      2 IQMTGPSPLSLASVDGYITTCRASQSISSTYNLMWQOKRGPRLIIYAASSLGSGVPSR 61  
        |||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
QY      61 FSGSSGSTSYSLTISRVEADAITYCCQMSNPPTEFGGTMLEIR 106  
        |||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
DB      62 FSGSSGGTDFTLTISLQPEDPATYYCOO-SYSTLTFFGGTGKVEIK 106  
        |||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
  
RESULT 11  
Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
   (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
   Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal  
   fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL EMBL; AF035033; AAD56269.1; -.  
DR HSSP; P01607; 1REI.  
DR InterPro: IPR003006; IG_MHC.  
DR InterPro: IPR003596; IG_V.  
PI Pfam; PF00047; 1g; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON_TER  
FT NON_TER  
SO SEQUENCE    107 AA; 107 MW; 070549FEDE0754748 CMC64;  
  
Query Match          58.8%; Score 327; DB 4; Length 107;  
Best Local Similarity 62.3%; Pred. No. 1.2e-25;  
Matches   66; Conservative 19; Indels 2; Gaps 2;  
  
QY      2 IVLSGSPALISAPGEKYTMTCRASSV-NVMHWQOKRGSSPKRWISATSNLASGVPAR 60  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
DB      2 IQMTGPSPLSLASVDGYITTCRASQSISSTYNLMWQOKRGPRLIIYAASSLGSGVPSR 61  
        |||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
QY      61 FSGSSGSTSYSLTISRVEADAITYCCQMSNPPTEFGGTMLEIR 106  
        |||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
DB      62 FSGSSGGTDFTLTISGLQAEPAITYCOO-SYSALTTPPGTKVIDIR 106  
        |||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
  
RESULT 12  
Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
```

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035037; AAD56273.1; -.
 DR HSSP; P01607; IREL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 FT NON_TER 1
 FT 108
 SQ SEQUENCE 108 AA; 11738 MW; C06681716CADI6F3 CRC64;
 Query Match 58.2%; Score 323.5; DB 4; Length 108;
 Best Local Similarity 60.4%; Pred. No. 2.7e-25;
 Matches 64; Conservative 19; Mismatches 22; Indels 1; Gaps 1;
 Oy 2 IVLSOSPATLSAPGKVTMTCRASSV--NYMHVYQKRGSSPKWISATSNLASGVP 60
 Db 2 IGMTOSPSLSASVGDVITTCRASOSISLYLWYQKRGKAPNLLIYATSSLSQSGVPSR 61
 Oy 61 FSGSGSGTSYSLTISRVEADATATYCCQWSSNPPTFGGCTMLEIR 106
 Db 62 FSGSGSGTDFLTITSLQPEDFATYCCQSYSTSWTFEGCTKVEIK 107
 RESULT 13
 ID 09UL85 PRELIMINARY; PRT; 109 AA.
 AC 09UL85;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -.
 DR HSSP; P80362; IWTI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 FT NON_TER 1
 FT 109
 SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACCC CRC64;
 Query Match 58.1%; Score 323; DB 4; Length 109;
 Best Local Similarity 57.4%; Pred. No. 3.1e-25;
 Matches 62; Conservative 23; Mismatches 21; Indels 2; Gaps 2;

Oy 1 QIVLSOSPATLSAPGKVTMTCRASSV--NYMHVYQKRGSSPKWISATSNLASGVP 59
 Db 1 EIVTOSPTLSVSPERATLSCWASOSISNLIAMVQKPGQAPRLIYTGSTRATGTPA 60
 Oy 60 FSGSGSGTSYSLTISRVEADATATYCCQWSSNPPTFGGCTMLEIR 106
 Db 61 FSGSGSGTEFTLTITSLQSEDFATYHCQYNSMPPLTFGGCTKVEIK 108
 RESULT 14
 ID 09UL86 PRELIMINARY; PRT; 109 AA.
 AC 09UL86;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035028; AAD56264.1; -.
 DR HSSP; P80362; IWTI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 FT NON_TER 1
 FT 109
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
 Query Match 57.4%; Score 319; DB 4; Length 109;
 Best Local Similarity 57.4%; Pred. No. 7.8e-25;
 Matches 62; Conservative 20; Mismatches 24; Indels 2; Gaps 1;
 Oy 1 QIVLSOSPATLSAPGKVTMTCRASSV--NYMHVYQKRGSSPKWISATSNLASGVP 58
 Db 1 EIVTOSPTLSVSPERATLSCWASOSISNLIAMVQKPGQAPRLIYTGSTRATGTP 60
 Oy 59 ARFSGSGTSYSLTISRVEADATATYCCQWSSNPPTFGGCTMLEIR 106
 Db 61 DRFSGSGTDFLTITSLQPEDFATYCCQYSSIFTFGCTKVDIK 108
 RESULT 15
 ID 0920E6 PRELIMINARY; PRT; 109 AA.
 AC 0920E6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE pterin-mimicking anti-idiotope kappa chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Jape A., Jennings I.G., Horvath O., Cotton R.G.H.,
 RT "Definition of the idiotope of pterin-mimicking antibodies expressed
 in mammalian cells".
 Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

Wed Nov 27 08:54:33 2002

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Page 6

DR EMBL AF307938: AAL09422.1; -
DR InterPro: IPR003006; IG-MHC.
DR Pfam: PF00047; 1g; 1.
FT NON_TER 1
FT 1
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;

Query Match	57.18;	Score 317.5;	DB 11;	Length 109;
Best Local Similarity	59.48;	Pred. No. 1.1e-24;		
Matches 63;	Conservative 15;	Mismatches 27;	Indels 1;	Gaps 1;

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Oy 2 IYLSOSPILSLSPKXYMTCRASSV-NYHHWYQOKRSGSPKIMASTSLACGPVR 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 IQMTGSPASLASVGEYTYITTCRASGNIHNILAWYQOKGRKSPOLLVYNAKTLAAGVSR 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 61 FSGSSGTSYLTISRVAEDAAATYTCQOQMSNPFTFGGTYLEIR.106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 FSGSSGTYSLKINSLOPEDRGSTYCCQHFMTPTWTFGGGTYLEIR.107
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: November 27, 2002, 07:22:55
Job time : 60.9344 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:17:51 : Search time 19.2355 Seconds

(without alignments)
162.139 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 556

Sequence: 1 QIVLSQSPALISASPEGEKV.....CQWSSNPRTFGGTMLEIR 106

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	526	94.6	106	3	US-08-783-853A-105
2	526	94.6	106	4	US-09-344-050-105
3	526	94.6	107	3	US-08-783-853A-11
4	526	94.6	107	4	US-09-344-050-11
5	526	94.6	112	3	US-08-783-853A-103
6	526	94.6	112	4	US-09-344-050-103
7	521	93.7	128	1	US-08-476-275-4
8	521	93.7	128	4	US-08-476-275-4
9	507	91.2	129	2	US-08-449-287-2
10	507	91.2	129	4	US-08-449-287-2
11	507	91.2	235	4	US-09-423-439-18
12	507	91.2	235	4	US-09-423-439-18
13	490	88.1	105	1	US-08-459-310-4
14	486	87.4	107	1	US-08-211-202-3
15	486	87.4	246	1	US-08-469-486-57
16	486	87.4	246	2	US-08-469-486-57
17	484	87.1	252	1	US-08-279-772A-6
18	484	87.1	252	4	US-08-902-486-9
19	482	86.7	237	2	US-08-468-252-5
20	482	86.7	237	3	US-08-668-706B-5
21	482	86.7	237	5	PCT-US95-10740-5
22	475	85.4	97	2	US-08-308-494A-11
23	473.5	85.2	110	3	US-08-836-561-33
24	471.5	84.8	105	1	US-08-211-202-110
25	469	84.4	97	4	US-09-280-028-4
26	466	83.8	129	2	US-08-116-778E-2
27	466	83.8	129	2	US-08-438-562-2

28	466	83.8	129	2	US-08-483-528B-92
29	464	83.5	128	4	US-08-619-491-2
30	464	83.5	128	5	PCT-US95-07302-2
31	462	83.1	128	2	US-08-656-586-2
32	457	82.2	222	2	US-08-190-199A-67
33	457	82.2	235	2	US-08-190-199A-61
34	456	82.0	281	4	US-09-423-439-44
35	456	82.0	666	4	US-09-423-439-51
36	455	81.8	106	3	US-08-397-411-9
37	455	81.8	129	3	US-08-783-853A-99
38	455	81.8	129	4	US-09-344-050-99
39	454	81.7	125	3	US-08-783-853A-78
40	454	81.7	125	4	US-09-344-050-78
41	453	81.5	127	1	US-08-483-882-80
42	453	81.5	127	2	US-08-483-389-80
43	453	81.5	127	2	US-08-487-113D-80
44	453	81.5	127	2	US-08-473-503-80
45	453	81.5	127	2	US-08-483-932-80

ALIGNMENTS

RESULT 1
US-08-783-853A-105
Sequence 105, Application US/08783853A
Patent No. 6005091

GENERAL INFORMATION:

APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783, 853A
FILING DATE: 16-JAN-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Sequence 92, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 67, Appl
Sequence 61, Appl
Sequence 44, Appl
Sequence 51, Appl
Sequence 9, Appl
Sequence 99, Appl
Sequence 99, Appl
Sequence 78, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 80, Appl

HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-783-853A-105

Query Match
Best Local Similarity 94.6%; Score 526; DB 3; Length 106;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNYMHYQOKPSSSPKPVISATSNLASCVPAR 60
DB 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNYMHYQOKPSSSPKPVISATSNLASCVPAR 60

QY 61 FSSGSGTSTSLTISRVEDATYTCQOQSSNPRTFGGTMLEIR 106
DB 61 FSSGSGTSTSLTISRVEDATYTCQOQSSNPRTFGGTMLEIR 106

RESULT 2

US-09-344-050-105
Sequence 105, Application US/09344050
Patent No. 6391299

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

US-09-344-050-105

Query Match
Best Local Similarity 94.6%; Score 526; DB 4; Length 106;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNYMHYQOKPSSSPKPVISATSNLASCVPAR 60
DB 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNYMHYQOKPSSSPKPVISATSNLASCVPAR 60

QY 61 FSSGSGTSTSLTISRVEDATYTCQOQSSNPRTFGGTMLEIR 106
DB 61 FSSGSGTSTSLTISRVEDATYTCQOQSSNPRTFGGTMLEIR 106

RESULT 3

US-08-783-853A-11
Sequence 11, Application US/08783853A
Patent No. 6005091

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-783-853A-11

Query Match
Best Local Similarity 94.6%; Score 526; DB 3; Length 107;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Matches 101: Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60
Db 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60

Qy 61 FSGSGSTSYSLTISRVEADATYCCOOWSNPTFGGCTMLEIR 106
Db 61 FSGSGSTSYSLTISRVEADATYCCOOWSNPTFGGCTMLEIR 106

RESULT 4
US-09-344-050-11

; Sequence 11, Application US/09344050

; Patent No. 6391299

; GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael

; APPLICANT: Church, William

; APPLICANT: Gross, Mitchell

; APPLICANT: Feuerstein, Gloria

; APPLICANT: Nichols, Andrew

; APPLICANT: Padlan, Eduardo

; APPLICANT: Patel, Arundhal

; APPLICANT: Sylvester, Daniel

; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/344,050

; FILING DATE: 24-JUN-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/783,853

; FILING DATE: 16-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Kirk

; REGISTRATION NUMBER: 33,833

; REFERENCE/DOCKET NUMBER: P50438

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5096

; TELEFAX:

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; US-09-344-050-11

Query Match 94.6%; Score 526; DB 4; Length 107;

Best Local Similarity 95.3%; Pred. NO. 1.7e-42;

Matches 101: Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60
Db 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60

Db 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60

Qy 61 FSGSGSTSYSLTISRVEADATYCCOOWSNPTFGGCTMLEIR 106
Db 61 FSGSGSTSYSLTISRVEADATYCCOOWSNPTFGGCTMLEIR 106

RESULT 5
US-08-783-853A-103

; Sequence 103, Application US/08783853A

; Patent No. 6005091

; GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael

; APPLICANT: Church, William

; APPLICANT: Gross, Mitchell

; APPLICANT: Feuerstein, Gloria

; APPLICANT: Nichols, Andrew

; APPLICANT: Padlan, Eduardo

; APPLICANT: Patel, Arundhal

; APPLICANT: Sylvester, Daniel

; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/783,853A

; FILING DATE: 16-JAN-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/029,119

; FILING DATE: 24-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Kirk

; REGISTRATION NUMBER: 33,833

; REFERENCE/DOCKET NUMBER: P50438

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5096

; TELEFAX:

; INFORMATION FOR SEQ ID NO: 103:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; US-08-783-853A-103

Query Match 94.6%; Score 526; DB 3; Length 112;

Best Local Similarity 95.3%; Pred. NO. 1.7e-42;

Matches 101: Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60
Db 1 QVLSQSPAILASPGKVTMTCRASSSVNHWYQOKPGSSPKPWISATSNLASGVPAR 60

Db 61 FSGSGCTSYSLTISRVEDAATYYCQOWSNPRTFGGCTKLEIK 106

RESULT 6

US-09-344-050-103

Sequence 103, Application US/09344050
Patent No. 6391299

GENERAL INFORMATION:

APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Gloria
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853

FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX:

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

US-09-344-050-103

Query Match 94.6%; Score 526; DB 4; Length 112;
Best Local Similarity 95.3%; Pred. No. 1.7e-42;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPAILSPGKVTMTCTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

Db 1 QIVLSOSPAILSPGKVTMTCTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

QY 61 FSGSGCTSYSLTISRVEDAATYYCQOWSNPRTFGGCTKLEIR 106

Db 61 FSGSGCTSYSLTISRVEDAATYYCQOWSNPRTFGGCTKLEIK 106

RESULT 7

US-08-476-275-4
Sequence 4, Application US/08476275
Patent No. 5776456

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,891

FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-155

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-476-275-4

Query Match 93.7%; Score 521; DB 1; Length 128;
Best Local Similarity 92.5%; Pred. No. 5.9e-42;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QIVLSOSPAILSPGKVTMTCTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

Db 23 QIVLSOSPAILSPGKVTMTCTCRASSSVNYMHYQOKPGSSPKPWISATSNLASGVPAR 60

QY 61 FSGSGCTSYSLTISRVEDAATYYCQOWSNPRTFGGCTKLEIK 106

Db 83 FSGSGCTSYSLTISRVEDAATYYCQOWSNPRTFGGCTKLEIK 128

RESULT 8

US-08-475-815B-7

Sequence 7, Application US/08475815B

Patent No. 6399061

GENERAL INFORMATION:

APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: LEONARD, JOHN E.

APPLICANT: NEMMAN, ROLAND A.
APPLICANT: REEF, MITCHELL E.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-815B-7

Query Match 93.7%; Score 521; DB 4; Length 128;
Best Local Similarity 92.5%; Pred. No. 5,9e-42;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QIVLSQSPALISASPEKVTMTGRASSSVNYMHVYQOKPSSSPKPMISATSNLASGVPR 60
DB 23 QIVLSQSPALISASPEKVTMTGRASSSVYIHVFOOKPSSSPKPMIVATSNLASGVPR 82

QY 61 FSGSGSGTSTLTISRVEADATYYCOQWSSNPFTFGGTMLEIR 106
DB 83 FSGSGSGTSTLTISRVEADATYYCOQWTSNPFTFGGTMLEIR 128

RESULT 9
US-08-449-287-2
Sequence 2, Application US/08449287
Patent No. 5877293
GENERAL INFORMATION:
APPLICANT: ADAIR, John Robert
APPLICANT: BODMER, Mark William
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
TITLE OF INVENTION: Their Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,287
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-287-2

Query Match 91.2%; Score 507; DB 2; Length 129;
Best Local Similarity 91.5%; Pred. No. 1,2e-40;
Matches 97; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QIVLSQSPALISASPEKVTMTGRASSSVNYMHVYQOKPSSSPKPMISATSNLASGVPR 60
DB 23 QIVLSQSPALISASPEKVTMTGRASSSVYIHVFOOKPSSSPKPMIVATSNLASGVPR 82

QY 61 FSGSGSGTSTLTISRVEADATYYCOQWSSNPFTFGGTMLEIR 106
DB 83 FSGSGSGTSTLTISRVEADATYYCOQWTSNPFTFGGTMLEIR 128

RESULT 10
US-09-423-439-18
Sequence 18, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423.439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match 91.2%; Score 507; DB 4; Length 235;
Best Local Similarity 91.5%; Pred. No. 2,4e-40;
Matches 97; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QIVLSQSPALLSASGKGVMTTCRASSSVNMYHMYQOKPGSSPKPWISATSNLASGVAPAR 60
DB 23 QTVLSQSPALLSASGKGVMTTCRASSSVTYIHMYQOKPGSSPKSWIATSNLASGVAPAR 82
QY 61 FSGSGSGTSTSLTISRVEAEDAATYYCOQWSSNPTEFGGTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEAEDAATYYCOHWSKPPTEFGGTKLEIK 128

RESULT 11
US-09-423-439-58
Sequence 58: Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423.439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-423-439-58

Query Match 91.2%; Score 507; DB 4; Length 235;

Best Local Similarity 91.5%; Pred. No. 2,4e-40;
Matches 97; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QIVLSQSPALLSASGKGVMTTCRASSSVNMYHMYQOKPGSSPKPWISATSNLASGVAPAR 60
DB 23 QTVLSQSPALLSASGKGVMTTCRASSSVTYIHMYQOKPGSSPKSWIATSNLASGVAPAR 82
QY 61 FSGSGSGTSTSLTISRVEAEDAATYYCOQWSSNPTEFGGTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEAEDAATYYCOHWSKPPTEFGGTKLEIK 128

RESULT 12
US-09-011-769A-23
Sequence 23: Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
BLAKEY, David C.
DAVIES, David H.
HENNAM, John F.
HENNEQUIN, Laurent F.A.
MARSHAM, Peter R.
DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011.769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-011-769A-23

Query Match 91.2%; Score 507; DB 4; Length 235;
Best Local Similarity 91.5%; Pred. No. 2,4e-40;
Matches 97; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QIVLSQSPALLSASGKGVMTTCRASSSVNMYHMYQOKPGSSPKPWISATSNLASGVAPAR 60
DB 23 QTVLSQSPALLSASGKGVMTTCRASSSVTYIHMYQOKPGSSPKSWIATSNLASGVAPAR 82
QY 61 FSGSGSGTSTSLTISRVEAEDAATYYCOQWSSNPTEFGGTMLEIR 106
DB 83 FSGSGSGTSTSLTISRVEAEDAATYYCOHWSKPPTEFGGTKLEIK 128

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RESULT 13
US-08-459-310-4
: Sequence 4, Application US/08459310
: Patent No. 5645817
: GENERAL INFORMATION:
: APPLICANT: Seemann, Gerhard
: APPLICANT: Bosslet, Klaus
: TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
: TITLE OF INVENTION: Their Preparation and Use
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,310
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/100,963
: FILING DATE: 03-AUG-1993
: APPLICATION NUMBER: DE P 422 58 53.7
: FILING DATE: 05-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Wadler, Linda A.
: REGISTRATION NUMBER: 33,218
: REFERENCE/DOCKET NUMBER: 02481.1317-00000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-408-4000
: TELEFAX: 202-408-4400
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 105 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-459-310-4

Query Match      88.1%; Score 490; DB 1; Length 105;
Best Local Similarity 91.3%; Pred. No. 3.8e-39;
Matches 95; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY      2      IVLSGPAIIASPEGEKTMTCRASSVSYVMHWYQOKPGSSPKPMISATSNLASGVPAF 61
      2      IQLTSPAILLASPEEKYTMTCRASSVSVMHWYQOKPGSSPKPMIYATSNLASGVPAF 61
DB      2      IQLTSPAILLASPEEKYTMTCRASSVSVMHWYQOKPGSSPKPMIYATSNLASGVPAF 61

OY      62      SGSGSGTSYSLTISRVEAEDATYTCQOMSSNPFFGGTLMLEI 105
      62      SGSGSGTSYSLTISRVEAEDATYTCQOMSSNPFFGGTLMLEI 105
DB      62      SGSGSGTSYSLTISRVEAEDATYTCQOMSSNPFFGGTLMLEI 105

RESULT 14
US-08-211-202-3
: Sequence 3, Application US/08211202
: Patent No. 5565332
: GENERAL INFORMATION:
: APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
: APPLICANT: BAIER, Michael
: APPLICANT: JESPERS, Laurent Stephane Anne Therese
: APPLICANT: WINTER, Gregory Paul
: TITLE OF INVENTION: Production of chimeric antibodies - a
: TITLE OF INVENTION: combinatorial approach
: NUMBER OF SEQUENCES: 144
: CORRESPONDENCE ADDRESS:

```

```

ADDRESSSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-3

Query Match      87.4% Score 486; DB 1; Length 107;
Best Local Similarity 88.6%; Pred. No. 9,1e-39;
Matches 93; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY    2 IVLSGPAIIASPEGEKWTTCRASSSYNYMHVYOQRPGSSPKPNIISATNSLASGVPARF 61
      2 IELTSPILIASPGKATITCTCRASSSVSMHWQKRFGSSKKPNIVATSNLASGVPTRF 61
DDB   62 SGGSGTSYSTLTISRVEAEDATYYCCQWSSNPFTFGGTMLEIR 106
      62 SGTSGTSYSTLTISRVEAEDATYYCCQWSSNPFTFGGTMLEIR 106

RESULT 15
US-08-469-486-57
Sequence 57, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Theogersen, Hans Christian
APPLICANT: Holtef, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:18:10 ; Search time 12.278 Seconds

(without alignments)
137.479 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 556
Sequence: I QIVLSQSPAILISASPEKVT.....COQSSNPPTFGCGTMLEIR 106Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCTI_NEM_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	106	US-09-893-615-89	Sequence 89, Appl
2	526	94.6	106	US-09-965-099-105	Sequence 105, App
3	526	94.6	106	US-10-051-852-105	Sequence 105, App
4	526	94.6	107	US-09-965-099-11	Sequence 11, Appl
5	526	94.6	107	US-10-051-852-11	Sequence 11, Appl
6	526	94.6	112	US-09-965-099-103	Sequence 103, App
7	526	94.6	112	US-10-051-852-103	Sequence 103, App
8	472	84.9	107	US-09-144-886-90	Sequence 90, Appl
9	464	83.5	109	US-09-144-886-91	Sequence 91, Appl
10	455	81.8	129	US-09-965-099-99	Sequence 99, Appl
11	455	81.8	129	US-10-051-852-99	Sequence 99, Appl
12	454	81.7	125	US-09-965-099-78	Sequence 78, Appl
13	454	81.7	125	US-10-051-852-78	Sequence 78, Appl
14	453	81.5	127	US-09-753-436-80	Sequence 80, Appl
15	451	81.1	107	US-09-965-099-62	Sequence 62, Appl
16	451	81.1	107	US-10-051-852-62	Sequence 62, Appl
17	449	80.8	107	US-09-144-886-82	Sequence 82, Appl
18	449	80.8	107	US-09-144-886-83	Sequence 83, Appl
19	448	80.6	106	US-09-976-787-24	Sequence 24, Appl

20	448	80.6	106	US-09-865-198-23	Sequence 23, Appl
21	448	80.6	108	US-09-976-787-8	Sequence 8, Appl
22	448	80.6	108	US-09-865-198-8	Sequence 8, Appl
23	448	80.6	238	US-09-976-787-29	Sequence 29, Appl
24	448	80.6	238	US-09-865-198-28	Sequence 28, Appl
25	448	80.6	240	US-09-976-787-28	Sequence 28, Appl
26	448	80.6	240	US-09-865-198-27	Sequence 27, Appl
27	447	80.4	105	US-09-982-107-12	Sequence 12, Appl
28	447	80.4	107	US-09-144-886-76	Sequence 76, Appl
29	447	80.4	107	US-09-965-099-57	Sequence 57, Appl
30	447	80.4	107	US-10-051-852-57	Sequence 57, Appl
31	446	80.2	109	US-09-965-099-95	Sequence 95, Appl
32	446	80.2	109	US-10-051-852-95	Sequence 95, Appl
33	445	80.0	235	US-09-910-059-17	Sequence 17, Appl
34	444	79.9	669	US-09-807-721-2	Sequence 2, Appl
35	443	79.7	108	US-09-910-059-9	Sequence 9, Appl
36	441	79.3	107	US-09-965-099-74	Sequence 74, Appl
37	441	79.3	107	US-10-051-852-74	Sequence 74, Appl
38	437	78.6	107	US-09-144-886-78	Sequence 78, Appl
39	437	78.6	119	US-09-808-037-28	Sequence 28, Appl
40	437	78.6	239	US-09-808-037-6	Sequence 6, Appl
41	434	78.1	107	US-09-144-886-88	Sequence 88, Appl
42	427	76.8	107	US-09-144-886-75	Sequence 75, Appl
43	422	75.9	109	US-09-144-886-97	Sequence 97, Appl
44	420	75.5	107	US-09-965-099-44	Sequence 44, Appl
45	420	75.5	107	US-10-051-852-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-893-615-89
; Sequence 89, Application US/09893615
; Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischeer, Gerald W.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSER: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-893-615-89

Query Match 100.0%; Score 556; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2,2e-33;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNMHYQOKPGSSPKPWISATSNLASGVPAR 60
DB 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNMHYQOKPGSSPKPWISATSNLASGVPAR 60
QY 61 FSSGSGTSTSLTISRVEADAAATYYCQWSSNPPTFGGTMLEIR 106
DB 61 FSSGSGTSTSLTISRVEADAAATYYCQWSSNPPTFGGTMLEIR 106

RESULT 2
US-09-965-099-105
Sequence 105, Application US/09965099
Patent No. US20020136725A1

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Giora

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/965,099

FILING DATE: 26-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/346,487

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Baumelster, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX: <Unknown>

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: linear

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-965-099-105

Query Match 94.6%; Score 526; DB 10; Length 106;
Best Local Similarity 95.3%; Pred. No. 2,8e-31;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNMHYQOKPGSSPKPWISATSNLASGVPAR 60

DB 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNMHYQOKPGSSPKPWISATSNLASGVPAR 60

QY 61 FSSGSGTSTSLTISRVEADAAATYYCQWSSNPPTFGGTMLEIR 106
DB 61 FSSGSGTSTSLTISRVEADAAATYYCQWSSNPPTFGGTMLEIR 106

RESULT 3
US-10-051-852-105

Sequence 105, Application US/10051852
Patent No. US20020146411A1

GENERAL INFORMATION:

APPLICANT: Blackburn, Michael

Church, William

Gross, Mitchell

Feuerstein, Giora

Nichols, Andrew

Padian, Eduardo

Patel, Arunbhai

Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,852

FILING DATE: 17-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/344,050

FILING DATE: 25-JUN-1999

APPLICATION NUMBER: 08/783,853

FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Baumelster, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX: <Unknown>

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: linear

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-051-852-105

Query Match 94.6%; Score 526; DB 12; Length 106;
Best Local Similarity 95.3%; Pred. No. 2,8e-31;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPALLSAPGKVTMTTCRASSSVNMHYQOKPGSSPKPWISATSNLASGVPAR 60

Db 1 QIVLSOSPAILISASPGKVTMTCRASSSVNMYMHYQOKPGSSPKPWITATSNLASGVPAR 60
QY 61 FSSGSGTSTSLTISRVEADATYYCOQWSSNPPTFGGTMLEIR 106
Db 61 FSSGSGTSTSLTISRVEADATYYCOQWSSNPPTFGGTMLEIR 106

RESULT 4
US-09-965-099-11
Sequence 11, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Giora
Patel, Arunbhai

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>

Prior APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-965-099-11
Query Match
Best Local Similarity 94.6%; Score 526; DB 10; Length 107;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPAILISASPGKVTMTCRASSSVNMYMHYQOKPGSSPKPWITATSNLASGVPAR 60
Db 1 QIVLSOSPAILISASPGKVTMTCRASSSVNMYMHYQOKPGSSPKPWITATSNLASGVPAR 60
QY 61 FSSGSGTSTSLTISRVEADATYYCOQWSSNPPTFGGTMLEIR 106
Db 61 FSSGSGTSTSLTISRVEADATYYCOQWSSNPPTFGGTMLEIR 106

RESULT 5

US-10-051-852-11
Sequence 11, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>

Prior APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-051-852-11
Query Match
Best Local Similarity 94.6%; Score 526; DB 12; Length 107;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QIVLSOSPAILISASPGKVTMTCRASSSVNMYMHYQOKPGSSPKPWITATSNLASGVPAR 60
Db 1 QIVLSOSPAILISASPGKVTMTCRASSSVNMYMHYQOKPGSSPKPWITATSNLASGVPAR 60
QY 61 FSSGSGTSTSLTISRVEADATYYCOQWSSNPPTFGGTMLEIR 106
Db 61 FSSGSGTSTSLTISRVEADATYYCOQWSSNPPTFGGTMLEIR 106

RESULT 6
US-09-965-099-103

Sequence 103, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Giora
Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS,
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-965-099-103

Query Match 94.6%, Score 526, DB 10, Length 112;
Best Local Similarity 95.3%, Pred. No. 3e-31;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 1 QIVLSQSPAILISASPGKVTMTCRASSSVNWMYQOKPGSSPKPWISATSLASGVAR 60
DB 1 QIVLSQSPAILISASPGKVTMTCRASSSVNWMYQOKPGSSPKPWIVATSLNLSAGVAP 60
OY 61 FSGSGSGTSTSLTISRVEAEDATYYCCQWSSNPPTFGGTMLEIR 106
DB 61 FSGSGSGTSTSLTISRVEAEDATYYCCQWSSNPPTFGGTMLEIR 106
RESULT 7
US-10-051-852-103
Sequence 103, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew

Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-051-852-103

Query Match 94.6%, Score 526, DB 12, Length 112;
Best Local Similarity 95.3%, Pred. No. 3e-31;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 1 QIVLSQSPAILISASPGKVTMTCRASSSVNWMYQOKPGSSPKPWISATSLASGVAR 60
DB 1 QIVLSQSPAILISASPGKVTMTCRASSSVNWMYQOKPGSSPKPWIVATSLNLSAGVAP 60
OY 61 FSGSGSGTSTSLTISRVEAEDATYYCCQWSSNPPTFGGTMLEIR 106
DB 61 FSGSGSGTSTSLTISRVEAEDATYYCCQWSSNPPTFGGTMLEIR 106
RESULT 8
US-09-144-886-90
Sequence 90, Application US/09144886
Patent No. US2002015514A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886

;; CURRENT FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 98
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 90
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-90

Query Match 84.9%; Score 472; DB 9; Length 107;
Best Local Similarity 86.4%; Pred. No. 1.8e-27;
Matches 89; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 4 LSQSALISASPEKVTMTCRASSSVNHYQOKPGSSPKWISATSNLASGVPA 63
DB 4 LTQSPALMSASPEKVTMTCRASSSVSYWYQOKPGSSPRIMTYDTSNLASGVPA 63

OY 64 SSGSGSYSLTISRVAEDATYCCQWSSNPPTFGGCTMLEIR 106
DB 64 SSGSGSYSLTISRVAEDATYCCQWSSNPPTFGGCTMLEIR 106

RESULT 9
US-09-144-886-91
;; Sequence 91, Application US/09144886
;; Patent No. US2002015114A1
;; GENERAL INFORMATION:
;; APPLICANT: Marks, James D
;; APPLICANT: Amersdorfer, Peter
;; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
;; TITLE OF INVENTION: Botulinum Neurotoxins
;; FILE REFERENCE: 2500.117USO
;; CURRENT APPLICATION NUMBER: US/09/144.886
;; CURRENT FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 98
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 91
;; LENGTH: 109
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
;; OTHER INFORMATION: 3H4 region VL epitope 2
US-09-144-886-91

Query Match 83.5%; Score 464; DB 9; Length 109;
Best Local Similarity 84.1%; Pred. No. 6.7e-27;
Matches 90; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

OY 2 IVLQSPALISASPEKVTMTCRASSSV--NYMHYQOKPGSSPKWISATSNLASGVPA 59
DB 2 IELTQSPALMSASPEKVTMTCRASSSVSYLVQWYQOKPGSSPRIMTYDTSNLASGVPA 61

OY 60 RFGSGSGSYSLTISRVAEDATYCCQWSSNPPTFGGCTMLEIR 106
DB 62 RFGSGSGSYSLTISRVAEDATYCCQWSSNPPTFGGCTMLEIR 106

RESULT 10
US-09-965-099-99
;; Sequence 99, Application US/09965099
;; Patent No. US20020136725A1
;; GENERAL INFORMATION:
;; APPLICANT: Blackburn, Michael
;; APPLICANT: Feuerstein, Gloria
;; APPLICANT: Patel, Arunbhai
;; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
;; TREATMENT OF THROMBOSIS
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: SmithKline Beecham Corporation
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/965,099
;; FILING DATE: 26-Sep-2001
;; CLASSIFICATION: <unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/346,487
;; FILING DATE: <unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baumeister, Kirk
;; REGISTRATION NUMBER: 33,833
;; REFERENCE/DOCKET NUMBER: P50438-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5096
;; TELEFAX: <unknown>
;; TELEX: <unknown>
;; INFORMATION FOR SEQ ID NO: 99:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 129 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: Internal
;; ORIGINAL SOURCE:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-09-965-099-99

Query Match 81.8%; Score 455; DB 10; Length 129;
Best Local Similarity 79.2%; Pred. No. 3.3e-26;
Matches 84; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 1 QIVLSQPAIISASPEKVTMTCRASSSVNHYQOKPGSSPKWISATSNLASGVPA 60
DB 20 QIVLQSPALMSASPEKVTMTCRASSSVNHYQOKPGKAPKPVITATSNLASGVPA 79

OY 61 FSGSGSGSYSLTISRVAEDATYCCQWSSNPPTFGGCTMLEIR 106
DB 80 FSGSGSGSYSLTISRVAEDATYCCQWSSNPPTFGGCTMLEIR 125

RESULT 11
US-10-051-852-99
;; Sequence 99, Application US/10051852
;; Patent No. US2002014641A1
;; GENERAL INFORMATION:
;; APPLICANT: Blackburn, Michael
;; APPLICANT: Church, William
;; APPLICANT: Gross, Mitchell
;; APPLICANT: Feuerstein, Gloria
;; APPLICANT: Nichols, Andrew
;; APPLICANT: Padlan, Eduardo
;; APPLICANT: Patel, Arunbhai
;; APPLICANT: Sylvester, Daniel
;; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
;; OF THROMBOSIS
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia

```

1 STATE: PA
2 COUNTRY: USA
3 ZIP: 19406
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Diskette
7 COMPUTER: IBM Compatible
8 OPERATING SYSTEM: DOS
9 SOFTWARE: FASTSEQ Version 1.5
10
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/10/051.852
13 FILING DATE: 17-Jan-2002
14 CLASSIFICATION: <unknown>
15
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 09/344,050
18 FILING DATE: 25-JUN-1999
19 APPLICATION NUMBER: 08/783,853
20 FILING DATE: 16-JAN-1997
21
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Baumelster, Kirk
24 REGISTRATION NUMBER: 33,833
25 REFERENCE/DOCKET NUMBER: P50438
26
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 610-270-5096
29 TELEFAX: <unknown>
30
31 INFORMATION FOR SEQ ID NO: 99:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 129 amino acids
34 TYPE: amino acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38
39 HYPOTHETICAL: NO
40
41 ANTI-SENSE: NO
42
43 FRAGMENT TYPE: Internal
44
45 ORIGINAL SOURCE:
46 SEQUENCE DESCRIPTION: SEQ ID NO: 99:
47
48 US-10-051-852-99
49
50 Query Match 81.8%, Score 455, DB 12, Length 129;
51 Best Local Similarity 79.2%, Pred. No. 3,3e-26;
52 Matches 84: Conservative 11; Mismatches 11; Indels 0; Gaps 0;
53
54 QY 1 QIVLSOSPALISASGEVYMTICRASSSVNYWHYQOKPGSSPKPMISATSLASGVPAR 60
55 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
56 Db 20 QIVLTQSSSLASASGDRVITTCRASSSVNYWHYQOKPGKAPKPMIYATSLASGVPSR 79
57 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
58 QY 61 FSGSGSGTYSLTISRVEAEDATYYCQOWSSNPTFGGTMLEIR 106
59 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 Db 80 FSGSGSGTDTLTITISLOPEDEPATYYCQOWSINPTFGGTMLEIK 125
61
62 RESULT 12
63 US-09-965-099-78
64 Sequence 78, Application US/09965099
65 Patent No. US20020136725A1
66
67 GENERAL INFORMATION:
68 APPLICANT: Blackburn, Michael
69 Feuerstein, Gloria
70 Patel, Arunbhai
71
72 TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
73 TREATMENT OF THROMBOSIS
74
75 NUMBER OF SEQUENCES: 111
76 CORRESPONDENCE ADDRESS:
77 ADDRESSEE: SmithKline Beecham Corporation
78 STREET: 709 Swedeland Road
79 CITY: King of Prussia
80 STATE: PA
81 COUNTRY: USA
82 ZIP: 19406
83
84 COMPUTER READABLE FORM:
85 MEDIUM TYPE: Diskette
86 COMPUTER: IBM Compatible
87

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: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ VERSION 1.5
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/965, 099
: FILING DATE: 26-Sep-2001
: CLASSIFICATION: <unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/346,487
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumelster, Kirk
: REGISTRATION NUMBER: 33,833
: REFERENCE/DOCKET NUMBER: P50438-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5096
: TELEFAX: <unknown>
:
: INFORMATION FOR SEQ ID NO: 78:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE:
: SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-965-099-78
:
: Query Match 81.7%; Score 454; DB 10; Length 125;
: Best Local Similarity 78.3%; Pred. NO.3.8e-26;
: Matches 83; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
:
: Oy 1 QIVLSQSPAILASPGKEVYMTCRASSSVNYMHVYQOKFGSSPKPMISATSNLASCVPAR 60
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
: Db 20 QIVLQSPATILSLSGERATLSGRASSVNYMHVYQORGCAPKPMIVATSNLASCVPAR 79
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
: Oy 61 FSGSGSGTYSILTISRVAEDATATYYCOOWSSNPRTFGGTYMLEIR 106
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
: Db 80 FSGSGSGTYDYLITSLPEDEFAVYYCOOWSNPRTFGGTYMLEIR 125
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:
: RESULT 13
: US-10-051-852-78
: Sequence 78, Application US/10051852
: Patent No. US2002014641A1
: GENERAL INFORMATION:
: APPLICANT: Blackburn, Michael
: Church, William
: Gross, Mitchell
: Feuerstein, Gloria
: Nichols, Andrew
: Padlan, Eduardo
: Patel, Arunbhai
: Sylvester, Daniel
: TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
: OF THROMBOSIS
: NUMBER OF SEQUENCES: 111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ VERSION 1.5
: CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-10-051-852-78

Query Match 81.7%; Score 454; DB 12; Length 125;
Best Local Similarity 78.3%; Pred. No. 3,8e-26;
Matches 83; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Oy 1 QIVLSQSPAILASPGKVTMTCRASSSVNWMYQOKPGSSPKPMISATNSLASGVAP 60
Db 20 QIVLSQSPAILASPGKVTMTCRASSSVNWMYQOKPGSSPKPMISATNSLASGVAP 79
Oy 61 FSGSGSGTSTLTISRVEADATYCCOOWSSNPFTFGGTMLEIR 106
Db 80 FSGSGSGTSTLTISRVEADATYCCOOWSSNPFTFGGTMLEIR 125

RESULT 14
US-09-753-436-80
Sequence 80, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-09-753-436-80

Query Match 81.5%; Score 453; DB 10; Length 127;
Best Local Similarity 81.1%; Pred. No. 4,6e-26;
Matches 86; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 1 QIVLSQSPAILASPGKVTMTCRASSSVNWMYQOKPGSSPKPMISATNSLASGVAP 60
Db 22 QIVLSQSPAILASPGKVTMTCRASSSVNWMYQOKPRSSPKPMIYLTSMLASGVAP 81
Oy 61 FSGSGSGTSTLTISRVEADATYCCOOWSSNPFTFGGTMLEIR 106
Db 82 FSGSGSGTSTLTISRVEADATYCCOOWSSNPFTFGGTMLEIR 127

RESULT 15
US-09-965-099-62
Sequence 62, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Gloria
Patel, Arunbhal
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-965-099-62

Query Match      81.1%  Score 451:  DB 10:  Length 107:
Best Local Similarity 77.4%  Pred. No. 5.5e-26:
Matches 82:  Conservative 11;  Mismatches 13;  Indels 0;  Gaps 0;

QY  1 QIVLSQSPAILLSAPGKVTMTGRASSVYMHMYOQKPGSSPKPMISATSNLAGVPAR 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 EIVLTQSPATLSLSPGERATLSCRASSVYMHMYOQRPQAPKPMIYATSNLAGVPAR 60

QY  61 FSGSGGTSTSLTISRVEADATYYCQOQSSNPTEGGTMEIR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 FSGSGGTDTLTITSLPEDFAVYCCQQWSINPTEGGTKVEIK 106
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Search completed: November 27, 2002, 07:26:00
Job time : 12.278 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:46:58 ; Search time 36.5677 Seconds
(without alignments)
3349.042 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318
Sequence: 1 CAATGTCCTCTCCAGTC.....GGACCATGCTGAATAAGA 318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PC1_NEM_PUB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	10	US-09-893-615-88 Sequence 88, Appl
2	300.4	94.5	321	10	US-09-965-099-6 Sequence 6, Appl
3	300.4	94.5	321	12	US-10-051-852-6 Sequence 6, Appl
4	293.6	93.0	318	10	US-09-965-099-104 Sequence 104, App
5	293.6	93.0	318	12	US-10-051-852-104 Sequence 104, App
6	293.6	93.0	335	12	US-09-965-099-102 Sequence 102, App
7	293.6	93.0	335	12	US-10-051-852-102 Sequence 102, App
8	266.4	84.4	390	10	US-09-753-436-79 Sequence 79, Appl
9	266.2	83.1	357	10	US-09-808-037-27 Sequence 27, Appl
10	266.2	83.1	717	10	US-09-808-037-5 Sequence 5, Appl
11	261	82.1	318	10	US-09-976-787-77 Sequence 26, Appl
12	261	82.1	318	10	US-09-865-198-26 Sequence 26, Appl
13	261	82.1	324	10	US-09-976-787-16 Sequence 16, Appl
14	261	82.1	324	10	US-09-865-198-16 Sequence 16, Appl
15	261	82.1	714	10	US-09-976-787-31 Sequence 31, Appl
16	261	82.1	720	10	US-09-976-787-30 Sequence 30, Appl
17	259.6	81.6	322	9	US-09-982-107-11 Sequence 11, Appl
18	257.8	81.1	357	10	US-09-910-059-8 Sequence 8, Appl
19	257.8	81.1	705	10	US-09-910-059-16 Sequence 16, Appl

20	251.4	79.1	717	8	US-08-940-544-3	Sequence 3, Appl
21	251.4	79.1	2059	9 <td>US-09-807-721-1<th>Sequence 1, Appl</th></td>	US-09-807-721-1 <th>Sequence 1, Appl</th>	Sequence 1, Appl
22	248.2	78.1	411	10 <td>US-09-881-823-5<th>Sequence 5, Appl</th></td>	US-09-881-823-5 <th>Sequence 5, Appl</th>	Sequence 5, Appl
23	241.8	76.0	5691	10 <td>US-09-897-006-11<th>Sequence 11, Appl</th></td>	US-09-897-006-11 <th>Sequence 11, Appl</th>	Sequence 11, Appl
24	198.6	62.5	321	10 <td>US-09-965-099-56<th>Sequence 56, Appl</th></td>	US-09-965-099-56 <th>Sequence 56, Appl</th>	Sequence 56, Appl
25	198.6	62.5	321	12 <td>US-10-051-852-56<th>Sequence 56, Appl</th></td>	US-10-051-852-56 <th>Sequence 56, Appl</th>	Sequence 56, Appl
26	198	62.3	412	10 <td>US-09-965-099-98<th>Sequence 98, Appl</th></td>	US-09-965-099-98 <th>Sequence 98, Appl</th>	Sequence 98, Appl
27	198	62.3	412	12 <td>US-10-051-852-98<th>Sequence 98, Appl</th></td>	US-10-051-852-98 <th>Sequence 98, Appl</th>	Sequence 98, Appl
28	197.8	62.2	357	10 <td>US-09-753-436-95<th>Sequence 95, Appl</th></td>	US-09-753-436-95 <th>Sequence 95, Appl</th>	Sequence 95, Appl
29	195.4	61.4	321	10 <td>US-09-965-099-61<th>Sequence 61, Appl</th></td>	US-09-965-099-61 <th>Sequence 61, Appl</th>	Sequence 61, Appl
30	195.4	61.4	321	12 <td>US-10-051-852-61<th>Sequence 61, Appl</th></td>	US-10-051-852-61 <th>Sequence 61, Appl</th>	Sequence 61, Appl
31	195.2	61.4	330	10 <td>US-09-965-099-94<th>Sequence 94, Appl</th></td>	US-09-965-099-94 <th>Sequence 94, Appl</th>	Sequence 94, Appl
32	195.2	61.4	330	12 <td>US-10-051-852-94<th>Sequence 94, Appl</th></td>	US-10-051-852-94 <th>Sequence 94, Appl</th>	Sequence 94, Appl
33	194.8	61.3	401	10 <td>US-09-965-099-77<th>Sequence 77, Appl</th></td>	US-09-965-099-77 <th>Sequence 77, Appl</th>	Sequence 77, Appl
34	194.8	61.3	401	12 <td>US-10-051-852-77<th>Sequence 77, Appl</th></td>	US-10-051-852-77 <th>Sequence 77, Appl</th>	Sequence 77, Appl
35	193.8	60.9	321	10 <td>US-09-965-099-43<th>Sequence 43, Appl</th></td>	US-09-965-099-43 <th>Sequence 43, Appl</th>	Sequence 43, Appl
36	193.8	60.9	321	12 <td>US-10-051-852-43<th>Sequence 43, Appl</th></td>	US-10-051-852-43 <th>Sequence 43, Appl</th>	Sequence 43, Appl
37	169.8	53.4	280	10 <td>US-09-965-099-34<th>Sequence 34, Appl</th></td>	US-09-965-099-34 <th>Sequence 34, Appl</th>	Sequence 34, Appl
38	169.8	53.4	280	12 <td>US-10-051-852-34<th>Sequence 34, Appl</th></td>	US-10-051-852-34 <th>Sequence 34, Appl</th>	Sequence 34, Appl
39	166	52.2	321	10 <td>US-09-965-099-73<th>Sequence 73, Appl</th></td>	US-09-965-099-73 <th>Sequence 73, Appl</th>	Sequence 73, Appl
40	166	52.2	321	12 <td>US-10-051-852-73<th>Sequence 73, Appl</th></td>	US-10-051-852-73 <th>Sequence 73, Appl</th>	Sequence 73, Appl
41	156.4	49.2	321	10 <td>US-09-910-059-64<th>Sequence 64, Appl</th></td>	US-09-910-059-64 <th>Sequence 64, Appl</th>	Sequence 64, Appl
42	156.4	49.2	705	10 <td>US-09-910-059-96<th>Sequence 96, Appl</th></td>	US-09-910-059-96 <th>Sequence 96, Appl</th>	Sequence 96, Appl
43	154.6	48.6	321	10 <td>US-09-910-059-70<th>Sequence 70, Appl</th></td>	US-09-910-059-70 <th>Sequence 70, Appl</th>	Sequence 70, Appl
44	154.6	48.6	705	10 <td>US-09-910-059-98<th>Sequence 98, Appl</th></td>	US-09-910-059-98 <th>Sequence 98, Appl</th>	Sequence 98, Appl
45	152.2	47.9	321	10 <td>US-09-910-059-60<th>Sequence 60, Appl</th></td>	US-09-910-059-60 <th>Sequence 60, Appl</th>	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-893-615-88
Sequence 88, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Mong, Hing
Schinson, Jeffrey L.
Schuman, Richard F.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESS: FINNEGAN, HENDERSON, FARABOW, GARRETT &
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudt, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995, 0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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?      MOLECULE TYPE: CDNA
?
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 1..318
?      SEQUENCE DESCRIPTION: SEQ ID NO: 88
US-09-893-615-88

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Query Match	100.0%	Score 318	DB 10	Length 318
Best Local Similarity	100.0%	Pred. No. 1.7e-88		
Matches 318	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	CAAAATGTTCTCTCCCACTCTCCAGCAATCCGTGTGATCTCCAGGGGAAAGGTGCACA	60
Db	1	CAAATGTGTCTCTCCCACTCTCCAGCAATCCGTGTGATCTCCAGGGGAAAGGTGCACA	60
QY	61	ATGACTTTCAGAGGGCAGCTCAAGTGTAAATTACATGCACTGGTACCAGACAGACGACAGA	12
Db	61	ATGACTTTCAGAGGGCAGCTCAAGTGTAAATTACATGCACTGGTACCAGACAGACGACAGA	12
QY	121	TCCTCCCCCAAAACCCGTGATTCTTCTCCATCCATCCACAGCTGGCTTGAGAGTCCCTCTGGC	18
Db	121	TCCTCCCCCAAAACCCGTGATTCTTCTCCATCCATCCACAGCTGGCTTGAGAGTCCCTCTGGC	18
QY	181	TTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAAATCAGCAGAGTGGAGGCTGAA	24
Db	181	TTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAAATCAGCAGAGTGGAGGCTGAA	24
QY	241	GATGCTGGCAGTATTACTTGCAGCAGAGTAGTAACCCACCCACAGCTTCGGAGGGGG	30
Db	241	GATGCTGGCAGTATTACTTGCAGCAGAGTAGTAACCCACCCACAGCTTCGGAGGGGG	30
QY	301	ACCATGCTGGAAATTAAGA 318	
Db	301	ACCATGCTGGAAATTAAGA 318	

RESULT 2
US-09-965-099-6

Sequence 6, Application US/0999650999
Patent No. US20020136725A1

;; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael

Feuerstein, Giora
Patel, Arunbhai

NUMBER OF SEQUENCES: 111

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation

ADDRESS: SMITHKLINE BEECHAM CORPORATION
STREET: 709 Swedeland Road
CITY: King of Prussia

CITY: KING OF PRUSSIA
STATE: PA
COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

```

;
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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```

;
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/965,095

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; FILING DATE: 26-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ;

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487

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; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;

```

NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
REFERENCE: 610 370 5005

TELEPHONE: 610-270-
TELEFAX: <Unknown>

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;
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 6:
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 321 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;
;

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; ; MOLECULE TYPE: CDNA
; ; HYPOTHETICAL: NO
; ; ANTI-SENSE: NO
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[illegible]

Db 241 GATGCTGCCACTTATTACTGCC

QY 301 ACCATGCTGGAATAAGA 318

Db 301 ACCAAGCTGAATCAA 318

Journal of
Business Ethics

RESOLUT 3
US-10-051-852-6
Source 6 Resolution INC/10051852

GENERAL INFORMATION:
; sequence 0, Application US/10051852
; Patent No. US20020146411A1

GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church: William

Gross, Mitchell
Feuerstein, Gloria

Nichols, Andrew
Padlan, Eduardo

Patel, Arunbhai
Sylvester, Daniel

TITLE OF INVENTION: ANTICOAG
OF THROM

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline B
STREET: 709 Swedeland R

```

; CITY: King of Prussia
; STATE: PA
;
```

```
COUNTRY: USA  
ZIP: 19406
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```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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;
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS

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; SOFTWARE: FASTSEQ Version 1.0
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-051-852-6

Query Match 94.5%; Score 300.4; DB 12; Length 321;
Best Local Similarity 96.5%; Pred. No. 4.3e-83;
Matches 307; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGATCTTCAGGGGAAAAGTCCACA 60
DB 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGATCTTCAGGGGAAAAGTCCACA 60
QY 61 ATGACTTGGAGGGCCAGCTCAAGTGAATTAATGACACTGGTACCAGCAAGAACCCAGGA 120
DB 61 ATGACTTGGAGGGCCAGCTCAAGTGAATTAATGACACTGGTACCAGCAAGAACCCAGGA 120
QY 121 TCCCTCCCAAAACCTGATTTCTGCCACATCCAACTGGGCTTCTGGAGTCCCTGCTCGC 180
DB 121 TCCCTCCCAAAACCTGATTTCTGCCACATCCAACTGGGCTTCTGGAGTCCCTGCTCGC 180
QY 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
DB 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
QY 241 GATGCTGCCACTTATTACGCCAGCAGTGGAGTAGTAACCCAGCCGCTTCGGAGGGGG 300
DB 241 GATGCTGCCACTTATTACGCCAGCAGTGGAGTAGTAACCCAGCCGCTTCGGAGGGGG 300
QY 301 ACCATGCTGGAATTAAGA 318
DB 301 ACCATGCTGGAATTAAGA 318

RESULT 4
US-09-965-099-104
Sequence 104, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Gloria
Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESS: Smitthkline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..318
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-965-099-104

Query Match 93.0%; Score 295.6; DB 10; Length 318;
Best Local Similarity 95.6%; Pred. No. 1.3e-81;
Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGATCTTCAGGGGAAAAGTCCACA 60
DB 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGATCTTCAGGGGAAAAGTCCACA 60
QY 61 ATGACTTGGAGGGCCAGCTCAAGTGAATTAATGACACTGGTACCAGCAAGAACCCAGGA 120
DB 61 ATGACTTGGAGGGCCAGCTCAAGTGAATTAATGACACTGGTACCAGCAAGAACCCAGGA 120
QY 121 TCCCTCCCAAAACCTGATTTCTGCCACATCCAACTGGGCTTCTGGAGTCCCTGCTCGC 180
DB 121 TCCCTCCCAAAACCTGATTTCTGCCACATCCAACTGGGCTTCTGGAGTCCCTGCTCGC 180
QY 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
DB 181 TTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
QY 241 GATGCTGCCACTTATTACGCCAGCAGTGGAGTAGTAACCCAGCCGCTTCGGAGGGGG 300
DB 241 GATGCTGCCACTTATTACGCCAGCAGTGGAGTAGTAACCCAGCCGCTTCGGAGGGGG 300
QY 301 ACCATGCTGGAATTAAGA 318
DB 301 ACCATGCTGGAATTAAGA 318

RESULT 5
US-10-051-852-104

Query Match	93.0%;	Score 295.6;	DB 10;	Length 335;
Best Local Similarity	95.6%;	Pred. NO. 1.3e-81;		
Matches 304;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;

QY	1	C A T T T G T T C T C C C A G T C C A G C A A A T C C T G T C T C A T T C C A G G G G A A A A G T C A C A	60
Db	1	C A G A T A G T A C T C T C C C A G T C C C A G C A A T C C T G T C T C A T T C C A G S G G A A A A G T C A C A	60
QY	61	A T G A C T T G C A G S G C C A G C T C A A G T A T G A A T T A C A T G C A C T G T T A C C A G C A A A G C C A G A	120
Db	61	A T G A C T T G C A G S G G C A G C T C A A G T A T G A A T T A C A T G C A C T G T T A C C A G C A A A G C C A G A	120
QY	121	T C C A C C C C C A A A C C C T G G A T T T T G C C A C A T C C A A C C T G G C T T T G G A G A C C C T G C T C G C	180
Db	121	T C C T C C C C C A A A C C C T G G A T T T A T G C C A C A T C C A A C C T G G C T T T G S A G T C C T G C T C G C	180
QY	181	T T C A G T G G C A C T G G G T C T G G A C C T T T A C T C T C T C A C A A T C A G C A G A G T G A A G G C T G A A	240
Db	181	T T C A G T G G C A C T G G G T C T G G A C C T T T A C T C T C T C A C A A T C A G C A A G A G T G A A G G C T G A A	240
QY	241	G A T C C T G G C A C T T T A T T A C T G C A C A G T G G A G T A A C C A C C A G C A T T C G G A G S G G G G	300
Db	241	G A T C C T G G C A C T T T A T T A C T G C A C A G T G G A G T A A C C A C C A G C A T T C G G A G S G G G G	300
QY	301	A C C A T G C T G A A A T P A G A 318	
Db	301	A C C A A G C T G G A A A T C A A A 318	

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RESULT 7
US-10-051-852-102
; Sequence 102, Application US/10051852
; Patent No. US20020146411A1
; GENERAL INFORMATION:

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?      APPLICANT: Blackburn, Michael
?      Church, William
?      Gross, Mitchell
?      Feuerstein, Gloria
?      Nichols, Andrew
?      Padman, Eduardo
?      Patel, Arunbhai
?      Sylvester, Daniel
?      TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
?      OF THROMBOSIS
?      NUMBER OF SEQUENCES: 111

```

?
?
? CORRESPONDENCE ADDRESS:
? ADDRESS: Smithkline Beecham Corporation
?
? STREET: 709 Swedeland Road
?
? CITY: King of Prussia
?
? STATE: PA
?
? COUNTRY: USA
?
? ZIP: 19406
?

```

1  COMPUTER READABLE FORM:
2
3  MEDIUM TYPE: diskette
4
5  COMPUTER: IBM compatible
6
7  OPERATING SYSTEM: DOS
8
9  SOFTWARE: PASTESQ Version 1.5
10
11 CURRENT APPLICATION DATA:
12
13 APPLICATION NUMBER: US/10/051,852
14
15 FILING DATE: 17-Jan-2002
16
17 CLASSIFICATION: <Unknown>

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 09/344,050
3 FILING DATE: 25-JUN-1999
4 APPLICATION NUMBER: 08/783,853
5 FILING DATE: 16-JAN-1997
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Baunmeister, Kirk
8 REGISTRATION NUMBER: 33,833
9 REFERENCE/DOCKET NUMBER: P50438
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: 610-270-5096
12 TELEFAX: <unknown>

```

1      TELEX: <UNKNOWN>
2      INFORMATION FOR SEQ ID NO: 102:
3      SEQUENCE CHARACTERISTICS:
4          LENGTH: 335 base pairs
5          TYPE: nucleic acid
6          STRANDEDNESS: single
7          TOPOLOGY: linear
8      MOLECULE TYPE: cDNA
9      HYPOTHETICAL: NO
10     ANTI-SENSE: NO
11     FRAGMENT TYPE: <UNKNOWN>
12     ORIGINAL SOURCE:
13     FEATURE:
14         NAME/KEY: Coding Sequence
15         LOCATION: 1..335
16     OTHER INFORMATION:
17     SEQUENCE DESCRIPTION: SEQ ID NO: 102
18
19     US-10-051-852-102

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Query Match	93.0%	Score 295.6	DB 12	Length 335
Best Local Similarity	95.6%	Pred. No. 1.3e-81		
Matches 304	Conservative	0	Mismatches 14	Indels 0
				Gaps 0

OY	1	C A A N T G T T C T C C C A G T C C C A G C A A N T C C T G C T C A T C C A G G C A A A G G T C A C A	60
Db	1	C A G A T A G T A C T C C C A C A T C C A G C A N A T C C T G T C T C A T C C A G G G A A A G G T C A C A	60
OY	61	A T G A C T T T C A G A G G C C A G C T C A A G T A A T T A C A T G C A C T G T A C C A G C A A A C C A G A	120
Db	61	A T G A C T T T C A G A G G C C A G C T C A A G T A A T T A C A T G C A C T G T A C C A G C A A A C C A G A	120
OY	121	T C C T C C C C C A A A C C C T G A A T T T C G C A C A T C C A A C C T G G C T T C T G A G T C C C T G C T C G C	180
Db	121	T C C T C C C C C A A A C C C T G A A T T T A T T A T T A T C C A T C C A A C C T G G C T T C T G A G T C C C T G C T C G C	180
OY	181	T T C A G T G C A G T G G G T C T G G A C C T T A C T C T C A C A A T C A G C A G A G T G A A G G C T G A A	240
Db	181	T T C A G T G C A G T G G G T C T G G A C C T T A C T C T C A C A A T C A G C A G A G T G A A G G C T G A A	240
OY	241	G A T G T G C C A C T T A T T A T C G C A C A G A G A G T A A C C A C C A C C G T T C G G A G G G G G	300
Db	241	G A T G T G C C A C T T A T T A T C G C A C A G A G A G T A A C C A C C A C C G T T C G G T G A A G G C	300
OY	301	A C C A T G C T G A A A T P A G A	318
Db	301	A C C A A G C T G A A A T C A A A	318

RESULT 8
US-09-753-436-79
; Sequence 79, Application US/09753436
; Patent No. US20010029293A1
; GENERAL INFORMATION:

1 APPLICANT: Gallatin, W. Michael
2
3 APPLICANT: Vazeux, Rosemary
4 TITLE OF INVENTION: ICAM-Related Materials and Methods
5
6 NUMBER OF SEQUENCES: 120
7
8 CORRESPONDENCE ADDRESS:
9
10 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
11
12 STREET: 6300 Sears Tower, 233 South Wacker Drive
13

? CITY: Chicago
 ? STATE: Illinois
 ? COUNTRY: United States of America
 ? ZIP: 60606-6402
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/753,436
 ? FILING DATE:
 ? CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/382,289
; FILING DATE:
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Joseph A., Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 33282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-753-436-79

Query Match      84.4%; Score 268.4; DB 10; Length 390;
Best Local Similarity 90.3%; Pred. No. 3.1e-73;
Matches 287; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGGTACA 60
DB 73 CAATTGTTCTCAACCGAGTCTCCAGCACTATGTCGATCTCCAGGGGAAAGGTACC 132
QY 61 ATGACTTGCAGGGCGAGCTCAAGTGTAAATTACATGCACTGGTACCAAGCAAGCCAGGA 120
DB 133 ATGACCTGCAGTGCAGCTCAAGTGTAAATTACATTTATTGTGTAACCAAGCAAGCCAGGA 192
QY 121 TCCGCCCCCAACCGCTGATTTCTGCCACATCCAACTGGCTTCTGGAGTCCCGCTCGCG 180
DB 193 TCCGCCCCCAACCGCTGATTTCTGCATCTCAATCCAACTGGCTTCTGGAGTCCCGCTCGCG 252
QY 181 TTCAGTGCAGTGGGTCTGGAGACTTCTACTCTCTCAATTCAGCAGAGTGGAGGCTGAA 240
DB 253 TTCAGTGCAGTGGGTCTGGAGGCTCTTACTCTCTCAATTCAGCAGATGAGAGGCTGAA 312
QY 241 GATGCTCCCACTTATTAATCTCCAGCACTGAGTGTAAACCAACCACTTCCAGGGGGG 300
DB 313 GATGCTCCCACTTATTAATCTCCAGCACTGAGTGTAAACCACTTCCAGGTTCCGTTGGG 372
QY 301 ACCATGCTGGAATTAAGA 318
DB 373 ACCAAGCTGGAAGCTGAAGA 390

RESULT 9
US-09-808-037-27
; Sequence 27, Application US/09808037
; Patent No. US20020052311A1
```

```

; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Bekka
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 357
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(357)
; US-09-808-037-27

Query Match      83.1%; Score 264.2; DB 10; Length 357;
Best Local Similarity 89.6%; Pred. No. 5.8e-72;
Matches 284; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2 AAATTGTTCTCTCCAGTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGGTACAA 61
DB 41 ACATCGAGCTCACTCACTCTCCAGCAATCTGTGTCATCTCCAGGGGAAAGGTACCA 100
QY 62 TGAATTGAGGCGAGCTCAAGTGTAAATTACATGCACTGTAACCAAGCAAGCAGAT 121
DB 101 TGACTGCACTGAGCTCAAGTGTAAATTACATGCACTGTAACCAAGCAGAT 160
QY 122 CTTCCGCCCAACCGCTGATTTCTGCCACATCCAACTGGCTTCTGGAGTCCCGCTCGCT 181
DB 161 CTTCCGCCCAACCGCTGATTTCTGCCACATCCAACTGGCTTCTGGAGTCCCGCTCGCT 220
QY 182 TCAAGTGCAGTGGGTCTGGAGACTTCTACTCTCTCAATTCAGCAGAGTGGAGGCTGAG 241
DB 221 TCAAGTGCAGTGGGTCTGGAGACTTCTACTCTCTCAATTCAGCAGAGTGGAGGCTGAG 280
QY 242 ATGCTGCACCTTATTAATCTCCAGCACTGAGTGTAAACCAACCACTTCCAGGGGGGA 301
DB 281 ATGCTGCACCTTATTAATCTCCAGCACTGAGTGTAAACCAACCACTTCCAGGGGGGG 340
QY 302 CCATGCTGGAATTAAGA 318
DB 341 CCAAGCTGGAATTAAGA 357

RESULT 10
US-09-808-037-5
; Sequence 5, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Bekka
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
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SOFTWARE: Patentin version 3.0

SEQ ID NO 5
LENGTH: 717
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(717)
US-09-808-037-5

Query Match 83.1%; Score 264.2; DB 10; Length 717;
Best Local Similarity 89.6%; Pred. No. 7.4e-72;
Matches 284; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2 AAATTGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTACAA 61
DB 401 ACATGAGCTCACTCACTCCTCAGCAATCATGTCTGCAATCTCCAGGGGGAAGTACCA 460
QY 62 TGACTTGAGGGGCGAGCTCAAGTGAATTAATACATGACAGTGTACAGAGCCAGGAT 121
DB 461 TGACTTGAGAGTCCAGCTCACTCAATTAATGATGATGATGATGATGATGATGATGAT 520
QY 122 CCTCCCAAAACCTGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTCGAT 181
DB 521 CCTCCCAAAAGATGATTTATGACATCAATCGGCTTCTGGAGTCCCTGCTCGCT 580
QY 182 TCAGTGGCAGTGGTGTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGCTGAAG 241
DB 581 TCAGTGGCAGTGGTGTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGCTGAAG 640
QY 242 ATGCTGCACATTATTACTGCCAGCAGAGTAGTAACCCAGCCGTTGCGAGGGGGA 301
DB 641 ATGCTGCACATTATTACTGCCAGCAGAGTAGTAACCCAGCTTACCATTCACGTTCCGAGGGGG 700
QY 302 CCATGCTGGAATTAAGA 318
DB 701 CCAGCTGGAATTAAGA 717

RESULT 11

US-09-976-787-27
Sequence 27, Application US/09976787
Patent No. US20020064528A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 27
LENGTH: 318
TYPE: DNA
ORGANISM: Mouse
US-09-976-787-27

Query Match 82.1%; Score 261; DB 10; Length 318;
Best Local Similarity 89.0%; Pred. No. 5.3e-71;
Matches 282; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AAATTGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTACAA 61
DB 2 ACATGAGCTCACTCACTCCTCAGCAATCATGTCTGCAATCTCCAGGGGGAAGTACCA 61
QY 62 TGACTTGAGGGGCGAGCTCAAGTGAATTAATACATGACAGTGTACAGAGCCAGGAT 121
DB 62 TAACCTGCGAGTGGCAGCTCAAGTGAATTAATACATGACAGTGTACAGAGCCAGGGA 121

QY 122 CCTCCCAAAACCTGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTCGCT 181
DB 122 CTTCCTCCAAATCTGATTTATAGCACAATCCAACTGGCTTCTGGAGTCCCTGCTCGCT 181
QY 182 TCAGTGGCAGTGGTGTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGCTGAAG 241
DB 182 TCAGTGGCAGTGGTGTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGCTGAAG 241
QY 242 ATGCTGCACATTATTACTGCCAGCAGAGTAGTAACCCAGCCGTTGCGAGGGGGA 301
DB 242 ATGCTGCACATTATTACTGCCAGCAGAGTAGTAACCCAGCTTACCATTCACGTTCCGAGGGGA 301
QY 302 CCATGCTGGAATTAAGA 318
DB 302 CCAGCTGGAATTAAGA 318

RESULT 12

US-09-865-198-26
Sequence 26, Application US/09865198
Patent No. US2002010345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 26
LENGTH: 318
TYPE: DNA
ORGANISM: Mouse
US-09-865-198-26

Query Match 82.1%; Score 261; DB 10; Length 318;
Best Local Similarity 89.0%; Pred. No. 5.3e-71;
Matches 282; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AAATTGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGGAAAAGTACAA 61
DB 2 ACATGAGCTCACTCACTCCTCAGCAATCATGTCTGCAATCTCCAGGGGGAAGTACCA 61
QY 62 TGACTTGAGGGGCGAGCTCAAGTGAATTAATACATGACAGTGTACAGAGCCAGGAT 121
DB 62 TAACCTGCGAGTGGCAGCTCAAGTGAATTAATACATGACAGTGTACAGAGCCAGGGA 121
QY 122 CCTCCCAAAACCTGATTTCTGCGACATCCAACTGGCTTCTGGAGTCCCTGCTCGCT 181
DB 122 CTTCCTCCAAATCTGATTTATAGCACAATCCAACTGGCTTCTGGAGTCCCTGCTCGCT 181
QY 182 TCAGTGGCAGTGGTGTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGCTGAAG 241
DB 182 TCAGTGGCAGTGGTGTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGCTGAAG 241
QY 242 ATGCTGCACATTATTACTGCCAGCAGAGTAGTAACCCAGCCGTTGCGAGGGGGA 301
DB 242 ATGCTGCACATTATTACTGCCAGCAGAGTAGTAACCCAGCTTACCATTCACGTTCCGAGGGGA 301
QY 302 CCATGCTGGAATTAAGA 318
DB 302 CCAGCTGGAATTAAGA 318

RESULT 13

US-09-976-787-16
Sequence 16, Application US/09976787
Patent No. US20020064528A1
GENERAL INFORMATION:

```
APPLICANT: Zhu, Zhenping
APPLICANT: Wille, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 16
LENGTH: 324
TYPE: DNA
ORGANISM: Mus musculus
US-09-976-787-16

Query Match
Best Local Similarity 82.1%; Score 261; DB 10; Length 324;
Best Local Similarity 89.0%; Pred. No. 5,4e-71;
Matches 282; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 2 AAATTGTTCTCTCCAGCTCCAGCAATCCTGCTGCATCTCCAGGGGAAAGGTACAA 61
DB 2 ACATCGAGCTCAGCTCAGCTCCAGCAATGCTGCTGCATCTCCAGGGGAGAGGTACAA 61
QY 62 TGACTTGACAGGGCCAGCTCAGTGTAAATTAATGACACTGGTACCAAGAGGCTAGAT 121
DB 62 TAACCTGACAGTGCAGCTCAGTGTAAATTAATGACACTGGTACCAAGAGGCTAGAT 121
QY 122 CTTCTCCCAAACTGTGATTTATAGACATCCAACTGGCTTCGGAGTCCCTGCTGCT 181
DB 122 CTTCTCCCAAACTGTGATTTATAGACATCCAACTGGCTTCGGAGTCCCTGCTGCT 181
QY 182 TCAGTGGCAGTGGGTGGGACCTTACTCTGTCACAAATGACAGGAGGCTGAG 241
DB 182 TCAGTGGCAGTGGGTGGGACCTTACTCTGTCACAAATGACAGGAGGCTGAG 241
QY 242 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 301
DB 242 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 301
QY 302 CCATGCTGGAATTAAGA 318
DB 302 CCATGCTGGAATTAAGA 318
```

```
RESULT 14
US-09-865-198-16
Sequence 16, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 16
LENGTH: 324
TYPE: DNA
ORGANISM: Mouse
US-09-865-198-16
```

```
Query Match
Best Local Similarity 82.1%; Score 261; DB 10; Length 324;
Best Local Similarity 89.0%; Pred. No. 5,4e-71;
Matches 282; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 2 AAATTGTTCTCTCCAGCTCCAGCAATCCTGCTGCATCTCCAGGGGAAAGGTACAA 61
```

```
DB 2 ACATCGAGCTCAGCTCAGCTCCAGCAATGCTGCTGCATCTCCAGGGGAGAGGTACAA 61
QY 62 TGACTTGACAGGGCCAGCTCAGTGTAAATTAATGACACTGGTACCAAGAGGCTAGAT 121
DB 62 TAACCTGACAGTGCAGCTCAGTGTAAATTAATGACACTGGTACCAAGAGGCTAGAT 121
QY 122 CTTCTCCCAAACTGTGATTTATAGACATCCAACTGGCTTCGGAGTCCCTGCTGCT 181
DB 122 CTTCTCCCAAACTGTGATTTATAGACATCCAACTGGCTTCGGAGTCCCTGCTGCT 181
QY 182 TCAGTGGCAGTGGGTGGGACCTTACTCTGTCACAAATGACAGGAGGCTGAG 241
DB 182 TCAGTGGCAGTGGGTGGGACCTTACTCTGTCACAAATGACAGGAGGCTGAG 241
QY 242 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 301
DB 242 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 301
QY 302 CCATGCTGGAATTAAGA 318
DB 302 CCATGCTGGAATTAAGA 318
```

```
RESULT 15
US-09-976-787-31
Sequence 31, Application US/09976787
Patent No. US20020064528A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Wille, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 31
LENGTH: 714
TYPE: DNA
ORGANISM: Mouse
US-09-976-787-31
```

```
Query Match
Best Local Similarity 82.1%; Score 261; DB 10; Length 714;
Best Local Similarity 89.0%; Pred. No. 7,1e-71;
Matches 282; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 2 AAATTGTTCTCTCCAGCTCCAGCAATCCTGCTGCATCTCCAGGGGAAAGGTACAA 61
DB 398 ACATCGAGCTCAGCTCAGCTCCAGCAATGCTGCTGCATCTCCAGGGGAGAGGTACAA 457
QY 62 TGACTTGACAGGGCCAGCTCAGTGTAAATTAATGACACTGGTACCAAGAGGCTAGAT 121
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QY 122 CTTCTCCCAAACTGTGATTTATAGACATCCAACTGGCTTCGGAGTCCCTGCTGCT 181
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DB 242 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 301
QY 638 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 697
DB 638 ATGCTGCACTTATTAATGACAGTGTAGTAACCAACCACTGCTGAGGAGGGA 697
QY 302 CCATGCTGGAATTAAGA 318
DB 302 CCATGCTGGAATTAAGA 318
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Wed Nov 27 08:54:28 2002

us-09-893-615-88.rnpb

Page 9

Db 698 CCAGCTGGAAATAAAA 714

Search completed: November 27, 2002, 05:31:02
Job time : 38.5677 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2002, 07:18:10 ; Search time 14.2471 Seconds
(without alignments)
137.479 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 646
Sequence: 1 EVMLVSGGGLVQPKGSLK.....SGIDYANDYWGQGTSLTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PCRT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646	100.0	123	10	US-09-893-615-87
2	532.5	82.4	143	10	US-09-881-823-16
3	519	80.3	117	10	US-09-835-087-8
4	519	80.3	117	10	US-09-809-739-12
5	519	80.3	117	10	US-09-840-459-10
6	519	80.3	148	10	US-09-840-459-100
7	493	76.3	117	10	US-09-835-087-13
8	493	76.3	117	10	US-09-809-739-23
9	493	76.3	117	10	US-09-840-459-20
10	489	75.7	117	10	US-09-835-087-12
11	489	75.7	117	10	US-09-809-739-22
12	488	75.5	117	10	US-09-840-459-19
13	488	75.5	117	10	US-09-835-087-11
14	488	75.5	117	10	US-09-809-739-21
15	488	75.5	117	10	US-09-840-459-18
16	487	75.4	117	10	US-09-835-087-10
17	487	75.4	117	10	US-09-809-739-20
18	487	75.4	117	10	US-09-840-459-17
19	487	75.4	119	10	US-09-840-459-104

20	483	74.8	101	10	US-09-840-459-34	Sequence 34, Appl
21	471.5	73.0	126	10	US-09-840-459-74	Sequence 74, Appl
22	468	72.4	100	10	US-09-840-459-35	Sequence 75, Appl
23	463	71.7	127	10	US-09-840-459-71	Sequence 4, Appl
24	460.5	71.3	120	12	US-10-025-687-4	Sequence 73, Appl
25	455.5	70.5	126	10	US-09-840-459-73	Sequence 3, Appl
26	444.5	68.8	263	9	US-09-956-086-3	Sequence 3, Appl
27	444.5	68.8	263	9	US-09-956-087-3	Sequence 6, Appl
28	444.5	68.8	283	9	US-09-983-580-6	Sequence 8, Appl
29	444.5	68.8	123	10	US-09-840-459-82	Sequence 4, Appl
30	443	68.4	140	10	US-09-286-240-4	Sequence 72, Appl
31	442	67.9	125	10	US-09-840-459-72	Sequence 9, Appl
32	438.5	67.9	125	10	US-09-840-459-91	Sequence 89, Appl
33	438	67.8	123	10	US-09-840-459-84	Sequence 84, Appl
34	436.5	67.6	124	10	US-09-840-459-84	Sequence 2, Appl
35	435	67.3	125	10	US-09-883-758-2	Sequence 3, Appl
36	434.5	67.3	298	10	US-09-811-123-3	Sequence 28, Appl
37	434	67.2	119	10	US-09-840-459-92	Sequence 90, Appl
38	434	67.2	121	10	US-09-229-200A-28	Sequence 131, App
39	433.5	67.1	124	10	US-09-840-459-90	Sequence 5, Appl
40	433.5	67.1	124	10	US-09-910-059-131	Sequence 5, Appl
41	433	67.0	473	10	US-09-756-301A-5	Sequence 5, Appl
42	432.5	67.0	119	10	US-09-927-703-5	Sequence 5, Appl
43	432.5	67.0	119	10	US-09-766-535A-5	Sequence 5, Appl
44	432.5	67.0	119	10	US-09-756-161A-5	Sequence 5, Appl
45	432.5	67.0	119	10	US-09-756-161A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-893-615-87
Sequence 87, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995, 0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION:	SEQ ID NO:	87:
US-09-893-615-87		

Query Match	100.0%;	Score 646;	DB 10;	Length 123;
Best Local Similarity	100.0%;	Pred. No. 1.5e-52;		
Matches 123; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

Qy 61 FYADSVKDRFTISRDDSQSMYLQMNLIKTEPTAMYYCVRRGASGIDYAMDYWGQGTSLT 120

Db 61 FYADSVKDRFTISRDDSQSMYLQMNLIKTEPTAMYYCVRRGASGIDYAMDYWGQGTSLT 120

Qy	121	VSS	123
		111	
Db	121	VSS	123

RESULT 2
US-09-881-823-16
Sequence 16 Application US/09881823

: PATENT NO. US2002006806A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: SHI, WENYUAN
 :
 : APPLICANT: ANDERSON, MAXWELL,

APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI

FILE REFERENCE: 22651-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15

PRIOR FILING DATE: 1999-08-20
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn version 3.0

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; TYPE: PRM
; ORGANISM: Murline
US-09-861-823-16

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Query Match	82.4%	Score 532.5	DB 10	Length 143
Best Local Similarity	84.8%	Pred. No. 3.9e-42		
Matches 106	Conservative	5	Mismatches 9	Indels 5
				Gaps 2

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Db
20 EQVLVERCGGLVQPKGSJLKLSCAASGFTEFNTAMNWNVAQPGCKLEWARIRRSKNINYAT 79

61 FADSVDFRTISRDDSGMLKLNNNLTETEDPAMCYCRRGASGLDVA--MDVWGQGS 118
OY :|||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 80 YADSVDEFRTISRDDSGMLKLNNNLTETEDPAMYCYR---NYDYDAWSATWVGQGY 136

Qy	119	LTSS	123
	:		
Db	137	VTSS	141

RESULT 3
US-09-835-087-8
: Sequence 8. Application US/09835087

PATENT NO.: 032002004.2/001
 GENERAL INFORMATION:
 APPLICANT: Wayne W. Hancock
 TITLE OF INVENTION: Method of Treating Graft Rejection Using

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: TITLE OF INVENTION: Inhibitors of CCR2 Function
:
: FILE REFERENCE: 1855.2008-003
:
: CURRENT APPLICATION NUMBER: US/09/835,087
:
: CURRENT FILING DATE: 2001-09-24
:

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; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
LENGTH: 117

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; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
US-09-835-087-8

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Query Match%	80.3%	Score 519;	DB 10;	length 117;
Best Local Similarity	80.5%	Pred. No. 5.4e-41;		
Matches	99;	Conservative	11;	Mismatches 7;
				Indeels 6;
				Gaps 1

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Db 1 EYQVLVESSGGGLVQPKGSLKLSCAAGFENNNYAMNNWVRAPGKGLEWARIKRSNNAT 60

[illegible]

QY	1.21	VSS	1.23
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Db	1.15	VSS	1.17

RESULT 4
US-09-809-739-12
: Sequence 12, Application US/09809739

RECEIVED NO. 0000000000

GENERAL INFORMATION:

APPLICANT: Horvath, Christopher J.

APPLICANT: Rao, Patricia E.

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:      SOFTWARE: FastSeq for Windows Version 4.0
:      SEQ ID NO 127

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? ORGANISM: Unknown
? FEATURE:
? NAME/KEY: STMS

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LOCATION: (1)...(117)
OTHER INFORMATION: Murine mab ID9 heavy chain variable region
NAME/KEY: SITE
LOCATION: (31)
LOCATION: (35)

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Db      61  YYADSVKDRYTTISRDSSEMLFLQNNLKTEDTAMYYCVTFYNGV-----WGTGTVTVT 114
QY      121 VSS 123
        |||
Db      115 VSS 117

RESULT 5
US-09-840-459-10
; Sequence 10, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-10

Query Match      80.3%; Score 519; DB 10; Length 117;
Best Local Similarity 80.5%; Pred. No. 5,4e-41;
Matches 99; Conservative 11; Mismatches 7; Indels 6; Gaps 1;

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Db      1  EVOLVESGGGLVQPKGSLKLSCAASGFSPFNAYAMNVRQAPGKGLEWVARIRTKNNVAT 60
QY      61  FYADSVKDRFTTSRDSSQSMLYLQNNLKTEDTAMYYCVRRAASGIDYAMDYGQTSILT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  YYADSVKDRYTTISRDSSEMLFLQNNLKTEDTAMYYCVTFYNGV-----WGTGTVTVT 114
QY      121 VSS 123
        |||
Db      115 VSS 117

RESULT 6
US-09-840-459-100
; Sequence 100, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-100

Query Match      80.3%; Score 519; DB 10; Length 148;
Best Local Similarity 80.5%; Pred. No. 6,9e-41;
Matches 99; Conservative 11; Mismatches 7; Indels 6; Gaps 1;
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```
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-100

Query Match      80.3%; Score 519; DB 10; Length 148;
Best Local Similarity 80.5%; Pred. No. 6,9e-41;
Matches 99; Conservative 11; Mismatches 7; Indels 6; Gaps 1;

QY      1  EVMLVESGGGLVQPKGSLKLSCAASGFSPFNAYAMNVRQAPGKGLEWVARIRSKSNVAT 60
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20  EVOLVESGGGLVQPKGSLKLSCAASGFSPFNAYAMNVRQAPGKGLEWVARIRTKNNVAT 79
QY      61  FYADSVKDRFTTSRDSSQSMLYLQNNLKTEDTAMYYCVRRAASGIDYAMDYGQTSILT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80  YYADSVKDRYTTISRDSSEMLFLQNNLKTEDTAMYYCVTFYNGV-----WGTGTVTVT 133
QY      121 VSS 123
        |||
Db      134 VSS 136

RESULT 7
US-09-835-087-13
; Sequence 13, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-13

Query Match      76.3%; Score 493; DB 10; Length 117;
Best Local Similarity 76.4%; Pred. No. 1,3e-38;
Matches 94; Conservative 14; Mismatches 9; Indels 6; Gaps 1;

QY      1  EVMLVESGGGLVQPKGSLKLSCAASGFSPFNAYAMNVRQAPGKGLEWVARIRSKSNVAT 60
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  EVOLVESGGGLVQPKGSLKLSCAASGFSPFNAYAMNVRQAPGKGLEWVARIRTKNNVAT 60
QY      61  FYADSVKDRFTTSRDSSQSMLYLQNNLKTEDTAMYYCVRRAASGIDYAMDYGQTSILT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  YYADSVKDRYTTISRDSKNTLYLQNNLKTEDTAMYYCVTFYNGV-----WGQGTLYVT 114
QY      121 VSS 123
        |||
```

```

Db          115 VSS 117

RESULT 8
US-09-809-739-23
: Sequence 23, Application US/09809739
: Patent No. US20020106369A1
: GENERAL INFORMATION:
: APPLICANT: Horvath, Christopher J.
: TITLE OF INVENTION: Method of Inhibiting Stenosis and
: TITLE OF INVENTION: Restenosis
: FILE REFERENCE: 1855.1069-003
: CURRENT APPLICATION NUMBER: US/09/809,739
: CURRENT FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: US 09/528,267
: PRIOR FILING DATE: 2000-03-17
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 23
: LENGTH: 117
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Humanized sequence
US-09-809-739-23

```

```

Query Match Similarity      76.3%: Score 493: DB 10: Length 117:
Best Local Similarity      76.4%: Pred. No. 1.3e+38:
Matches 94: Conservative 14: Mismatches 9: Indels 6: Gaps 1:

OY      1 EVMLEYSGGGLVQPKGSLKLSGCAAGTFENNAYMMWRQAPGKGLEWVARIRKSNNTAT 60
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 EVQLVDSGGGLVKKPGSGSLRLSCAAGCFSPNAYMMWRQAPGKGLEWVARIRTKNNYAF 60
OY      61 FYADSVKRRFTISRPDSQSMLYLGNNNLKTEPTAMYYCYRRASGIDYAMDYWGQTSILT 120
      61 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      61 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 FYADSVKRRFTISRPDSKNTLYLGNNNLKTEPTAVYYCYVTFYNGV-----WGQTLVAT 114
OY      121 VSS 123
      121 | | |
Db      115 VSS 117

RESULT 9
US-09-840-459-20
: Sequence 20, Application US/09840459
: Patent No. US20020150576A1
: GENERAL INFORMATION:
: APPLICANT: Larosa, Gregory J.
: APPLICANT: Horvath, Christopher
: APPLICANT: Newman, Walter
: APPLICANT: Jones, S. Tarran
: APPLICANT: O'Brien, Slobhan H.
: APPLICANT: O'Keefe, Theresa
: TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR
: FILE REFERENCE: 1855.1052-012
: CURRENT APPLICATION NUMBER: US/09/840.459
: CURRENT FILING DATE: 2001-02-02
: PRIOR APPLICATION NUMBER: PCT/US01/03537
: PRIOR FILING DATE: 2001-02-02
: PRIOR APPLICATION NUMBER: 09/497,625
: PRIOR FILING DATE: 2000-02-03
: PRIOR APPLICATION NUMBER: 09/359,193
: PRIOR FILING DATE: 1999-07-22
: PRIOR APPLICATION NUMBER: 09/121,781
: PRIOR FILING DATE: 1998-07-23
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 20
: LENGTH: 117
: TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-20

```

Query	March	Similarity	76.3%	Score	493	DB	10	Length	117
Best	Local	Similarity	76.4%	Pred.	No. 1.3e-38				
Matches	94	Conservative	14	Mismatches	9	Indels	6	Gaps	1

QY	1	EYMLVESGGGLVQPGKSLKSLCAASGFTFNNYAMNVRQAPGKGLEVARIRKSNNTAT	60
Db	1	EQQLVESGGGLKPPGKSLRLSCAASGFSFNAYAMNVRQAPGKGLEVARIRTKNNNTAT	60
QY	61	FYADSVKDRFTISRPDSQSMLYLQNNKLTETPTAMYYCYRRASGIDYAMDYGGGTSLT	120
Db	61	YYADSVKDRYTRISRPDSKNTLYLQNNKLTETPTAVYYCYCTFYNGCV-----WGQGLTAVT	114
QY	121	VSS	123
Db	115	VSS	117

```

RESULT 10
US-09-835-087-12
; Sequence 12, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 117
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-12

```

```

Query Match          75.7%: Score 489; DB 10; Length 117;
Best Local Similarity 75.6%: Pred. No. 3e-38;
Matches 93; Conservative 14; Mismatches 10; Indels 6; Gaps 1.

OY      1 EYMLVESGGGLVQPQGSILKSCAAGFTFNNYAMNVRQAPKGLGEMVARIKSNNTYAT 60
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1 EQVLVESGGGLVYKPGGSLRLSCAAGSFSFNAAMNVRAPKGLGEMVARIKNNNTYAT 60
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      61 FYADVSKDRFTLSRDDSQSMLYLQNNLNKTEDTAMYYCVYRCAGSGIDVAMDYWGQGTSLT 120
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      61 YYADVSKDRFTLSRDDSKNTLYLQNNLSKTEDTAVYYCTTFYNGGV-----WGQGTLYT 114
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      121 VSS 123
      |||

DB      115 VSS 117

```


Best Local Similarity 75.6%; Pred. No. 3.7e-38;
Matches 93; Conservative 13; Mismatches 11; Indels 6; Gaps 1;

```
QY 1 EVMVESGGGLVOPKGLIKSCAASGFTFNNYAMNWRQAPGKLEWVARIRSKSNYYAT 60
  |||
Db 1 EVOLVESGGGLVOPKGLIKSCAASGFTFNNYAMNWRQAPGKLEWVARIRSKSNYYAT 60
  |||
QY 61 FYADSVADRFTISRDSQSMILYLOMNNLKTEDTAMYYCVRRGASGIDYAMDYMGQTSLT 120
  |||
Db 61 YYADSVADRFTISRDSQSMILYLOMNNLKTEDTAMYYCVRRGASGIDYAMDYMGQTSLT 114
  |||
QY 121 VSS 123
  |||
Db 115 VSS 117
```

```
RESULT 15
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. US20020150576a1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Slobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 185.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-18
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Query Match 75.5%; Score 488; DB 10; Length 117;
Best Local Similarity 75.6%; Pred. No. 3.7e-38;
Matches 93; Conservative 13; Mismatches 11; Indels 6; Gaps 1;

QY 1 EVMVESGGGLVOPKGLIKSCAASGFTFNNYAMNWRQAPGKLEWVARIRSKSNYYAT 60
  |||
Db 1 EVOLVESGGGLVOPKGLIKSCAASGFTFNNYAMNWRQAPGKLEWVARIRSKSNYYAT 60
  |||
QY 61 FYADSVADRFTISRDSQSMILYLOMNNLKTEDTAMYYCVRRGASGIDYAMDYMGQTSLT 120
  |||
Db 61 YYADSVADRFTISRDSQSMILYLOMNNLKTEDTAMYYCVRRGASGIDYAMDYMGQTSLT 114
  |||
QY 121 VSS 123
  |||
Db 115 VSS 117
```

Search completed: November 27, 2002, 07:26:00
Job time : 15.2471 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2002, 07:18:10 : Search time 1.73745 Seconds
(Without alignments)
137.479 Million cell updates/sec

Title: US-09-893-615-1
Perfect score: 91
Sequence: 1 WRMYFSHRHAHLRSP 15

Scoring table: BLOSUM62
Gap 10.0, Capext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published.Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	91	100.0	15	10	US-09-893-615-1
2	91	100.0	19	10	US-09-893-615-27
3	91	100.0	19	10	US-09-893-615-29
4	91	100.0	19	10	US-09-893-615-33
5	91	100.0	19	10	US-09-893-615-35
6	91	100.0	19	10	US-09-893-615-37
7	91	100.0	19	10	US-09-893-615-65
8	66	72.5	19	10	US-09-893-615-31
9	41	45.1	127	10	US-09-864-761-44155
10	41	45.1	191	10	US-09-828-644-87
11	40	44.0	300	10	US-09-728-721-4
12	40	44.0	300	12	US-10-105-931-4
13	40	44.0	540	10	US-09-748-537-1
14	40	44.0	540	10	US-09-728-721-2
15	40	44.0	540	10	US-09-771-161A-184
16	40	44.0	540	10	US-09-862-027-28
17	40	44.0	540	12	US-10-133-780-1
18	40	44.0	540	12	US-10-105-931-2
19	40	44.0	544	10	US-09-925-301-1015

20	40	44.0	616	10	US-09-925-300-1519	Sequence 1519, Ap
21	39	42.9	92	9	US-10-032-159A-18	Sequence 18, Appl
22	39	42.9	139	9	US-10-032-159A-16	Sequence 16, Appl
23	39	42.9	378	10	US-09-864-761-43251	Sequence 43251, A
24	39	42.9	1004	10	US-09-767-215-2	Sequence 2, Appl1
25	39	42.9	1138	10	US-09-767-215-5	Sequence 5, Appl1
26	38	41.8	29	10	US-09-880-901-2	Sequence 2, Appl1
27	38	41.8	39	10	US-09-864-761-48462	Sequence 48462, A
28	38	41.8	65	10	US-09-912-020-395	Sequence 395, App
29	38	41.8	65	10	US-09-815-242-10177	Sequence 10177, A
30	38	41.8	293	10	US-09-815-242-5614	Sequence 5614, Ap
31	38	41.8	303	9	US-09-828-523A-20	Sequence 12527, A
32	38	41.8	303	9	US-09-815-242-12527	Sequence 86, Appl
33	38	41.8	311	9	US-09-828-523A-86	Sequence 43222, A
34	38	41.8	379	10	US-09-864-761-43222	Sequence 43, Appl
35	37	40.7	29	10	US-09-995-297-34	Sequence 35570, A
36	37	40.7	69	10	US-09-864-761-35570	Sequence 49114, A
37	37	40.7	121	10	US-09-864-761-49114	Sequence 868, App
38	37	40.7	189	10	US-09-987-967-2	Sequence 2, Appl1
39	37	40.7	220	10	US-09-925-301-1209	Sequence 1209, Ap
40	37	40.7	224	10	US-09-885-188-11	Sequence 11, Appl
41	37	40.7	224	10	US-09-885-189-11	Sequence 63, Appl
42	37	40.7	267	10	US-09-726-643-63	Sequence 170, App
43	37	40.7	329	9	US-09-895-913A-170	Sequence 12, Appl
44	37	40.7	628	10	US-09-828-447-12	
45	37	40.7				

ALIGNMENTS

RESULT 1
US-09-893-615-1
Sequence 1, Application US/09893615
Patent NO. US20020082395A1

GENERAL INFORMATION:

APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.

TITLE OF INVENTION: ONSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

DUNNER, LLP

STREET: 1300 I Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/893,615

FILING DATE: 29-Jun-2001

ATTORNEY/AGENT INFORMATION:

NAME: Etinudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 04995, 0041-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: Linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-893-615-1

Query Match 100.0%; Score 91; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
DB 1 WRMYFSHRHAHLRSP 15

RESULT 2
US-09-893-615-27
Sequence 27, Application US/09893615
Patent No. US20020082395A1

GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001

ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-893-615-27

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
DB 3 WRMYFSHRHAHLRSP 17

RESULT 3
US-09-893-615-29
Sequence 29, Application US/09893615
Patent No. US20020082395A1

GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.

Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-893-615-29

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WRMYFSHRHAHLRSP 15
DB 3 WRMYFSHRHAHLRSP 17

RESULT 4
US-09-893-615-33
Sequence 33, Application US/09893615
Patent No. US20020082395A1

GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/893.615
:   FILING DATE: 29-Jun-2001
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Elnaudi, Carol P.
:     REGISTRATION NUMBER: 32,220
:   REFERENCE/DOCKET NUMBER: 04995.0041-00000
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 202-408-4400
:     TELEFAX: 202-408-4400
:   INFORMATION FOR SEQ ID NO: 33:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 19 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:     MOLECULE TYPE: protein
:     SEQUENCE DESCRIPTION: SEQ ID NO: 33:
:
: US-09-893-615-33
:
: Query Match      100.0%; Score 91; DB 10; Length 19;
: Best Local Similarity 100.0%; Pred. No. 3.7e-08;
: Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy      1 WRWFSHRHAHLRSP 15
:         ||||||||||||
:         3 WRWFSHRHAHLRSP 17
:
: Db
:
: RESULT 5
: US-09-893-615-35
:   Sequence 35, Application US/09893615
:   Patent No. US20020082395A1
:   GENERAL INFORMATION:
:     APPLICANT: Fischer, Gerald W.
:       Schuman, Richard F.
:       Wong, Hing
:       Stinson, Jeffrey L.
:   TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
:     CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
:     POSITIVE BACTERIA
:   NUMBER OF SEQUENCES: 89
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
:       STREET: 1300 I Street, NW
:       CITY: Washington
:       STATE: DC
:       COUNTRY: USA
:       ZIP: 20005-3315
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/893.615
:     FILING DATE: 29-Jun-2001
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Elnaudi, Carol P.
:       REGISTRATION NUMBER: 32,220
:     REFERENCE/DOCKET NUMBER: 04995.0041-00000
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 202-408-4400
:     TELEFAX: 202-408-4400
:   INFORMATION FOR SEQ ID NO: 35:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 19 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:     MOLECULE TYPE: protein
:     SEQUENCE DESCRIPTION: SEQ ID NO: 35:
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: US-09-893-615-35
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: Query Match      100.0%; Score 91; DB 10; Length 19;
: Best Local Similarity 100.0%; Pred. No. 3.7e-08;
: Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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: Oy      1 WRWFSHRHAHLRSP 15
:         ||||||||||||
:         3 WRWFSHRHAHLRSP 17
:
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: RESULT 6
: US-09-893-615-37
:   Sequence 37, Application US/09893615
:   Patent No. US20020082395A1
:   GENERAL INFORMATION:
:     APPLICANT: Fischer, Gerald W.
:       Schuman, Richard F.
:       Wong, Hing
:       Stinson, Jeffrey L.
:   TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
:     CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
:     POSITIVE BACTERIA
:   NUMBER OF SEQUENCES: 89
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
:       STREET: 1300 I Street, NW
:       CITY: Washington
:       STATE: DC
:       COUNTRY: USA
:       ZIP: 20005-3315
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/893.615
:     FILING DATE: 29-Jun-2001
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Elnaudi, Carol P.
:       REGISTRATION NUMBER: 32,220
:     REFERENCE/DOCKET NUMBER: 04995.0041-00000
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 202-408-4400
:     TELEFAX: 202-408-4400
:   INFORMATION FOR SEQ ID NO: 37:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 19 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:     MOLECULE TYPE: protein
:     SEQUENCE DESCRIPTION: SEQ ID NO: 37:
:
: US-09-893-615-37
:
: Query Match      100.0%; Score 91; DB 10; Length 19;
: Best Local Similarity 100.0%; Pred. No. 3.7e-08;
: Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Oy      1 WRWFSHRHAHLRSP 15
:         ||||||||||||
:         3 WRWFSHRHAHLRSP 17
:
: Db
:
: RESULT 7
: US-09-893-615-65
:   Sequence 65, Application US/09893615
:   Patent No. US20020082395A1
:   GENERAL INFORMATION:
:     APPLICANT: Fischer, Gerald W.
:       Schuman, Richard F.
:       Wong, Hing
:       Stinson, Jeffrey L.
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TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Version #1.30
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-893-615-65
Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 3 WRMYFSHRHAHLRSP 17
QY 1 WRMYFSHRHAHLRSP 15
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RESULT 8
US-09-893-615-31
Sequence 31, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Skinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Version #1.30
APPLICATION NUMBER: US/09/893,615

FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-893-615-31
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Best Local Similarity 73.3%; Pred. No. 0.00023;
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DB 3 WRMYFSHRHAHLRSP 17
QY 1 WRMYFSHRHAHLRSP 15
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US-09-864-761-44155
Sequence 44155, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmlca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408

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2  PRIOR APPLICATION NUMBER: US 09/774, 203
3  PRIOR FILING DATE: 2001-01-29
4  NUMBER OF SEQ. ID NOS: 49117
5  SOFTWARE: Annemax Sequence Listing Engine vers. 1.1
6  SEQ. ID NO 44135
7  LENGTH: 127
8  TYPE: PRT
9  ORGANISM: Homo sapiens
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11  FEATURE:
12
13  OTHER INFORMATION: MAP TO AC004622.1
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15  OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
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19  OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
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21  OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
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23  OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
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25  OTHER INFORMATION: EST_HUMAN HIT: AW023622.1, EVALU0 5.00e-40
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27  US-09-864-761-44135

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; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-748-537-1
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Best Local Similarity 33.3%; Pred. No. 57;
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; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
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; ORGANISM: Homo sapiens
; US-09-728-721-2
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Best Local Similarity 33.3%; Pred. No. 57;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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; Sequence 184, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
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; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
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Best Local Similarity 33.3%; Pred. No. 57;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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Job time : 1.73745 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

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Title: US-09-893-615-2

Perfect score: 91

Sequence: 1 WHMRRIRPLQLAGR 15

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Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	91	100.0	19	US-09-893-615-9	Sequence 9, Appli
3	91	100.0	19	US-09-893-615-17	Sequence 17, Appli
4	91	100.0	19	US-09-893-615-19	Sequence 19, Appli
5	91	100.0	19	US-09-893-615-41	Sequence 41, Appli
6	91	100.0	19	US-09-893-615-57	Sequence 57, Appli
7	80	87.9	19	US-09-893-615-15	Sequence 15, Appli
8	50	54.9	139	US-09-864-761-33721	Sequence 33721, A
9	44.5	48.9	323	US-09-816-087-4	Sequence 9, Appli
10	44.5	48.9	343	US-09-985-694A-9	Sequence 4, Appli
11	43	47.3	51	US-09-864-761-42937	Sequence 42937, A
12	43	47.3	1298	US-09-982-610-33	Sequence 33, Appli
13	42	46.2	68	US-09-920-920-81	Sequence 81, Appli
14	41	45.1	54	US-09-925-297-466	Sequence 466, App
15	41	45.1	99	US-09-864-761-40505	Sequence 40505, A
16	41	45.1	379	US-09-804-682-72	Sequence 72, Appli
17	41	45.1	379	US-09-804-682-73	Sequence 73, Appli
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20	40	44.0	136	US-09-728-479-9	Sequence 9, Appli
21	40	44.0	136	US-09-263-689-13	Sequence 13, Appli
22	40	44.0	802	US-09-964-899-41	Sequence 41, Appli
23	40	44.0	1074	US-09-509-106A-2	Sequence 2, Appli
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26	39	42.9	253	US-09-815-242-11842	Sequence 11842, A
27	39	42.9	338	US-09-318-271-8	Sequence 8, Appli
28	38.5	42.3	343	US-09-985-664A-2	Sequence 2, Appli
29	38	41.8	25	US-09-864-761-43467	Sequence 43467, A
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31	38	41.8	133	US-09-867-550-372	Sequence 372, App
32	38	41.8	577	US-09-815-242-11760	Sequence 11760, A
33	38	41.8	797	US-09-815-242-5071	Sequence 5071, Ap
34	38	41.8	824	US-09-932-145-3	Sequence 3, Appli
35	37.5	41.2	189	US-09-815-242-11799	Sequence 11799, A
36	37.5	41.2	264	US-09-815-242-13980	Sequence 13980, A
37	37.5	41.2	417	US-09-815-242-10165	Sequence 10165, A
38	37	40.7	73	US-09-764-887-288	Sequence 288, App
39	37	40.7	79	US-09-867-550-860	Sequence 860, App
40	37	40.7	178	US-09-966-546-2	Sequence 2, Appli
41	37	40.7	178	US-09-966-545-2	Sequence 2, Appli
42	37	40.7	610	US-09-748-107-2	Sequence 2, Appli
43	36.5	40.1	295	US-09-815-242-10104	Sequence 10104, A
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45	36	39.6	11	US-09-780-070-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-09-893-615-2
; Sequence 2, Application US/09893615
; Patent No. US20020082395A1
; GENERAL INFORMATION:
; APPLICANT: Filscher, Gerald W.
; Schuman, Richard F.
; Wong, Hing
; Stinson, Jeffrey L.
; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GF
; POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
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; CITY: Washington
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Elnaoui, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 04995.0041-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: Linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-893-615-2

Query Match 100.0%; Score 91; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 WHMRHRIPLQLAGR 15

RESULT 2
US-09-893-615-9
Sequence 9, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudt, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-893-615-9

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPLQLAGR 15
Db 3 WHMRHRIPLQLAGR 17

RESULT 3
US-09-893-615-17
Sequence 17, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.

Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-893-615-17

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHMRHRIPLQLAGR 15
Db 3 WHMRHRIPLQLAGR 17

RESULT 4
US-09-893-615-19
Sequence 19, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/893,615
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-893-615-19

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHRRRIPQLAAGR 15
Db 3 WHRRRIPQLAAGR 17

RESULT 5
US-09-893-615-41
Sequence 41, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-893-615-41

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHRRRIPQLAAGR 15
Db 3 WHRRRIPQLAAGR 17

RESULT 6
US-09-893-615-57
Sequence 57, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-893-615-57

Query Match 100.0%; Score 91; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHRRRIPQLAAGR 15
Db 3 WHRRRIPQLAAGR 17

RESULT 7
US-09-893-615-15
Sequence 15, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Mong, Hing
Stinson, Jeffrey L.

TITLE OF INVENTION: OPOSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-893-615-15
Query Match 87.9%; Score 80; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 HMRHRIPLOLAGR 15
DB 4 HMRHRIPLOLAGR 17
RESULT 8
US-09-864-761-33721
Sequence 33721, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33721
LENGTH: 139
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000046.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
OTHER INFORMATION: EST_HUMAN HIT: AA853678.1, EVALUATE 2.00e-21
US-09-864-761-33721
Query Match 54.9%; Score 50; DB 10; Length 139;
Best Local Similarity 72.7%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 WHMRHRIPLOL 11
DB 98 WHMRHRIPLOL 108
RESULT 9
US-09-816-087-4
Sequence 4, Application US/09816087
Patent No. US20020064822A1
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
FILE REFERENCE: CL000749-CIP
CURRENT APPLICATION NUMBER: US/09/816,087
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 323
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-816-087-4
Query Match 48.9%; Score 44.5; DB 10; Length 323;

Best Local Similarity 57.1%; Pred. No. 9.7;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Oy 1 WHHRRIPQLAAG 14
Db 138 WYRRR-PKRLSAG 150

RESULT 10

US-09-985-694A-9
; Sequence 9, Application US/09985694A
; Patent No. US20020150980A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: G-Protein Coupled Receptor
; FILE REFERENCE: P145P1C1
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 08/461,989
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/13296
; PRIOR FILING DATE: 1994-11-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 343
; TYPE: PRT
; ORGANISM: human
US-09-985-694A-9

Query Match 48.9%; Score 44.5; DB 10; Length 343;
Best Local Similarity 57.1%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Oy 1 WHHRRIPQLAAG 14
Db 150 WYRRR-PKRLSAG 162

RESULT 11

US-09-864-761-42937
; Sequence 42937, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263, 6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42937
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049594.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EST_HUMAN HIT: BF338634.1, EVALU 4.00e-21
; OTHER INFORMATION: SWISSPROT HIT: P42128, EVALU 5.20e-01
US-09-864-761-42937

Query Match 47.3%; Score 43; DB 10; Length 51;
Best Local Similarity 44.4%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 8; Gaps 1;

Oy 1 WHR-----HRIPQL 10
Db 30 WDMRLGRCGRGPHRLPLQ 47

RESULT 12

US-09-982-610-33
; Sequence 33, Application US/09982610
; Patent No. US20020146420A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/982,610
; FILING DATE: 17-Oct-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,648
; FILING DATE: 1996-MAY-23
; APPLICATION NUMBER: 08/222616

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013627.3.
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5
; OTHER INFORMATION: SWISSPROT HIT: P28476, EVALUE 2.50e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA843600.1, EVALUE 2.60e-01
US-09-864-761-40505

Query Match 45.1%; Score 41; DB 10; Length 99;
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
OY 1 WHWRHR--IPLOLAG 14
|||:| ||:|
Db 57 WHMNRKRFAPLRMLPG 72

Search completed: November 27, 2002, 07:25:59
Job time : 2.73745 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:23:05 : Search time 1.44788 Seconds
(without alignments)
429.695 Million cell updates/sec

Title: US-09-893-615-2

Sequence: 1 MWMHRRIPLQLAGR 15

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	40.0	203	FLA1_ARCFU	O29208 archaeoglob
2	6	40.0	342	YM22_YEAST	P40214 saccharomyc
3	6	40.0	367	DP3B_PSEPU	P13455 pseudomonas
4	6	40.0	510	GARD_BACSU	P42240 bacillus su
5	6	40.0	536	CBP8_HUMAN	P22792 homo sapien
6	6	40.0	558	BCHD_RHOSH	O34845 rhodobacter
7	6	40.0	666	Y079_SCHPO	O13670 schizosacch
8	6	40.0	778	FTSK_COXBU	P39920 coxiella bu
9	6	40.0	1144	DP3A_NEIMA	O91vx8 neisseria m
10	6	40.0	1144	DP3A_NEIMA	O91vx2 neisseria m
11	5	33.3	29	HOXY_RHOOP	P22660 rhodococcus
12	5	33.3	93	REP1_ECOLI	P05830 escherichia
13	5	33.3	98	FER1_CVAPA	P17007 cyanophora
14	5	33.3	99	FER2_APHSA	P00251 aphanothece
15	5	33.3	102	YAIY_ECOLI	P77669 escherichia
16	5	33.3	105	YB59_YEAST	P38311 saccharomyc
17	5	33.3	108	NIFH_NOSMU	Q09158 nostoc musc
18	5	33.3	112	OL11_MOUSE	Q60890 mus musculu
19	5	33.3	114	Y118_ARCFU	O30118 archaeoglob
20	5	33.3	136	YAGP_ECOLI	P75684 escherichia
21	5	33.3	148	MBR1_ECOLI	P08097 escherichia
22	5	33.3	156	COAD_HAETN	P44805 haemophilus
23	5	33.3	157	VE6_HPV36	P50810 human papil
24	5	33.3	157	YM75_YEAST	Q05022 saccharomyc
25	5	33.3	158	TPC1_BALNU	P21797 balanus nub
26	5	33.3	162	UL33_HSVB	P28953 equine herp
27	5	33.3	170	YFCR_ECOLI	P76501 escherichia
28	5	33.3	171	MSG2_MOUSE	P47759 mus musculu
29	5	33.3	179	HSIV_LISIN	Q32C74 listeria in
30	5	33.3	179	HSIV_LISMO	O6Y719 listeria mo
31	5	33.3	179	YAJI_ECOLI	P61122 escherichia
32	5	33.3	180	HSIV_BACDI	O8k42z bacillus ha
33	5	33.3	181	HSIV_BACSU	P39070 bacillus su

34	5	33.3	184	YDJA_HAETN	P45244 haemophilus
35	5	33.3	192	MOBA_NEIMB	P58847 neisseria m
36	5	33.3	195	AANT_HDYM1	P25881 hepatitis d
37	5	33.3	196	UHPA_SALTY	P27667 salmonella
38	5	33.3	201	PCP_BACHD	O9K64 bacillus ha
39	5	33.3	203	IAAS_HORVU	P07596 hordeum vul
40	5	33.3	204	KGUA_XYLEA	O9pd76 xylella fas
41	5	33.3	205	YTCG_ECOLI	P31432 escherichia
42	5	33.3	210	V593_CAME	O9phs3 campylobact
43	5	33.3	215	ISPD_AQUAE	O67343 aquilex aeo
44	5	33.3	215	HEX8_ADEMI	P19722 mouse adeno
45	5	33.3	215	TRPF_BACSU	P20167 bacillus su

ALIGNMENTS

RESULT 1

FLA1_ARCFU STANDARD: PRT: 203 AA.

AC O29208: 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable flagellin 1 precursor.

GN FLA1 OR AF1054.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=96049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kinkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Goeyne J.D., Weidman J.F., McDonald L., Uterback T.,

RA Cottrell M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,

RA Sadov P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997).

CC -!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO

CC FORM THE FILAMENTS OF FLAGELLA.

CC -!- SIMILARITY: BELONGS TO THE ARCHAEAL FLAGELLIN FAMILY.

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CC or send an email to license@sib-sib.ch).

CC EMBL; AE001030; AAB90186.1; -

DR TIGR; AF1054; -

DR InterPro; IPR002774; Arch_flagellin.

DR Pfam; PF01917; Arch_flagellin; 1.

DR KEGG; MultiGene family; Complete proteome.

FT PROPEP 1 11 POTENTIAL.

FT CHAIN 12 203 PROBABLE FLAGELLIN 1.

SO SEQUENCE 203 AA; 21665 MM; C1C9B1210D79809D C1C64;

Query Match 40.0%; Score 6; DB 1; Length 203;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      9 LQLAAG 14
        |||
Db      85 LQLAAG 90

RESULT 2
YM22_YEAST
ID      YM22_YEAST      STANDARD:      PRT:      342 AA.
AC      P40214;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DE      01-NOV-1997 (Rel. 35, Last annotation update)
DE      Hypothetical 38.6 kDa protein in RPS16A-TIF34 intergenic region.
GN      YMR144W OR YM9375.13.
OS      Saccharomyces cerevisiae (Baker's Yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=5288c / AB972;
RA      Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL      Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      or send an email to license@isb-sib.ch).
DR      EMBL; 247071; CAA87358.1; -
DR      SGD; S0004752; YMR144W.
KW      Hypothetical protein.
SQ      SEQUENCE 342 AA; 38570 MW; AEA7FE5E1080CA6 CRC64;

Query Match
Best Local Similarity 40.0%; Score 6; DB 1; Length 342;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9 LQLAAG 14
        |||
Db      274 LQLAAG 279

RESULT 3
DP3B_PSEPU
ID      DP3B_PSEPU      STANDARD:      PRT:      367 AA.
AC      P13455;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      DNA polymerase III, beta chain (EC 2.7.7.7).
GN      DNAN.
OS      Pseudomonas putida.
OC      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC      Pseudomonas.
OX      NCBI_TaxID=303;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=7N2100;
RA      MEDLINE=89218947; PubMed=2540413;
RA      Fujita M.O., Yoshikawa H., Ogasawara N.;
RT      Structure of the dna region of Pseudomonas putida: conservation
RT      among three bacteria, Bacillus subtilis, Escherichia coli and P.
RT      putida.
RL      Mol. Genet. 215:381-387(1989).
CC      -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC      RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC      THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC      THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT
CC      IS CLAMPED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-

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CC      INDEPENDENT) ALONG DUPLEX DNA (BY SIMILARITY).
CC      -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate;
CC      + [DNA](N).
CC      -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND
CC      THETA CHAINS) THAT CAN REPAIR SHORT GAPS CREATED BY NUCLEASE
CC      IN DUPLEX DNA. FOR EFFICIENT REPLICATION OF THE LONG, SINGLE-
CC      STRANDED TEMPLATES, POL III REQUIRES THE AUXILIARY CHAINS BETA,
CC      GAMMA, AND DELTA.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -----
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CC      or send an email to license@isb-sib.ch).
DR      EMBL; X14791; CAA32894.1; -
DR      PIR; JY0002; DIPS3P.
DR      HSSP; P00583; 2POL.
DR      InterPro: IPR001001; DNA_polIII_beta.
DR      Pfam: PF02767; DNA_pol3_beta.1.
DR      Pfam: PF02768; DNA_pol3_beta_3; 1.
DR      SMART; SM00480; POL3Bc; 1.
DR      TIGRFAMs; TIGR00663; dnan; 1.
KW      Transference; DNA-directed DNA polymerase; DNA replication.
SQ      SEQUENCE 367 AA; 40718 MW; FE65ABBA6D65FEAD CRC64;

Query Match
Best Local Similarity 40.0%; Score 6; DB 1; Length 367;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9 LQLAAG 14
        |||
Db      284 LQLAAG 289

RESULT 4
GARD_BACSU
ID      GARD_BACSU      STANDARD:      PRT:      510 AA.
AC      P42240; P42241.
DT      01-NOV-1995 (Rel. 32, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Probable D-galactarate dehydratase (EC 4.2.1.42) (Galco).
GN      GARD.
OS      Bacillus subtilis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1423;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      MEDLINE=95219079; PubMed=7704254;
RA      Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
RT      Determination of a 21548 bp nucleotide sequence around the 24
RT      degrees region of the Bacillus subtilis chromosome.
RT      Microbiology 141:269-275(1995).
RN      (2)
RP      SEQUENCE FROM N.A.
RC      STRAIN=168;
RA      MEDLINE=98044033; PubMed=9384377;
RA      Kunst F., Ogasawara N., Moszer I., Albertini A.M., Allion G.,
RA      Azevedo V., Bertoro M.C., Bessieres P., Bolotin A., Borchert S.,
RA      Borriis R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA      Brouillet S., Brusch C.V., Caldwell B., Capano V., Carter N.M.,
RA      Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA      Dentzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmertson P.T.,
RA      Britlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA      Fritz C., Fujita M., Fujita Y., Funo S., Galizzi A., Galleron N.,
RA      Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA      Guisepi G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,

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RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasanara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetle D., Porwollik S., Prescott A.M.,
 RA Priesen E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Setguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
 RA Takuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarelli A.,
 RA Viari A., Mamout R., Wedler E., Wedler H., Wetzinger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT subtilis."

RT Nature 390:249-256(1997).
 CC -I- CATALYTIC ACTIVITY: D-galactarate = 5-dehydro-4-deoxy-D-glucarate
 CC + H2O.
 CC -I- PATHWAY: FIRST STEP IN THE METABOLISM OF D-GALACTARATE.
 CC -I- SIMILARITY: BELONGS TO THE UXA FAMILY.
 CC -I- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
 CC FRAMESHIFTS.

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 CC EMBL: D30808; BAA06472.1; ALT_FRAME.
 DR EMBL: D30808; BAA06473.1; ALT_FRAME.
 DR EMBL: Z99105; CAB12045.1; -
 DR Subtilisin: BG1163; gard.
 KW Lyase: Complete proteome.
 SQ SEQUENCE 510 AA; 54792 MW; C7283A007174CDE3 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 510;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQIAG 14
 | | | | |
 DB 412 LQIAG 417

RESULT 5
 CBB8_HUMAN STANDARD; PRT; 536 AA.
 ID CBB8_HUMAN STANDARD; PRT; 536 AA.
 AC P22792;
 DT 01-AUG-1991 (rel. 19, Created)
 DT 01-AUG-1991 (rel. 19, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Carboxypeptidase N 83 kDa chain (Carboxypeptidase N regulatory
 DE subunit) (Fragment).
 GN CPN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90094386; PubMed=2378615;
 RA Tan F., Weerasinghe D.K., Skidgel R.A., Tamei H., Kaul R.K.,
 RA Roninson I.B., Schilling J.W., Erdoes E.G.;
 RT "The deduced protein sequence of the human carboxypeptidase N high

RT molecular weight subunit reveals the presence of leucine-rich tandem
 RT repeats.";
 RT J. Biol. Chem. 265:13-19(1990).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=88309120; PubMed=3408501;
 RA Skidgel R.A., Bennett C.D., Schilling J.W., Tan F., Weerasinghe D.K.,
 RA Erdoes E.G.;
 RT "Amino acid sequence of the N-terminus and selected tryptic peptides
 RT of the active subunit of human plasma carboxypeptidase N: comparison
 RT with other carboxypeptidases.";
 RL Biochem. Biophys. Res. Commun. 154:1323-1329(1988).
 CC -I- FUNCTION: THE 83 KDA SUBUNIT BINDS AND STABILIZES THE CATALYTIC
 CC SUBUNIT AT 37 DEGREES CELSIUS AND KEEPS IT IN CIRCULATION. UNDER
 CC SOME CIRCUMSTANCES IT MAY BE AN ALLOSTERIC MODIFIER OF THE
 CC CATALYTIC SUBUNIT.
 CC -I- SUBUNIT: TETRAMER OF TWO CATALYTIC CHAINS AND TWO GLYCOSYLATED
 CC INACTIVE CHAINS.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- PTM: O-GLYCOSYLATED IN THE SER/THR-RICH REGION (POTENTIAL).
 CC -I- PTM: WHETHER OR NOT ANY CYS RESIDUES PARTICIPATE IN INTRACHAIN
 CC BONDS IS UNKNOWN, BUT THEY DO NOT FORM INTERCHAIN DISULFIDE BONDS
 CC WITH THE 50 KDA CATALYTIC SUBUNIT.
 CC -I- DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOT CONSIDERED TO BE
 CC COMPATIBLE WITH LIFE.
 CC -I- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC EMBL: J05158; AAA51921.1; -
 DR PIR: A34901; A34901.
 DR Genew: HGNC:2313; CPN2.
 DR MIM: 603104; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Lyp.
 DR Pfam: PF00560; LRR; 11.
 DR SMART: SM00013; LRRNT; 1.
 DR SMART: SM00369; LRR_TYP; 10.
 KW Repeat, Leucine-rich repeat, Glycoprotein.
 KM NON_TER
 FT REPEAT 1
 FT REPEAT 51 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 123 146 LRR 4.
 FT REPEAT 148 170 LRR 5.
 FT REPEAT 171 194 LRR 6.
 FT REPEAT 196 218 LRR 7.
 FT REPEAT 220 242 LRR 8.
 FT REPEAT 243 266 LRR 9.
 FT REPEAT 268 290 LRR 10.
 FT REPEAT 291 314 LRR 11.
 FT REPEAT 316 338 LRR 12.
 FT REPEAT 339 362 LRR 13.
 FT REPEAT 362 379 SER/THR-RICH.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 536 AA; 58649 MW; D524011243C9B2A6 CkC64;

Query Match 40.0%; Score 6; DB 1; Length 536;
 Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 8 PLOLAA 13
Db 384 PLOLAA 389

RESULT 6

BCHD_RHOSH STANDARD; PRT: 558 AA.
ID BCBD_RHOSH O34845;
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Magnesium-chelatase 60 kDa subunit (Mg-protoporphyrin IX chelatase)
DE (Mg-chelatase subunit D).
GN BCBD.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria: Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE-20115911; PubMed=10648776;
RT "Rhodobacter sphaeroides bchl and bchd encoding two subunits of
RT magnesium chelatase.";
RL (in) Plant Gene Register PGR97-190.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE-20115911; PubMed=10648776;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
RT sphaeroides 2.4.1.";
RL Nucleic Acids Res. 28:862-867 (2000).
RN [3]
RP CHARACTERIZATION.
RC STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE-95199269; PubMed=7892204;
RA Gibson L.C.D., Willows R.D., Kannangara C.G., von Wettstein D.,
RA Hunter C.N.;
RT "Magnesium-protoporphyrin chelatase of Rhodobacter sphaeroides:
RT reconstitution of activity by combining the products of the bchH, -I,
RT and -D genes expressed in *Escherichia coli*.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11941-11944 (1995).
CC -1- FUNCTION: Involved in bacteriochlorophyll biosynthesis; introduces
CC a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
CC IX.
CC -1- PATHWAY: Bacteriochlorophyll biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.
CC
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CC
CC -----
CC DR EMBL: AJ010302; CAB38736.1;
CC DR EMBL: AF017642; AB97157.1;
CC DR EMBL: AF195122; AF24286.1;
CC DR InterPro: IPR002035; VMF_A.
CC DR SMART: SM00327; VMA_1.
CC DR PROSITE: PS50234; VMFA_1.
CC KM Photosynthesis: Bacteriochlorophyll biosynthesis.
CC FT DOMAIN 376 555 VMFA.
CC FT DOMAIN 238 272 GUA/PRO-RICH.
CC SQ SEQUENCE 558 AA; 58548 MW; 2A16F62C1266FB3A CRC64;
Query Match 40.0%; Score 6; DB 1; Length 558;

Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 10 OLAGR 15
Db 289 OLAGR 294

RESULT 7

Y079_SCHPO STANDARD; PRT: 666 AA.
ID Y079_SCHPO O13670;
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Hypothetical protein C30B4.06 in chromosome II.
DE SPCC30B4.06C OR P1079.
GN Schizosaccharomyces pombe (fission yeast).
OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE-20089027; PubMed=10620777;
RA Machida M., Yamazaki S., Kunihito S., Tanaka T., Kushida N., Jinno K.,
RA Hatakeyama Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
RA Yanagida M.;
RT "A 38 kb segment containing the cdc2 gene from the left arm of fission
RT yeast chromosome II: sequence analysis and characterization of the
RT genomic DNA and cDNAs encoded on the segment.";
RL Yeast 16:71-80 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE-21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Spouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M., Squares R., Stevens S., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicakeert G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Botzys K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Egger P., Zimmermann W., Wedler H., Wambolt R., Punnett B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leclaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
RT "The genome sequence of *Schizosaccharomyces pombe*.";
RL Nature 415:871-880 (2002).
CC -1- SIMILARITY: BELONGS TO THE GIDA FAMILY.
CC
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CC

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CC -----
DR EMBL: AB004539; BAA21461.1; -
DR EMBL: AL001262; CAA20319.1; -
DR InterPro: IPR002218; GIDA.
DR InterPro: IPR000205; NAD_binding.
DR Pfam: PF01134; GIDA.1.
DR ProDom: PD003738; GIDA.1.
DR PROSITE: PS01280; GIDA_1; 1.
DR PROSITE: PS01281; GIDA_2; 1.
DR Hypothetical protein.
KW SEQUENCE 666 AA; 74230 MW; 703D4529BDEBA83 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QLAAG 15
|11111
DB 185 QLAAGR 190

RESULT 8
FTSK_COXBU STANDARD; PRT; 778 AA.
ID FTSK_COXBU
AC P39920;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cell division protein ftsk homolog.
GN FTSK OR SPOIIE.
OS Coccidia burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coccidia group; Coccidia.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile phase I / Bratislava;
RX MEDLINE=94055499; PubMed=8237209;
RA Oswald W., Thiele D.;
RL J. Vet. Med. B 40:366-370(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE FTSK/SPOIIE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X75627; CAA53289.1; -
DR InterPro: IPR002543; FTSK_SPOIIE.
DR Pfam: PF01580; FTSK_SPOIIE; 1.
KW Cell division; ATP-binding; Transmembrane.
FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT NP_BIND 436 443 ATP (POTENTIAL).
SQ SEQUENCE 778 AA; 85169 MW; FCE6C15100422061 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 778;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LQLAAG 14
|11111
DB 340 LQLAAG 345

RESULT 9

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DP3A_NEIMA STANDARD; PRT; 1144 AA.
ID DP3A_NEIMA
AC Q93VX8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAP OR NMA0632.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate -> N diphosphate
+ {DNA}(n).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
DIMERIZATION TO FORM THE POLIII' COMPLEX. POLIII' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAP
SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL162753; CAB83921.1; -
DR InterPro: IPR004013; PHP.C.
DR InterPro: IPR003141; PHP.N.
DR InterPro: IPR004805; POLC_alpha.
DR InterPro: IPR004365; tRNA_antl.
DR Pfam: PF01336; tRNA_antl; 1.
DR Pfam: PF02231; PHP_N; 1.
DR Pfam: PF02811; PHP_C; 1.
DR SMART: SM00481; POLIIC; 1.
DR TIGRFAMs: TIGR00594; polC; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.
SQ SEQUENCE 1144 AA; 126975 MW; 95270191E29EB412 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RIPIQL 11
|11111
DB 1097 RIPIQL 1102

RESULT 10
DP3A_NEIMB STANDARD; PRT; 1144 AA.
ID DP3A_NEIMB

```

AC Q9JXZ2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase III alpha subunit (EC 2.7.7.7).
 GN DNAE OR NMB1827.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=491;
 RX SEQUENCE FROM N.A.
 RC STRAIN=MC58 / Serogroup B;
 RA MEDLINE=20175755; PubMed=10710307;
 RA Tectelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Clecko A., Partsey D.S., Blair E., Ciftone H., Clark E.B.,
 RA Cotton M.D., Ullrich V., Maignan V., Qian H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignan V., Pizsa M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappaport R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).
 CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
 CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
 CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
 CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate -> N diphosphate
 CC + [DNA](N).
 CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
 CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
 CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH
 CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
 CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAE
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AE002532; AAF42162.1; -;
 DR TIGR: NMB1827; -;
 DR InterPro: IPR004013; PHP_C.
 DR InterPro: IPR003141; PHP_N.
 DR InterPro: IPR004805; POLC_alpha.
 DR InterPro: IPR004365; trna_antl.
 DR Pfam: PF01336; trna_antl.1.
 DR Pfam: PF02231; PHP_N.1.
 DR Pfam: PF02811; PHP_C.1.
 DR SMART: SM00481; POLIITAC.1.
 DR TIGRFAMs: TIGRF00594; POLC.1.
 KW Transferase: DNA-directed DNA polymerase; DNA replication;
 KM Complete proteome.
 SQ SEQUENCE 1144 AA; 127134 MW; 4CEABB86F90DD7FA CRC64;

Query Match 40.0%; Score 6; DB 1; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RLPQL 11
 |||||
 DB 1097 RLPQL 1102

RESULT 11
 HOXY_RHOOP

ID HOXY_RHOOP STANDARD: PRT; 29 AA.
 AC P22660;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NAD-reducing hydrogenase hoxs delta subunit (EC 1.1.2.1.2) (Fragment).
 GN HOXY.
 OS Rhodococcus opacus (Nocardia opaca).
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 NCBI_TaxID=37919;
 RX SEQUENCE.
 RC STRAIN=1B;
 RA MEDLINE=89231684; PubMed=2496982;
 RA Zaborosch C., Schneider K., Schlegel H.G., Kratzin H.;
 RT "Comparison of the NH2-terminal amino acid sequences of the four non-
 RT identical subunits of the NAD-linked hydrogenases from Nocardia opaca
 RT 1b and Alcaligenes eutrophus H16.";
 RL Eur. J. Biochem. 181:175-180(1989).
 CC -1- CATALYTIC ACTIVITY: H(2) + NAD(+) -> H(+) + NADH.
 CC -1- COFACTOR: FMN, NICKEL, TWO 4FE-4S, A 3FE-4S, AND A 2FE-2S
 CC CLUSTER.
 CC -1- SUBUNIT: TETRAMER OF AN ALPHA AND A GAMMA SUBUNITS (FLAVIN-
 CC CONTAINING DIMER), AND A DELTA AND A NICKEL-CONTAINING BETA
 CC SUBUNIT (HYDROGENASE DIMER).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: TO OTHER [NIFE] OR [NIFES] HYDROGENASES SMALL
 CC SUBUNIT.
 DR PIR: S03947; S03947.
 KW Oxidoreductase; NAD; Iron-sulfur; 3fe-4s; Plasmid.
 FT NON_TER 29
 SQ SEQUENCE 29 AA; 3159 MW; 1F54BC68F6AED6A CRC64;

Query Match 33.3%; Score 5; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 LAAGR 15
 |||||
 DB 23 LAAGR 27

RESULT 12
 REPI_ECOLI STANDARD: PRT; 93 AA.
 AC P05830;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE Regulatory protein repi (Fragment).
 GN REPI.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NCBI_TaxID=562;
 RX SEQUENCE FROM N.A.
 RC MEDLINE=87040771; PubMed=2430262;
 RA Kim K., Meyer R.J.;
 RT "Copy-number of broad host-range plasmid R1162 is regulated by a
 RT small RNA.";
 RL Nucleic Acids Res. 14:8027-8046(1986).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN REGULATING THE PLASMID
 CC COPY-NUMBER, INCREASING THE LEVEL OF THIS PROTEIN RESULTS IN A
 CC HIGHER PLASMID COPY-NUMBER.
 CC -----
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 CC -----
 DR EMBL: X04499; CAA28184.1; -.
 DR PIR: A25346; RGECDL.
 KW Plasmid; Plasmid copy control.
 FT NON_TER 93
 SO SEQUENCE 93 AA; 9413 MW; 0E767AC26C7634A CRC64;
 Query Match 33.3%; Score 5; DB 1; Length 93;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 LQIAA 13
 Db 48 LQIAA 52
 RESULT 13
 ID FER1_CVAPA STANDARD; PRT; 98 AA.
 AC P17007; Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ferredoxin I.
 GN PFME.
 OS Cyanophora paradoxa.
 OG Cyanelle.
 OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
 OX NCBI_TaxID=2762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LB555 / Pringsheim;
 RA Neumann-Spallart C., Brandtner M., Kraus M., Jakovitch J.,
 RA Bayer M.G., Maier T.L., Schenk H.E.A., Loeffelhardt W.;
 RT "The petf gene encoding ferredoxin I is located close to the str
 RT operon on the cyanelle genome of Cyanophora paradoxa.";
 RL FEBS Lett. 268:35-38(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91200662; PubMed=1901820;
 RA Bryant D.A., Schluchter W.M., Stirewalt V.L.;
 RT "Ferredoxin and ribosomal protein S10 are encoded on the cyanelle
 RL genome of Cyanophora paradoxa.";
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LB555 / Pringsheim;
 RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
 RA Bryant D.A.;
 RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
 RL Plant Mol. Biol. Rep. 13:327-332(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LB555 / Pringsheim;
 RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
 RA Farley J.Y., Schluchter W.M., Chung S., Neumann-Spallart C.,
 RA Steiner J.M., Jakovitch J., Bohnert H.J., Bryant D.A.;
 RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:
 RT the genetic complexity of a primitive plastid.";
 RL (in) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
 RL Schwemmler W. (eds.);
 RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
 RL (1997).
 RN [5]
 RP SEQUENCE OF 1-12
 RA Stevanovic S., Bayer M.G., Troger W., Schenk H.E.A.;
 RT "Cyanophora paradoxa korsch.: ferredoxin partial amino-terminal
 RT amino acid sequence, phylogenetic/taxonomic evidence.";
 RL Endocyt. Cell Res. 6:219-226(1990).

CC -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
 CC ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
 CC -!- COFACTOR: BINDS 1 2FE-2S CLUSTER.
 CC -!- SUBCELLULAR LOCATION: CYANELLE.
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 CC -----
 DR EMBL: X52143; CAA36387.1; -.
 DR EMBL: M35206; AAA31699.1; -.
 DR EMBL: U30821; AAA81236.1; -.
 DR PIR: S10427; FEKTL.
 DR PIR: J00459; J00459.
 DR HSSP: P00246; 4FXC.
 DR InterPro: IPR000564; 2FE2S_ferredoxin.
 DR InterPro: IPR001041; Ferredoxin.
 DR Pfam: PF00111; fer2; 1.
 DR PRINTS: PR00159; 2FE2SERDOXIN.
 DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
 KW Electron transport; Iron-sulfur; Cyanelle.
 FT INIT_MET 0
 FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 46 46 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 49 49 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 SQ SEQUENCE 98 AA; 10595 MW; 05061C34542FF77A CRC64;
 Query Match 33.3%; Score 5; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 10 QIAAG 14
 Db 70 QIAAG 74

RESULT 14
 ID FER2_APHSA STANDARD; PRT; 99 AA.
 AC P00251; Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last annotation update)
 DE Ferredoxin II.
 OS Aphanothece sacrum.
 OC Bacteria; Cyanobacteria; Chroococcales; Aphanothece.
 OX NCBI_TaxID=1122;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78150873; PubMed=417074;
 RA Hase T., Wakabayashi S., Wada K., Matsubara H.;
 RT "Amino acid sequence of Aphanothece sacrum Ferredoxin II (minor
 RT component). Structural characteristics and evolutionary
 RT implications.";
 RL J. Biochem. 83:761-770(1978).
 CC -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
 CC ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
 CC -!- COFACTOR: BINDS 1 2FE-2S CLUSTER.
 CC -----
 DR PIR: A00255; FEAH2.
 DR HSSP: P00246; 4FXC.
 DR InterPro: IPR000564; 2FE2S_ferredoxin.
 DR InterPro: IPR001041; Ferredoxin.
 DR Pfam: PF00111; fer2; 1.
 DR PRINTS: PR00159; 2FE2SERDOXIN.
 DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
 KW Electron transport; Iron-sulfur.
 FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 46 46 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

```

FT METAL 49 49 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 80 80 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 99 AA: 10354 MW: 28D256A1CE86E00F CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QLAG 14
   |||||
Db 71 QLAG 75

RESULT 15
YAIY ECOLI STANDARD: PRT: 102 AA.
ID YAIY ECOLI
AC P77669:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yaiY.
GN YAIY OR B0379 OR Z0475 OR ECS0429.
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schraum S., Davis R.W.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans F.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [5]
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL: AE000144; AAC73482.1; -.
DR EMBL: U73857; AAB18102.1; -.
DR EMBL: AE005217; AAC54725.1; -.
DR EMBL: AP002551; BAB3852.1; -.
DR EcoGene: EG14279; yaiY.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 25 45
FT TRANSMEM 75 95
SQ SEQUENCE 102 AA: 11424 MW: CA87D5A5E0F89F32 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWRHR 6
   |||||
Db 96 HWRHR 100

```

Search completed: November 27, 2002, 07:28:46
 Job time : 5.44788 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:24:25 : Search time 4.2278 Seconds
(Without alignments) 731.044 Million cell updates/sec

Title: US-09-893-615-2
Perfect score: 15

Sequence: 1 MHWNRHRIQLAAGR 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_fodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	46.7	160	09FTM6	Q9fmg6 Oryza sativ
2	7	46.7	160	0988K1	Q988K1 rhizobium 1
3	7	46.7	523	4 096DU2	Q96du2 homo sapien
4	7	46.7	524	11 09R0H5	Q9r0h5 mus musculu
5	7	46.7	594	3 09P4A3	Q9p4a3 emericella
6	7	46.7	1549	3 09VP01	Q9vp01 drosophila
7	7	46.7	1869	16 092JV3	Q92jv3 rhizobium m
8	7	46.7	82	16 09KEX7	Q9kex7 bacillus ha
9	6	40.0	111	16 09X2T9	Q9x2t9 escherichia
10	6	40.0	142	2 044529	Q44529 azotobacter
11	6	40.0	158	16 09CLH6	Q9clh6 pasteurella
12	6	40.0	176	5 09V103	Q9v103 drosophila
13	6	40.0	211	17 029897	Q29897 archaeoglob
14	6	40.0	218	2 P94955	P94955 micrococcus
15	6	40.0	231	15 056309	O56309 walleys epi
16	6	40.0	254	17 027483	O27483 methanobact

17	6	40.0	261	2 09KWS4	Q9kws4 pseudomonas
18	6	40.0	262	17 08ZZA7	Q8zza7 pyrobaculum
19	6	40.0	266	2 056187	Q56187 streptomyc
20	6	40.0	272	11 09CS07	Q9csq7 mus musculu
21	6	40.0	283	11 08R3S2	Q8r3s2 mus musculu
22	6	40.0	291	5 09NJV2	Q9njv2 haemochus
23	6	40.0	307	11 09EPG0	Q9epg0 mus musculu
24	6	40.0	309	16 08VPH0	Q8vph0 brucella me
25	6	40.0	317	16 09EBW3	Q9ebw3 streptomyc
26	6	40.0	330	16 09CC52	Q9cc52 mycobacteri
27	6	40.0	334	16 0920K3	Q920k3 rhizobium m
28	6	40.0	344	16 09RWF7	Q9rwf7 delinococcus
29	6	40.0	345	5 09VE32	Q9ve32 drosophila
30	6	40.0	347	11 054764	Q54764 mus musculu
31	6	40.0	358	13 057434	Q57434 fuqu rubrip
32	6	40.0	387	11 09D845	Q9d845 mus musculu
33	6	40.0	395	12 092283	Q92283 molluscum c
34	6	40.0	413	6 028665	Q28665 oryctolagus
35	6	40.0	413	6 028665	Q28665 oryctolagus
36	6	40.0	413	6 007298	Q07298 oryctolagus
37	6	40.0	423	13 057433	Q57433 fuqu rubrip
38	6	40.0	440	16 069661	Q69661 mycobacteri
39	6	40.0	449	10 09LIV0	Q9liv0 oryza sativ
40	6	40.0	450	16 099U27	Q99u27 staphylococ
41	6	40.0	450	16 0931T9	Q931t9 staphylococ
42	6	40.0	456	6 062663	Q62663 oryctolagus
43	6	40.0	458	16 08RHY2	Q8rhy2 fuscobacteri
44	6	40.0	467	2 09X4H6	Q9x4h6 streptomyc
45	6	40.0	475	16 08VIV5	Q8viv5 mycobacteri

ALIGNMENTS

RESULT 1

Q9FTM6 PRELIMINARY: PRT: 160 AA.
AC 09FTM6:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE P0005A05.23 protein (P0482C06.6 protein).
OS P0005A05.23 OR P0482C06.6.
GN Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0005A05.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0482C06.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002863; BAB16919.1; -;
DR EMBL; AP002845; BAB78610.1; -;
SQ SEQUENCE 160 AA; 16198 MW; 86560C2B6AC8F777 CRC64;

Query Match 46.7%; Score 7; DB 10; Length 160;
Best local similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 PQLAAG 14
|||||||
Db 38 PQLAAG 44

RESULT 2

0988K1

ID 0988K1 PRELIMINARY; PRT: 518 AA.

AC 0988K1: 01-OCT-2001 (TREMBLrel. 18, Created)

DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Hypothetical protein ml16708.

GN ML16708.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.,

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti."

RL DNA Res. 7:331-338(2000).

DR EMBL: AP003009; BAB52949.1; -.

DR InterPro: IPR001633; EAL.

DR InterPro: IPR000160; GGDEF.

DR Pfam: PF00563; EAL.1.

DR Pfam: PF00990; GGDEF.1.

DR SMART: SM00267; DUF1.1.

DR SMART: SM00052; DUF2.1.

DR TIGRFAWS: TIGR00254; GGDEF.1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 518 AA; 56502 MW; ED3361CD737C363E CRC64;

Query Match 46.7%; Score 7; DB 16; Length 518;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LQLAAGR 15

Db 142 LQLAAGR 148

RESULT 3

096DU2

ID 096DU2 PRELIMINARY; PRT: 523 AA.

AC 096DU2: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Keratin 6 lrs.

GN KRT6LRS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SCALP;

RA Rogers M.A., Langbein L., Winter H., Praetzel S., Ehmman C.,

RT "K6lrs, a new cytokeratin in the human hair follicle."

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: A308599; CAC43429.1; -.

DR InterPro: IPR001664; IF.

DR Pfam: PF00038; Filament.1.

DR PROSITE: PS00226; IF; UNKNOWN.1.

SQ SEQUENCE 523 AA; 57291 MW; 797F5655EE3A62D7 CRC64;

Query Match 46.7%; Score 7; DB 4; Length 523;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LQLAAGR 15

Db 330 LQLAAGR 336

RESULT 4

09ROH5

ID 09ROH5 PRELIMINARY; PRT: 524 AA.

AC 09ROH5: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Type II cytokeratin (Keratin protein K6lrs).

GN KRT2-6G.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Aoki N., Tsujimoto T.;

RT "Isolation and characterization of a novel mouse type II

RT cytokeratin."

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Porter R.M., McLean W.;

RT "Keratin K6lrs is specific to the inner root sheath of hair follicles

RT in mouse and humans."

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1-SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

DR EMBL: AB033744; BA85657.1; -.

DR MGD: AY033497; AAK5110.1; -.

DR EMBL: MGI:1861586; Krt2-6g.

DR InterPro: IPR001664; IF.

DR InterPro: IPR002957; Keratin_I.

DR InterPro: IPR003054; Keratin_II.

DR Pfam: PF00038; Filament.1.

DR PRINTS: PR01248; TYPE1KERATIN.

DR PRINTS: PR01276; TYPE2KERATIN.

DR PROSITE: PS00226; IF.1.

KW Coiled coil; Intermediate filament.

SQ SEQUENCE 524 AA; 57382 MW; 45FF0C44B440A72A CRC64;

Query Match 46.7%; Score 7; DB 11; Length 524;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LQLAAGR 15

Db 331 LQLAAGR 337

RESULT 5

09P4A3

ID 09P4A3 PRELIMINARY; PRT: 594 AA.

AC 09P4A3: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Camptothecin resistance conferring protein rcaA.

OS Emericella nidulans.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiiales; Trichocomaceae; Emericella.

OX NCBI_TaxID=162425;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21258791; PubMed=11361337;

RA Bruschi G.C., de Souza C.C., Fagundes M.R., Dani M.A., Goldman M.H.,
 RA Morris N.R., Liu L., Goldman G.H.,
 RT "Sensitivity to camptothecin in *Aspergillus nidulans* identifies a
 RT novel gene, *scatA*, related to the cellular DNA damage response."
 RL Mol. Genet. Genomics 265:264-275(2001).
 DR EMBL: AF228504; AAF81094.1; -
 SQ SEQUENCE 594 AA; 67513 MW; 19C4BE8E3DBD4505 CRC64;

Query Match 46.7%; Score 7; DB 3; Length 594;
 Best Local Similarity 100.0%; Pred. No. 34;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RHRIPLQ 10
 |||||
 DB 489 RHRIPLQ 495

RESULT 6

Q9VP01 PRELIMINARY; PRT; 1549 AA.

DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE CG11250 protein.
 GN CG11250.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George R.A., Blazer V.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Brandon R.C., Rogers Y.H.C., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butris K.C., Busch D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Doolittle K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jajala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).

DR EMBL: AE003595; AAF51761.1; -
 DR FlyBase: FBgn0037113; CG11250.

DR InterPro: IPR002110; ANK_PQZ.
 DR InterPro: IPR002110; BTB_PQZ.
 DR InterPro: IPR01087; Lipase_GDSL.

DR Pfam: PF00023; ank; 4.
 DR Pfam: PF00651; BTB; 1.
 DR SMART: SM00248; ANK; 2.

DR SMART: SM00225; BTB; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 1.

DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50097; BTB; 1.
 DR PROSITE: PS50108; LIPASE_GDSL_SER; UNKNOWN_1.

DR ANK repeat. Repeat.
 KW ANK repeat. Repeat.
 SQ SEQUENCE 1549 AA; 166717 MW; ED837D9A83114DCF CRC64;

Query Match 46.7%; Score 7; DB 5; Length 1549;
 Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PIQLANG 14
 |||||
 DB 1100 PIQLANG 1106

RESULT 7

Q92JV3 PRELIMINARY; PRT; 1869 AA.

AC Q92JV3;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Hypothetical signal peptide protein SMC03096.
 GN R02997 OR SMC03096.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capata D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godfrid T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT *Sinorhizobium meliloti* strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL: AL591792; CAC47576.1; -
 DR InterPro: IPR00425; MIP_family.
 DR PROSITE: PS00221; MIP; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1869 AA; 191305 MW; 32B51E6678708F9B CRC64;

Query Match 46.7%; Score 7; DB 16; Length 1869;
 Best Local Similarity 100.0%; Pred. No. 93;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RIPLQA 12
 |||||
 DB 813 RIPLQA 819

RESULT 8

Q9KEX7 PRELIMINARY; PRT; 82 AA.

AC Q9KEX7;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Hypothetical protein BH0722.

GN BH0722.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001509; BAB04441.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 82 AA; 8895 MW; 2747633A66928A81 CRC64;

Query Match 40.0%; Score 6; DB 16; Length 82;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAG 14
 |||||
 DB 18 LQLAG 23

RESULT 9

OBX279 PRELIMINARY; PRT; 111 AA.
 ID OBX279;
 AC OBX279;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein ECS4472.
 GN ECS4472.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shitagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:11-22(2001).
 DR EMBL: AP002566; BAB37895.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 111 AA; 12340 MW; 9C49517DED123AD7 CRC64;

Query Match 40.0%; Score 6; DB 16; Length 111;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PLQLAA 13
 |||||
 DB 89 PLQLAA 94

RESULT 10

O44529 PRELIMINARY; PRT; 142 AA.
 ID O44529;
 AC O44529;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Potential molybdenum-pterin-binding-protein.

GN MODG.
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DW136;
 RX MEDLINE=95394849; PubMed=7665518;
 RA Mouncey N.J., Mitchener L.A., Pau R.N.;
 RT "Mutational analysis of genes of the mod locus involved in molybdenum
 RT transport, homeostasis, and processing in Azotobacter vinelandii."
 RL J. Bacteriol. 177:5294-5302(1995).
 DR EMBL: Z49882; CAA90038.1; -;
 DR InterPro: IPR004606; MOP.
 DR InterPro: IPR005116; TOBE.
 DR Pfam: PF03459; TOBE; 2.
 DR TrifRAMS: TIGR00638; MOP; 2.
 SQ SEQUENCE 142 AA; 14359 MW; 514A7D97AEC2ED93 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LQLAG 14
 |||||
 DB 47 LQLAG 52

RESULT 11

O9CLH6 PRELIMINARY; PRT; 158 AA.
 ID O9CLH6
 AC O9CLH6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical protein PM1255.
 GN PM1255.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AE006164; AAK03339.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 158 AA; 18065 MW; C9135DF60FAD7ADA CRC64;

Query Match 40.0%; Score 6; DB 16; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QLAAGR 15
 |||||
 DB 32 QLAAGR 37

RESULT 12

O9V103 PRELIMINARY; PRT; 176 AA.
 ID O9V103
 AC O9V103;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG10919 protein.
 GN CG10919.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
 OC Ephydriidae: Drosophilidae: Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.O., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriell J.F., Abmayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.A., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doop L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jafarli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
 RA Relter K., Remington K., Saunders R.D.C., Scheeler J., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupsky M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003676; AAF54142.1; -;
 DR Flybase: FBgn0037514; CG10919.
 SQ SEQUENCE 176 AA; 21226 MW; D707C2448AAE5E53 CRC64;
 Query Match 40.0%; Score 6; DB 5; Length 176;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 HRIPLQ 10
 Db 87 HRIPLQ 92
 RESULT 13
 ID 029897 PRELIMINARY; PRT; 211 AA.
 AC 029897;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE Conserved hypothetical transmembrane protein.
 GN AFO350.
 OS Archaeoglobus fulgidus.
 OC Archaea: Euryarchaeota: Archaeoglobi: Archaeoglobales:
 OC Archaeoglobaceae: Archaeoglobus.
 OC NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Claydon R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kurlavsky A.R., Graham D.E., Kyriades N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.C., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon *Archaeoglobus fulgidus*.";
 RL Nature 390:364-370(1997).
 DR EMBL: AE001080; AAB90884.1; -;
 DR TIGR: AF0350; -;
 DR InterPro: IPR002781; DUF81.
 DR Pfam: PF01925; DUF81.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 SQ SEQUENCE 211 AA; 23303 MW; 927825BC1EFC1B46 CRC64;
 Query Match 40.0%; Score 6; DB 17; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 RPLQL 11
 Db 37 RPLQL 42
 RESULT 14
 ID P94955 PRELIMINARY; PRT; 218 AA.
 AC P94955;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE H(+)-transporting ATP synthase (EC 3.6.1.34) (Fragment).
 GN ATP H.
 OS Micrococcus luteus (Micrococcus lysodeikticus).
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
 OC Actinomycetales: Micrococcales: Micrococcaceae: Micrococcus.
 OC NCBI_TaxID=1270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 4698;
 RA Gruber G., Dose K., Nawroth T., Diel P., Cattaruzza M., Flach R.,
 RT "Cloning and analysis of the *atp*-operon genes H and A from *Micrococcus*
 RT luteus.";
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X84791; CAA59262.1; -;
 DR InterPro: IPR000711; ATPsyn_OSCP.
 DR Pfam: PF00213; OSCP; 1.
 DR PRINTS: PR00125; ATPASEDELTA
 DR TIGRfams: TIGR01145; ATP_synth_delta; 1.
 KW Hydrolase.
 FT NON_TER
 SQ SEQUENCE 1 1
 Query Match 40.0%; Score 6; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 LQLAAG 14
 Db 166 LQLAAG 171
 RESULT 15
 ID 056309 PRELIMINARY; PRT; 231 AA.
 AC 056309

AC 056309:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cyclin homolog.
OS walleye epidermal hyperplasia virus' type 2.
OC Viruses; Retroid viruses; Retroviridae; Epsilonretrovirus.
OX NCBI_TaxID=64461;
RN [1]
RP SEQUENCE FROM N.A.
RA Lapierre L.A., Casey J.W., Holtschu D.L.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Lapierre L.A., Holtschu D.L., Bowser P.R., Casey J.W.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AF037569; AAC68475.1; -;
DR EMBL: AF133052; AAC30056.1; -;
DR InterPro: IPR004366; Cyclin.
DR Pfam: PF00134; cyclin; 1.
DR SMART: SM00385; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 231 AA; 25367 MW; 95EA643029F27236 CRC64;

Query Match 40.0%; Score 6; DB 15; Length 231;
Best Local Similarly 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 9 LQLAAG 14
| | | | |
Db 64 LQLAAG 69

Search completed: November 27, 2002, 07:30:24
Job time : 10.4778 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:26:06 : Search time 2.08494 Seconds
(without alignments)
211.682 Million cell updates/sec

Title: US-09-893-615-2

Sequence: 1 WHWHRIRPLQLAGR 15

Scoring table: OLIGO

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	2	US-08-592-646A-28 Sequence 28, Appl
2	15	100.0	15	2	US-08-592-646A-48 Sequence 48, Appl
3	15	100.0	15	4	US-09-165-422-28 Sequence 28, Appl
4	15	100.0	15	4	US-09-165-422-48 Sequence 48, Appl
5	15	100.0	37	2	US-08-592-646A-59 Sequence 59, Appl
6	15	100.0	37	4	US-09-165-422-59 Sequence 59, Appl
7	14	93.3	15	2	US-08-592-646A-27 Sequence 27, Appl
8	14	93.3	15	2	US-08-592-646A-29 Sequence 29, Appl
9	14	93.3	15	4	US-09-165-422-27 Sequence 27, Appl
10	14	93.3	15	4	US-09-165-422-29 Sequence 29, Appl
11	13	86.7	15	2	US-08-592-646A-26 Sequence 26, Appl
12	13	86.7	15	2	US-08-592-646A-30 Sequence 30, Appl
13	13	86.7	15	4	US-09-165-422-26 Sequence 26, Appl
14	13	86.7	15	4	US-09-165-422-30 Sequence 30, Appl
15	12	80.0	15	2	US-08-592-646A-25 Sequence 25, Appl
16	12	80.0	15	2	US-08-592-646A-31 Sequence 31, Appl
17	12	80.0	15	4	US-09-165-422-25 Sequence 25, Appl
18	12	80.0	15	4	US-09-165-422-31 Sequence 31, Appl
19	11	73.3	11	2	US-08-592-646A-7 Sequence 7, Appl
20	11	73.3	11	4	US-09-165-422-7 Sequence 7, Appl
21	11	73.3	15	2	US-08-592-646A-9 Sequence 9, Appl
22	11	73.3	15	2	US-08-592-646A-24 Sequence 24, Appl
23	11	73.3	15	4	US-09-165-422-9 Sequence 9, Appl
24	11	73.3	15	4	US-09-165-422-24 Sequence 24, Appl
25	10	66.7	15	2	US-08-592-646A-23 Sequence 23, Appl
26	10	66.7	15	2	US-08-592-646A-32 Sequence 32, Appl
27	10	66.7	15	2	US-08-592-646A-40 Sequence 40, Appl

28	10	66.7	15	4	US-09-165-422-23 Sequence 23, Appl
29	10	66.7	15	4	US-09-165-422-32 Sequence 32, Appl
30	10	66.7	15	4	US-09-165-422-40 Sequence 40, Appl
31	9	60.0	15	2	US-08-592-646A-22 Sequence 22, Appl
32	9	60.0	15	2	US-08-592-646A-33 Sequence 33, Appl
33	9	60.0	15	2	US-08-592-646A-41 Sequence 41, Appl
34	9	60.0	15	4	US-09-165-422-22 Sequence 22, Appl
35	9	60.0	15	4	US-09-165-422-33 Sequence 33, Appl
36	9	60.0	15	4	US-09-165-422-41 Sequence 41, Appl
37	8	53.3	15	2	US-08-592-646A-21 Sequence 21, Appl
38	8	53.3	15	2	US-08-592-646A-34 Sequence 34, Appl
39	8	53.3	15	2	US-08-592-646A-43 Sequence 43, Appl
40	8	53.3	15	4	US-09-165-422-21 Sequence 21, Appl
41	8	53.3	15	4	US-09-165-422-34 Sequence 34, Appl
42	8	53.3	15	4	US-09-165-422-43 Sequence 43, Appl
43	7	46.7	15	2	US-08-592-646A-20 Sequence 20, Appl
44	7	46.7	15	2	US-08-592-646A-35 Sequence 35, Appl
45	7	46.7	15	2	US-08-592-646A-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-592-646A-28
: Sequence 28, Application US/08592646A
: Patent No. 5851535
: GENERAL INFORMATION:
: APPLICANT: JOLIVET-REYNAUD, Colette
: TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
: NUMBER OF INVENTIONS: GONDII AND APPLICATIONS
: CORRESPONDENCE ADDRESSES:
: ADDRESS: OLIFF & BERTRIDGE, PLC
: STREET: P.O. Box 19928
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/592,646A
: FILING DATE: 26-JAN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BertrIDGE, William P.
: REGISTRATION NUMBER: 30,024
: REFERENCE/DOCKET NUMBER: WPB 36923
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703 836-6400
: TELEFAX: 703 836-2787
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-592-646A-28

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

OY 1 WHWHRIRPLQLAGR 15
DB 1 WHWHRIRPLQLAGR 15

RESULT 2
US-08-592-646A-48
Sequence 48, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVIER & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-48

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHRRRIPQLAAGR 15
DB 1 WHRRRIPQLAAGR 15

RESULT 3
US-09-165-422-28
Sequence 28, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVIER & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422

FILING DATE: 02-Oct-1998
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-165-422-28

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHRRRIPQLAAGR 15
DB 1 WHRRRIPQLAAGR 15

RESULT 4
US-09-165-422-48
Sequence 48, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVIER & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-165-422-48

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHMRRIPQLAAGR 15
|||||
Db 1 WHMRRIPQLAAGR 15

RESULT 5

US-08-592-646A-59
Sequence 59, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-59
Query Match 100.0%; Score 15; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4,7e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHMRRIPQLAAGR 15
|||||
Db 10 WHMRRIPQLAAGR 24

RESULT 6

US-09-165-422-59
Sequence 59, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-165-422-59
Query Match 100.0%; Score 15; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 4,7e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHMRRIPQLAAGR 15
|||||
Db 10 WHMRRIPQLAAGR 24

RESULT 7

US-08-592-646A-27
Sequence 27, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-592-646A-27

Query Match 93.3%; Score 14; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHHRRIPQLAAG 14

DB 2 WHHRRIPQLAAG 15

RESULT 8

US-08-592-646A-29
Sequence 29, Application US/08592646A
Patent No. 5851535

GENERAL INFORMATION:

APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MITOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC

STREET: P.O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,646A

FILING DATE: 26-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703 836-6400

TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-592-646A-29

Query Match 93.3%; Score 14; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.2e-08;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHHRRIPQLAAG 15

DB 1 WHHRRIPQLAAG 14

RESULT 9

US-09-165-422-27
Sequence 27, Application US/09165422
Patent No. 6372897

GENERAL INFORMATION:

APPLICANT: JOLIVET-REYNAUD, Colette

TITLE OF INVENTION: MITOTOPIC POLYPEPTIDES OF TOXOPLASMA

TITLE OF INVENTION: GONDII AND APPLICATIONS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC

STREET: P.O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,422

FILING DATE: 02-Oct-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703 836-6400

TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 27;

US-09-165-422-27

Query Match 93.3%; Score 14; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.2e-08;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHHRRIPQLAAG 14

DB 2 WHHRRIPQLAAG 15

RESULT 10

US-09-165-422-29
Sequence 29, Application US/09165422
Patent No. 6372897

GENERAL INFORMATION:

APPLICANT: JOLIVET-REYNAUD, Colette

TITLE OF INVENTION: MITOTOPIC POLYPEPTIDES OF TOXOPLASMA

TITLE OF INVENTION: GONDII AND APPLICATIONS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC

STREET: P.O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,422

FILING DATE: 02-Oct-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703 836-6400

TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29;
US-09-165-422-29

Query Match 93.3%; Score 13; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HWRHRIPQLAAGR 15
DB 1 HWRHRIPQLAAGR 14

RESULT 11
US-08-592-646A-26
Sequence 26 Application US/08592646A
Patent No. 5651535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-30

Query Match 86.7%; Score 13; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WRRHRIPQLAAGR 13
DB 1 WRRHRIPQLAAGR 13

RESULT 13
US-09-165-422-26
Sequence 26 Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-26

Query Match 86.7%; Score 13; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHRRHRIPQLAAG 13
DB 3 WHRRHRIPQLAAG 15

RESULT 12
US-08-592-646A-30
Sequence 30 Application US/08592646A
Patent No. 5651535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette

TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-30

Query Match 86.7%; Score 13; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WRRHRIPQLAAGR 15
DB 1 WRRHRIPQLAAGR 13

RESULT 13
US-09-165-422-26
Sequence 26 Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-26

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-165-422-26

Query Match 86.7%; Score 13; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHHRRIPLOLA 13
DB 3 WHHRRIPLOLA 15

RESULT 14
US-09-165-422-30
Sequence 30, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVE & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-165-422-30

Query Match 86.7%; Score 13; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WHHRRIPLOLA 15
DB 1 WHHRRIPLOLA 13

RESULT 15
US-08-592-646A-25
Sequence 25, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVE & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-Jan-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-25

Query Match 80.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WHHRRIPLOLA 12
DB 4 WHHRRIPLOLA 15

Search completed: November 27, 2002, 07:32:09
Job time: 3.08494 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:28:06 : Search time 1.38996 Seconds
(without alignments)
171.849 Million cell updates/sec

Title: US-09-893-615-2

Perfect score: 15
Sequence: 1 WHMRHRIPLQLAGR 15

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 102317 seqs, 15924203 residues

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Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	15	100.0	19	10	US-09-893-615-9
4	15	100.0	19	10	US-09-893-615-17
5	15	100.0	19	10	US-09-893-615-19
6	15	100.0	19	10	US-09-893-615-41
7	14	93.3	19	10	US-09-893-615-15
8	6	40.0	228	10	US-09-893-737-142
9	6	40.0	290	10	US-09-815-242-12356
10	6	40.0	411	10	US-09-815-242-5746
11	6	40.0	585	10	US-09-815-242-11923
12	6	40.0	741	9	US-09-891-762-2
13	5	33.3	29	10	US-09-982-172-16
14	5	33.3	29	10	US-09-982-172-215
15	5	33.3	41	10	US-09-864-761-45173
16	5	33.3	46	10	US-09-864-761-46783
17	5	33.3	50	10	US-09-864-761-48053
18	5	33.3	54	10	US-09-925-297-888
19	5	33.3	57	10	US-09-864-761-48156

20	5	33.3	62	10	US-09-864-761-33340	Sequence 33340, A
21	5	33.3	80	10	US-09-864-761-48387	Sequence 48387, A
22	5	33.3	83	10	US-09-726-643-84	Sequence 84, Appl
23	5	33.3	88	8	US-08-424-550B-275	Sequence 275, App
24	5	33.3	92	10	US-09-867-550-494	Sequence 494, App
25	5	33.3	97	10	US-09-864-761-43414	Sequence 43414, A
26	5	33.3	97	12	US-10-036-342-16	Sequence 16, Appl
27	5	33.3	97	12	US-10-052-586-468	Sequence 468, App
28	5	33.3	111	10	US-09-764-898-295	Sequence 295, App
29	5	33.3	133	10	US-09-867-550-372	Sequence 372, App
30	5	33.3	140	10	US-09-864-761-43849	Sequence 43849, A
31	5	33.3	155	10	US-09-734-569-118	Sequence 118, App
32	5	33.3	180	10	US-09-771-730-131	Sequence 131, App
33	5	33.3	184	10	US-09-764-864-827	Sequence 827, App
34	5	33.3	190	9	US-09-895-913A-132	Sequence 132, App
35	5	33.3	193	10	US-09-941-936A-2	Sequence 2, Appl
36	5	33.3	202	10	US-09-811-284-151	Sequence 151, App
37	5	33.3	203	10	US-09-912-020-338	Sequence 338, App
38	5	33.3	215	10	US-09-924-256A-36	Sequence 36, Appl
39	5	33.3	216	10	US-09-771-730-50	Sequence 50, Appl
40	5	33.3	216	10	US-09-771-730-143	Sequence 143, App
41	5	33.3	216	10	US-09-771-730-146	Sequence 146, App
42	5	33.3	216	10	US-09-747-155-427	Sequence 427, App
43	5	33.3	218	12	US-10-011-033-2	Sequence 2, Appl
44	5	33.3	218	12	US-10-011-033-6	Sequence 6, Appl
45	5	33.3	218	12	US-10-011-033-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-893-615-2
Sequence 2, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Flischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Slinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elinaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-893-615-2

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHMRHRIPQLAAGR 15
Db 1 WHMRHRIPQLAAGR 15

RESULT 2
US-09-893-615-9
Sequence 9, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995, 0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-893-615-9

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHMRHRIPQLAAGR 15
Db 3 WHMRHRIPQLAAGR 17

RESULT 3
US-09-893-615-17
Sequence 17, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995, 0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-893-615-17

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WHMRHRIPQLAAGR 15
Db 3 WHMRHRIPQLAAGR 17

RESULT 4
US-09-893-615-19
Sequence 19, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995, 0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-893-615-19
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-893-615-19

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHMRRIPQLAAGR 15
|||||
Db 3 WHMRRIPQLAAGR 17

RESULT 5
US-09-893-615-41
Sequence 41, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-893-615-41

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHMRRIPQLAAGR 15
|||||
Db 3 WHMRRIPQLAAGR 17

RESULT 6
US-09-893-615-57
Sequence 57, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-893-615-57

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WHMRRIPQLAAGR 15
|||||
Db 3 WHMRRIPQLAAGR 17

RESULT 7
US-09-893-615-15
Sequence 15, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOPEPTIC ACID OF GRAM
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/893,615
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elinaudi, Carol P.
REGISTRATION NUMBER: 37,220
REFERENCE/DOCKET NUMBER: 04995-0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-893-615-15
Query Match 93.3%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 HMRHRIPLQLAGR 15
DB 4 HMRHRIPLQLAGR 17
RESULT 8
US-09-893-737-142
Sequence 142, Application US/09893737
Patent No. US20020110853A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 142
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-893-737-142
Query Match 40.0%; Score 6; DB 10; Length 228;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 QLAAGR 15
DB 200 QLAAGR 205

RESULT 9
US-09-815-242-12356
Sequence 12356, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12356
LENGTH: 290
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12356
Query Match 40.0%; Score 6; DB 10; Length 290;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 7 IPLQLA 12
DB 241 IPLQLA 246
RESULT 10
US-09-815-242-5746
Sequence 5746, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5746
LENGTH: 411
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5746

Query Match 40.0%; Score 6; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 IPLOLA 12
|||||
DB 371 IPLOLA 376

RESULT 11
US-09-815-242-11923
Sequence 11923, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zysek, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11923
LENGTH: 585
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11923

Query Match 40.0%; Score 6; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 IOLAAG 14
|||||

DB 142 IOLAAG 147

RESULT 12
US-09-891-762-2
Sequence 2, Application US/09891762
Patent No. US20020156253A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 48000 AND 52920, NOVEL HUMAN CALCIUM
CHANNELS AND USES THEREOF
FILE REFERENCE: MNT-170
CURRENT APPLICATION NUMBER: US/09/891,762
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,176
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 741
TYPE: PRT
ORGANISM: Homo sapiens
US-09-891-762-2

Query Match 40.0%; Score 6; DB 9; Length 741;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PLOLA 13
|||||
DB 344 PLOLA 349

RESULT 13
US-09-982-172-16
Sequence 16, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBIO
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 29
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-16

Query Match 33.3%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 LAAGR 15
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DB 25 LAAGR 29

RESULT 14
US-09-982-172-215
Sequence 215, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBIO
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE

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; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-215

Query Match          33.3%; Score 5; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LAAGR 15
   11111
DB 25 LAAGR 29

RESULT 15
US-09-864-761-45173
; Sequence 45173; Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45173
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL157392.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.46
; OTHER INFORMATION: EST_HUMAN HIT: BF224452.1, EVALU6 7.00e-17
; OTHER INFORMATION: SWISSPROT HIT: P25109, EVALU6 8.30e+00
US-09-864-761-45173

Query Match          33.3%; Score 5; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IPLQL 11
   11111
DB 24 IPLQL 28
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Search completed: November 27, 2002, 07:32:52
Job time: 1.38996 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 04:43:17 : Search time 1454.52 Seconds

(without alignments)
7383.171 Million cell updates/sec

Title: US-09-893-615-86

Perfect score: 369

Sequence: 1 GAAGTGAATGCTGCTGAGTCTC...CCATCCTCCTCCTCA 369

Scoring table: OLIGO_NUC

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Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: gb.htg:*

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12: gb.sy:*

13: gb.un:*

14: gb.vl:*

15: em.ba:*

16: em.fun:*

17: em.hum:*

18: em.in:*

19: em.mu:*

20: em.om:*

21: em.or:*

22: em.ov:*

23: em.pat:*

24: em.ph:*

25: em.pl:*

26: em.ro:*

27: em.sts:*

28: em.un:*

29: em.vl:*

30: em.htg.hum:*

31: em.htg.in:*

32: em.htg.inv:*

33: em.htg.other:*

34: em.htg.mus:*

35: em.htg.pln:*

36: em.htg.tod:*

37: em.htg.vrt:*

38: em.sy:*

39: em.htgo.hum:*

40: em.htgo.mus:*

41: em.htgo.other:*

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	145	39.3	366	10 AF178591	AF178591 Mus muscu
3	145	39.3	366	10 AF178595	AF178595 Mus muscu
4	145	39.3	366	10 AF178596	AF178596 Mus muscu
5	144	39.0	312	10 MUSIGHACT	M34735 Mouse Ig H-
6	144	39.0	337	10 MMU5546	U55546 Mus musculu
7	144	39.0	357	10 MUSIGHXT	M21470 Mouse Ig ac
8	144	39.0	360	10 MUSIGHVRA	D50376 Mouse mRNA
9	144	39.0	474	10 MUSIGHCLT	M20829 Mouse IgG2a
10	144	39.0	661	10 AF064446	AF064446 Mus muscu
11	143	38.8	300	10 MMIGH1	X59104 M. musculus
12	143	38.8	663	10 AF064445	AF064445 Mus muscu
13	141	38.2	299	10 AF072804	AF072804 Mus muscu
14	138	37.4	360	10 MDIGHVAQ	Z22080 M. domestlicu
15	132	35.8	242	10 AF023222	AF023222 Mus muscu
16	132	35.8	330	6 AR108680	AR108680 Sequence
17	131	35.5	247	10 AF023223	AF023223 Mus muscu
18	130	35.2	345	6 AR108686	AR108686 Sequence
19	116	31.4	315	10 MMU55466	U55466 Mus musculu
20	112	30.4	353	10 AF321939	AF321939 Mus muscu
21	107	29.0	421	10 MMIGHIHW	X78107 M. musculus
22	98	26.6	375	10 S63182	S63182 Ig VH-antli-
23	93	25.2	301	10 MMU55465	U55465 Mus musculu
24	93	25.2	337	10 MMU55545	U55545 Mus musculu
25	87	23.6	348	10 AF468835	AF468835 Mus muscu
26	86	22.3	360	10 MDIGHVAR	Z22082 M. domestlicu
27	84	22.8	332	10 MMU55520	U55520 Mus musculu
28	80	21.7	357	6 I73737	I73737 Sequence 1
29	80	21.7	1797	6 I73745	I73745 Sequence 17
30	76	20.6	304	10 S40679	S40679 AbJ heavy c
31	76	20.6	305	10 AF072799	AF072799 Mus muscu
32	76	20.6	351	10 AF006586	AF006586 Mus muscu
33	76	20.6	475	10 MUSIGHAAAC	M60022 Mouse Ig he
34	76	20.6	663	10 AF064443	AF064443 Mus muscu
35	76	20.6	185591	2 AC073561	AC073561 Mus muscu
36	74	20.1	360	10 AF006574	AF006574 Mus muscu
37	72	19.5	333	10 MMU55544	U55544 Mus musculu
38	69	18.7	322	10 AF118987	AF118987 Mus muscu
39	69	18.7	663	10 AF064444	AF064444 Mus muscu
40	68	18.4	231	10 S60842	S60842 Ab2 heavy c
41	68	18.4	351	10 AF030229	AF030229 Mus muscu
42	64	17.3	366	10 MUSIGH339A	L30140 Mus Musculu
43	63	17.1	357	10 MUSIGHUHF	M59948 Mouse Ig ac
44	63	17.1	360	10 MDIGHVAT	Z22093 M. domestlicu
45	61	16.5	251	10 AF133813	AF133813 Mus muscu

ALIGNMENTS

RESULT 1

AF118969 316 bp mRNA linear ROD 22-APR-1999

LOCUS Mus musculus AE0203 Immunoglobulin heavy chain VH10-JH4 region

DEFINITION mRNA, partial cds.

ACCESSION AF118969

VERSION AF118969.1 GI:4633367

KEYWORDS

SOURCE Mus musculus.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 316)

Seidl,R.J., Wilshtre,J.A., Mackenzie,J.D., Kantor,A.B., Herzenberg,L.A. and Herzenberg,L.A.

TITLE Predominant VH genes expressed in innate antibodies are associated with distinctive antigen-binding sites
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2262-2267 (1999)
MEDLINE 99162992
PUBMED 10051629
REFERENCE 2 (bases 1 to 316)
AUTHORS Seidl, K.J., Wlshire, J.A., Mackenzie, J.D., Herzenberg, L.A., Herzenberg, L.A. and Kantor, A.B.
JOURNAL Submitted (08-JUN-1999) Department of Genetics, Stanford University School of Medicine, Beckman Center, B007, Stanford, CA 94305-5125, USA

FEATURES
source
Location/Qualifiers
1. 316
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="AE0203"
<1..316
/codon_start=-2
/product="immunoglobulin heavy chain VH10-JH4 region"
/protein_id="A026740.1"
/db_xref="GI:4633368"
/translation="GGLVOPKSLKSCAASGFTNTYAMNVRQAPGKLEWVARISKSNNVATRYADSVKDRFTISRDSSQSMYTLQNNLKTEDTAMTCVRCSTIGNNAMD YWC"

CDS
BASE COUNT 95 a 65 c 79 g 77 t
ORIGIN

Query Match 39.3%; Score 145; DB 10; Length 316;
Best Local Similarity 99.5%; Pred. No. 3.5e-77;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 TGGGTCGCCAGGCTCCAGGAAGGGTTTGGAAATGGTGTGCTCCCATTAAGATAAAAGT 165
|||||
Db 83 TGGGTCGCCAGGCTCCAGGAAGGGTTTGGAAATGGTGTGCTCCCATTAAGATAAAAGT 142
|||||

QY 166 AATAATTATGCAACATTTTATGCCGATTCACTGAAAGACAGCTTCACCATCTCCAGAGAT 225
|||||
Db 143 AATAATTATGCAACATTTTATGCCGATTCACTGAAAGACAGCTTCACCATCTCCAGAGAT 202
|||||

QY 226 GATTACACAAGCATGCTCTATCTCAATGAACACTTGAACACTGAGGACACAGCCATG 285
|||||
Db 203 GATTACACAAGCATGCTCTATCTCAATGAACACTTGAACACTGAGGACACAGCCATG 262
|||||

QY 286 TATTACTGTGTGAGAC 301
|||||
Db 263 TATTACTGTGTGAGAC 278
|||||

RESULT 2
AF178591 366 bp mRNA linear ROD 22-MAY-2000
LOCUS Mus musculus 23-7 immunoglobulin heavy chain variable region mRNA,
DEFINITION partial cds.
ACCESSION AF178591
VERSION AF178591.1 GI:5853171
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 366)
AUTHORS Puterman, C., Deocharan, B. and Diamond, B.
TITLE Molecular analysis of the autoantibody response in peptide-induced autoimmunity
JOURNAL J. Immunol. 164 (5), 2542-2549 (2000)
MEDLINE 20143847
PUBMED 10679092
REFERENCE 2 (bases 1 to 366)
AUTHORS Puterman, C., Deocharan, B. and Diamond, B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein

FEATURES
source
Location/Qualifiers
1. 366
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="23-7"
/cell_type="hybridoma"
/note="from peptide-immunized mouse"
<1..366
/note="anti-peptide antibody"
/codon_start=-1
/product="immunoglobulin heavy chain variable region"
/protein_id="A054347.1"
/db_xref="GI:5853172"
/translation="DVKVVEGGGLVOPKSLKSCAASGFTNTYAMNVRQAPGKLEWVARIRSKSNVATRYADSVKDRFTISRDSSQSMYTLQNNLKTEDTAMTCVRRSGSRKYVDVWGAGTYTVSS"

CDS
BASE COUNT 101 a 84 c 95 g 86 t
ORIGIN

Query Match 39.3%; Score 145; DB 10; Length 366;
Best Local Similarity 99.5%; Pred. No. 3.6e-77;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 TGGGTCGCCAGGCTCCAGGAAGGGTTTGGAAATGGTGTGCTCCCATTAAGATAAAAGT 165
|||||
Db 106 TGGGTCGCCAGGCTCCAGGAAGGGTTTGGAAATGGTGTGCTCCCATTAAGATAAAAGT 165
|||||

QY 166 AATAATTATGCAACATTTTATGCCGATTCACTGAAAGACAGCTTCACCATCTCCAGAGAT 225
|||||
Db 166 AATAATTATGCAACATTTTATGCCGATTCACTGAAAGACAGCTTCACCATCTCCAGAGAT 225
|||||

QY 226 GATTACACAAGCATGCTCTATCTCAATGAACACTTGAACACTGAGGACACAGCCATG 285
|||||
Db 226 GATTACACAAGCATGCTCTATCTCAATGAACACTTGAACACTGAGGACACAGCCATG 285
|||||

QY 286 TATTACTGTGTGAGAC 301
|||||
Db 286 TATTACTGTGTGAGAC 301
|||||

RESULT 3
AF178595 366 bp mRNA linear ROD 22-MAY-2000
LOCUS Mus musculus 8-3 immunoglobulin heavy chain variable region mRNA,
DEFINITION partial cds.
ACCESSION AF178595
VERSION AF178595.1 GI:5853179
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 366)
AUTHORS Puterman, C., Deocharan, B. and Diamond, B.
TITLE Molecular analysis of the autoantibody response in peptide-induced autoimmunity
JOURNAL J. Immunol. 164 (5), 2542-2549 (2000)
MEDLINE 20143847
PUBMED 10679092
REFERENCE 2 (bases 1 to 366)
AUTHORS Puterman, C., Deocharan, B. and Diamond, B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
FEATURES
source
Location/Qualifiers
1. 366
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="8-3"
/cell_type="hybridoma"

	CDS	/note="from peptide-immunized mouse"
		<1..>366
		/note="anti-peptide antibody"
		/codon_start=1
		/product="Immunoglobulin heavy chain variable region"
		/protein_id="AADS4351.1"
		/db_xref="GI:5851180"
		/translation="DVRVSVSGGLVPKSLKLSCAASGTFENTYAMNWRQAPGKG
		LEWAIIRSRSSNNATAYADSVSKDRFTISRDSQSMTYLQNNNKETBDTMYCYVRHG
		LGRWYEDVMAGTTVVSS"
BASE COUNT	99 a 82 c 99 g 86 t	
ORIGIN		
Query Match	39.3%	Score 145; DB 10; Length 366;
Best Local Similarity	99.5%	Pred. No. 3.6e-77;
Matches 195; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;
QY 106 TGGGTCCGCCAGGCCTCCAGAAAGGGTTTGGAATGGTGGTCGCATTAAGAATAAAGT	165	
Dd 106 TGGGTCCGCCAGGCCTCCAGAAAGGGTTTGGAATGGTGGTCGCATTAAGAATAAAGT	165	
QY 166 AATATTATGCAACATTATATGCGCATTCAGTGAAGACAGGTTACCATCTCCAGAGAT	225	
Dd 166 AATATTATGCAACATTATATGCGCATTCAGTGAAGACAGGTTACCATCTCCAGAGAT	225	
QY 226 GATTTCACAACCATGCTTATATCGCAATGAACAACCTGAAAACAGTAGAGACACAGCATT	285	
Dd 226 GATTTCACAACCATGCTTATATCGCAATGAACAACCTGAAAACAGTAGAGACACAGCATT	285	
QY 286 TATTACTGTGTGAGAC 301		
Dd 286 TATTACTGTGTGAGAC 301		

RESULT	4
LOCUS	AF178596
DEFINITION	AF178596 366 bp mRNA linear ROD 22-MAY-2000 Mus musculus 39-9 immunoglobulin heavy chain variable region mRNA,
ACCESSION	AF178596
VERSION	AF178596.1 GI:5853181
KEYWORDS	
SOURCE	Mus musculus.
ORGANISM	Mus musculus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 366) Puterman,C., Deocharan,B. and Diamond,B. Molecular analysis of the autoantibody response in peptide-induced autoimmunity J. Immunol. 164 (5), 2542-2549 (2000)
JOURNAL	J. Immunol. 164 (5), 2542-2549 (2000)
MEDLINE	20143847
PUBMED	10679092
REFERENCE	2 (bases 1 to 366) Puterman,C., Deocharan,B. and Diamond,B. Direct Submission Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
AUTHORS	
TITLE	Location/Qualifiers
JOURNAL	1..366
FEATURES	/organism="Mus musculus" /strain="BALB/c" /db_xref="taxon:10090" /cell_line="39-9" /cell_type="hybridoma" /note="from peptide-immunized mouse" <1..>366 /note="anti-peptide antibody" /codon_start=1 /product="immunoglobulin heavy chain variable region" /protein_id="AA054352.1" /db_xref="GI:5853182" /translation="DVKVVESGGGLVPGKSLIKLSCAASGFETFTYAMNVRQAPGKG
CDS	

BASE COUNT	100 a	82 c	98 g	86 t	
ORIGIN					LEWVARIRSKSNNAATFYVADSVKDRFLISDDSGSMUYLOMNLNKTEDTAMMYCVRRIG
Query Match					LGRWYEDWAGACTTIVSS*
Best Local Similarity					39.3%; Score 145; DB 10; Length 366;
Matches 195; Conservative					99.5%; Pred. No. 3,66-77;
					0; Mismatches 1; Indels 0; Gaps 0;
QY	106	TGGTGCCGCCAGGCTCCAGAAAGGGTTTGGAAATGGGTGCTCGCATAGAAGATAAAAGT	165		
Db	106	TGGTGCCGCCAGGCTCCAGAAAGGGTTTGGAAATGGGTGCTCGCATAGAAGATAAAAGT	165		
QY	166	AATATTATGCAACATTATATGCGATTCAGTGAAGAAGACAGGTCACCATCTCCAGAGAT	225		
Db	166	AATATTATGCAACATTATATGCGATTCAGTGAAGAAGACAGGTCACCATCTCCAGAGAT	225		
QY	226	GATTTCACAAAGCATGCTCTATCTGCAANTGAACAATTGAAAACCTGAGGACACAGCCATG	285		
Db	226	GATTTCACAAAGCATGCTCTATCTGCAANTGAACAATTGAAAACCTGAGGACACAGCCATG	285		
QY	286	TATTACTGTGTGAGAC	301		
Db	286	TATTACTGTGTGAGAC	301		
RESULT 5					
MUSIGHACT					
LOCUS					
DEFINITION	MUSIGHACT	312 bp	mrna	linear	ROD 27-Apr-1993
ACCESSION	Mouse_Ig_H-chain mRNA VDJ-region, partial cds.				
VERSION	M34735				
KEYWORDS	M34735.1	GI:194746			
	D-region; J-region; V-region; immunoglobulin heavy chain; processed				

SOURCE	Mouse (strain BALB/c) adult spleen anti-HA hybridoma H220-3, CDNA to mRNA.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.					
AUTHORS	1 (bases 1 to 312) Clarke,S.H., Strudel,L.M., Kavalier,J., Schwartz,D., Gerhard,W.U. and Weigert,M.G.					
TITLE	V region gene usage and somatic mutation in the primary and secondary responses to influenza virus hemagglutinin					
JOURNAL	J. Immunol. 144 (7), 2795-2801 (1990)					
MEDLINE	90203619					
PUBMED	2108213					
FEATURES						
SOURCE	Location/Qualifiers 1..312 /organism="Mus musculus" /db_xref="taxon:10090" <1..>312 /note="Ig H-chain VDJ-region" /codon_start=2 /protein_id="AAA8022.1" /db_xref="GI:194747" /translation="(PKGSLKLSCAAGFTNTAMNVROAPGKLEIMVARIRSKNN YARYAVSDVKDRFIIISRDQSMLYLDNMNLKTEDTAMYCYBRAAYVAMDYWGCGTSV TV") BASE COUNT 95 a 69 c 73 g 75 t					
ORIGIN						
Query Match	39.0%; Score 144; DB 10; Length 312;					
Best Local Similarity	99.5%; Pred. No. 1.5e-76;					
Matches 194:	Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
OY	166	TGGGTCCGCCAGGCTCCAGAAAGGTTTGAATGGTGTCGCATTAAGAATAAAAGT	165			
Dd	68	TGGGTCCGCCAGGCTCCAGAAAGGTTTGAATGGTGTCGCATTAAGAATAAAAGT	127			
OY	166	AATTAATTATGCAACATTTTATATGCCGATTCAAGTGAAGACAGCTTACCATCTCCAGAGAT	225			
Dd	128	AATTAATTATGCAACATTTTATATGCCGATTCAAGTGAAGACAGCTTACCATCTCCAGAGAT	187			

QY 226 GATTACAAAGCATGCTCTATCTGCAATGAACAACCTTGAAAGCTGAGACACAGCCATG 285
|||||
Db 188 GATTACAAAGCATGCTCTATCTGCAATGAACAACCTTGAAAGCTGAGACACAGCCATG 247
|||||
QY 286 TATTACTGTGTGAGA 300
|||||
Db 248 TATTACTGTGTGAGA 262
|||||

RESULT 6
MMUS5546 337 bp mRNA linear ROD 14-SEP-2001
LOCUS Mus musculus anti-DNA immunoglobulin heavy chain IgG mRNA, antibody
DEFINITION 452p.108, partial cds.
ACCESSION U55546
VERSION U55546.1 GI:1872412
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 337)
AUTHORS Krishnan,M.R., Jou,N.T. and Marion,T.N.
TITLE Correlation between the amino acid position of arginine in VH-CDR3
and specificity for native DNA among autoimmune antibodies
JOURNAL J. Immunol. 157 (6), 2430-2439 (1996)
MEDLINE 96399071
PUBMED 8805642
REFERENCE 2 (bases 1 to 337)
AUTHORS Marion,T.N.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1996) Dept. of Microbiology/Immunology,
University of Tennessee, 858 Madison Ave., Memphis, TN 38163, USA
FEATURES
source location/Qualifiers.
1..337
/organism="Mus musculus"
/strain="(NZB x NZW) F1"
/db_xref="taxon:10090"
/cell_line="452p.108"
/cell_type="hybridoma"
/note="mouse number 452; clonally related to hybridomas
452p.119 and 452p.84"
<1..>337
/codon_start=2
/product="anti-DNA immunoglobulin heavy chain IgG"
/protein_id="AAB49145.1"
/db_xref="GI:1872413"
/translation="VQREGSLKUSCAAGSFSPNTAMNWRQAPGKLEWVARIRSKS
NNATYVADSVKDRFTISRDSOSMLYIQNNLKTEDTAMYCVREGSYSLYWXDVW
GAGTIVVSS"

V_region
BASE COUNT 96 a 75 c 82 g 80 t 4 others
ORIGIN
Query Match 39.0%; Score 144; DB 10; Length 337;
Best Local Similarity 99.5%; Pred. No. 1.5e-76;
Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 TGGGTCCGCCAGGCTCCAGGAAGGTTTGAATGGGTTGCTCGCATTAAGATAAAAGT 165
|||||
Db 74 TGGGTCCGCCAGGCTCCAGGAAGGTTTGAATGGGTTGCTCGCATTAAGATAAAAGT 133
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QY 166 AATAATTATGACATTTATATGCGGATTCAGTGAAGACAGGTCACCATCCAGAGAT 225
|||||
Db 134 AATAATTATGACATTTATATGCGGATTCAGTGAAGACAGGTCACCATCCAGAGAT 193
|||||

QY 226 GATTACAAAGCATGCTCTATCTGCAATGAACAACCTTGAAAGCTGAGACACAGCCATG 285
|||||
Db 194 GATTACAAAGCATGCTCTATCTGCAATGAACAACCTTGAAAGCTGAGACACAGCCATG 253
|||||

QY 286 TATTACTGTGTGAGA 300
|||||

Db 254 TATTACTGTGTGAGA 268
|||||

RESULT 7
MUSIGHXT 357 bp mRNA linear ROD 27-APR-1993
LOCUS Mouse Ig active H chain mRNA V-region, MRL-DNA4.
DEFINITION M21470.1 GI:196220
ACCESSION M21470.1
VERSION M21470.1 GI:196220
KEYWORDS C-region; V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse spleen hybridoma (haplotype 1gh) CDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 357)
AUTHORS Kofler,R.
TITLE A new murine Ig VH gene family
JOURNAL J. Immunol. 140 (11), 4031-4034 (1988)
MEDLINE 88229103
PUBMED 3131427
FEATURES
source location/Qualifiers
1..357
/organism="Mus musculus"
/db_xref="taxon:10090"
1..>357
/note="Ig heavy chain MRL-DNA4 V-region precursor"
/codon_start=1
/protein_id="AAA38634.1"
/db_xref="GI:196221"
/translation="MLGLKWFVFVFCVGHCHVCLVETGGGLVQPKGSLKUSCPAS
GFSPNTAMNWRQAPGKLEWVARIRSKSNVATYVADSVKDRFTISRDSOSMLYL
QNNLKTEDTAMYCVR"
1..57
/note="Ig heavy chain V-region signal peptide"
58..>357
mat_peptide
BASE COUNT 99 a 65 c 92 g 101 t
ORIGIN
Query Match 39.0%; Score 144; DB 10; Length 357;
Best Local Similarity 99.5%; Pred. No. 1.5e-76;
Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 TGGGTCCGCCAGGCTCCAGGAAGGTTTGAATGGGTTGCTCGCATTAAGATAAAAGT 165
|||||
Db 163 TGGGTCCGCCAGGCTCCAGGAAGGTTTGAATGGGTTGCTCGCATTAAGATAAAAGT 222
|||||

QY 166 AATAATTATGACATTTATATGCGGATTCAGTGAAGACAGGTTACCATCTCCAGAGAT 225
|||||
Db 223 AATAATTATGACATTTATATGCGGATTCAGTGAAGACAGGTTACCATCTCCAGAGAT 282
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QY 226 GATTACAAAGCATGCTCTATCTGCAATGAACAACCTTGAAAGCTGAGACACAGCCATG 285
|||||
Db 283 GATTACAAAGCATGCTCTATCTGCAATGAACAACCTTGAAAGCTGAGACACAGCCATG 342
|||||

QY 286 TATTACTGTGTGAGA 300
|||||
Db 343 TATTACTGTGTGAGA 357
|||||

RESULT 8
MUSHCVRA 360 bp mRNA linear ROD 26-MAR-2002
LOCUS Mouse mRNA for immunoglobulin heavy chain variable region, partial
DEFINITION sequence.
ACCESSION D50376
VERSION D50376.1 GI:804892
KEYWORDS immunoglobulin heavy chain variable region.
SOURCE Mus musculus (strain BALB/c) hybridoma producing anti-human
procollagenase antibody, cell-line K166 CDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 360)
 AUTHORS Yamanaoka, H. I., Kiril, Y. and Ohmoto, H.
 TITLE An improved phage display antibody cloning system using newly
 designed PCR primers optimized for Pfu DNA polymerase
 JOURNAL J. Biochem. 117 (6), 1218-1227 (1995)
 MEDLINE 96104992
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Yamanaoka, H.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-1995) Hachiro Yamanaoka, New Drug Research
 Laboratories, Kanebo Ltd.; 5-90 Tomobuchi-cho 1-chome,
 Miyakojima-ku, Osaka, Osaka 534, Japan (Tel:06-921-1281(ex.3609),
 Fax:06-923-3381)
 COMMENT Submitted (21-Apr-1995) to DDBJ by:
 Hachiro Yamanaoka
 New Drug Research Laboratories
 Kanebo Ltd.
 1-5-90 Tomobuchi-cho Miyakojima-ku
 Osaka, Osaka 534
 Japan
 Phone: 06-921-1281 x3609
 Fax: 06-923-3381.

FEATURES
 source
 1..360
 /organism="Mus musculus"
 /strain="BALB/c"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 /cell_line="K1E6"
 /cell_type="hybridoma producing anti-human procollagenase
 antibody"
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 /product="immunoglobulin heavy chain variable region"
 /db_xref="IMG/Link:DS0376"
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 /note="PCR primer"
 complement(339..360)
 /note="PCR primer"

BASE COUNT 104 a 77 c 95 g 84 t
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Query Match 39.0%; Score 144; DB 10; Length 360;
 Best Local Similarity 99.5%; Pred. No. 1.5e-76;
 Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 TGGGTCGCCAGGCTCCAGAAAGGTTGGATGGGTTGCTGCATTAAGATAAAGT 165
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 DB 109 TGGGTCGCCAGGCTCCAGAAAGGTTGGATGGGTTGCTGCATTAAGATAAAGT 168
 |||||||

QY 166 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACATCCAGAGAT 225
 |||||||
 DB 169 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACATCCAGAGAT 228
 |||||||

QY 226 GATTCAAAAGCATGCTATCTGCAAAATGAACACTTGAAACTGAGGACAGGCATG 285
 |||||||
 DB 229 GATTCAAAAGCATGCTATCTGCAAAATGAACACTTGAAACTGAGGACAGGCATG 288
 |||||||

QY 286 TATTACTGTGTGAGA 300
 |||||||
 DB 289 TATTACTGTGTGAGA 303
 |||||||

RESULT 9
 MUSIGKCLT 474 bp mRNA linear ROD 27-APR-1993
 LOCUS anti-DNA autoantibody.
 DEFINITION anti-DNA autoantibody.
 ACCESSION M20829.1 GI:196951
 VERSION M20829.1
 KEYWORDS V-region; autoantibody; immunoglobulin heavy chain.
 SOURCE Mouse (strain MRL/Mp -lpr/lpr) spleen hybridoma cell line MRL-DNA4,
 cDNA to mRNA.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 474)
 AUTHORS Kofler, R., Strohal, R., Balderas, R. S., Johnson, M. E., Noonan, D. J.,
 Duchsosal, M. A., Dixon, F. J. and Theofilopoulos, A. N.
 TITLE Immunoglobulin kappa light chain variable region gene complex
 organization and immunoglobulin genes encoding anti-DNA
 autoantibodies in lupus mice
 JOURNAL J. Clin. Invest. 82 (3), 852-860 (1988)
 MEDLINE 88331394
 PUBMED 3138286
 COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
 R. Kofler 28-JUL-1988.

FEATURES
 source
 1..474
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 1..>474
 /product="IgG2ak mRNA"
 52..>474
 /note="IgG2ak heavy chain precursor"
 /codon_start=1
 /protein_id="AAA38849.1"
 /db_xref="GI:196952"
 /translation="MLGLKWFVFPVQGVHCEVQVETGGGLVQPKSLKSCPAS
 GSPFNMANMYRQAPKGLKLEVAIRSRNNRYADSVDRFTISRDSSMLYL
 QNNLTKEDTAMTCVDRDANNSAMFAIWGGLTVSA"
 52..>474
 /product="Ig heavy chain"
 52..111
 /note="Ig heavy chain signal peptide"

BASE COUNT 120 a 95 c 119 g 140 t
 ORIGIN Chromosome 12.

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 Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 TGGGTCGCCAGGCTCCAGAAAGGTTGGATGGGTTGCTGCATTAAGATAAAGT 165
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 DB 214 TGGGTCGCCAGGCTCCAGAAAGGTTGGATGGGTTGCTGCATTAAGATAAAGT 273
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QY 166 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACATCCAGAGAT 225
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 DB 274 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACATCCAGAGAT 333
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QY 226 GATTCAAAAGCATGCTATCTGCAAAATGAACACTTGAAACTGAGGACAGGCATG 285
 |||||||
 DB 334 GATTCAAAAGCATGCTATCTGCAAAATGAACACTTGAAACTGAGGACAGGCATG 393
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QY 286 TATTACTGTGTGAGA 300
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 DB 394 TATTACTGTGTGAGA 408
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RESULT 10
 AF064446 661 bp DNA linear ROD 04-JAN-2000
 LOCUS AF064446
 DEFINITION gene, Vh10.3a allele, partial cds.
 ACCESSION AF064446
 VERSION AF064446.1 GI:3420274
 KEYWORDS
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 661)
 REFERENCE Whitcomb, E. A., Haines, B. B., Parmelee, A. P., Pearlman, A. M. and
 Brodeur, P. H.
 TITLE Germ-line structure and differential utilization of Igba and Ighb
 Vh10 genes
 JOURNAL J. Immunol. 162 (3), 1541-1550 (1999)

MEDLINE 99138634
 PUBMED 9973411
 REFERENCE 2 (bases 1 to 661)
 AUTHORS Whitcomb,E.A., Haines,B.B., Parmelee,A.P., Perlman,A.M. and Brodeur,P.H.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAY-1998) Pathology, Tufts University, 136 Harrison Ave, Boston, MA 02111, USA
 FEATURES
 source location/Qualifiers
 1..661
 /organism="Mus musculus"
 /strain="BALB/cBYJ"
 /db_xref="taxon:10090"
 /chromosome="12"
 /tissue_type="liver"
 /germline
 56..>661
 /gene="Vh10.3"
 /allele="Vh10.3a"
 56..63
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 82..87
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 join(<176..221,310..>622)
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 /codon_start=1
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 sig_peptide 176..220
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 <176..221
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 join(221,310..>622)
 /gene="Vh10.3"
 310..622
 /gene="Vh10.3"
 /note="variable region exon"
 623..661
 /gene="Vh10.3"
 /note="recombination signal sequence RSS"
 BASE COUNT 186 a 129 c 159 g 187 t
 ORIGIN
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 Best Local Similarity 99.5%; Pred. No. 1.5e-76;
 Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
 MMIGH1 300 bp mRNA linear ROD 05-DEC-1998
 LOCUS M.musculus mRNA (L1-5A1) for Igh heavy chain V region.
 DEFINITION X59104
 ACCESSION X59104.1 GI:51920
 VERSION 1g heavy chain; 1g variable region; immunoglobulin; rearranged.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 300)
 AUTHORS Kavalier,J.
 TITLE Direct Submission
 JOURNAL Submitted (15-APR-1991) J. Kavalier, Wistar Institute, 3601 Spruce Street, Philadelphia PA 19104, USA
 REFERENCE 2 (bases 1 to 300)
 AUTHORS Kavalier,J.
 JOURNAL Unpublished
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 source location/Qualifiers
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 /organism="Mus musculus"
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 /tissue_type="hybridoma"
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 /partial
 /codon_start=1
 /product="Igh heavy chain V region"
 /protein_id="CAA1850.1"
 /db_xref="GI:3980166"
 /translation="MYOPKCSLKLLKLSAASGFPTNANMVRQAPGKGLEWVARIR SKSNVATYADSVKRFETISRDQSMLYLOMNNIKTEDTAMYYCVSDFSHMGQ"
 CDS
 BASE COUNT 91 a 67 c 69 g 73 t
 ORIGIN
 Query Match 38.8%; Score 143; DB 10; Length 300;
 Best Local Similarity 99.5%; Pred. No. 6e-76;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TITLE Germline structure and differential utilization of Igna and Iggh
VH10 genes
JOURNAL J. Immunol. 162 (3), 1541-1550 (1999)
MEDLINE 99138834
PUBMED 9973411
REFERENCE 2 (bases 1 to 663)
AUTHORS Whitcomb,E.A., Haines,B.B., Parmelee,A.P., Perlman,A.M. and Brodeur,P.H.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1998) Pathology, Tufts University, 136 Harrison Ave, Boston, MA 02111, USA
FEATURES
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/chromosome="12"
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/allele="VH10.2a"
57..64
/gene="VH10.2"
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83..88
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/protein_id="AAC31897.1"
/db_xref="GI:3420273"
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OMNKLKTEPTARYCVS"
178..222
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/note="leader exon"
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/gene="VH10.2"
312..624
/gene="VH10.2"
/note="variable region exon"
625..663
/gene="VH10.2"
/note="recombination signal sequence RSS"
BASE COUNT 182 a 129 c 159 g 193 t
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Best Local Similarity 99.5%; Pred. No. 6,1e-76;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 106 TGGGTCGGCCAGGCTCCAGGAAGGGTTTGGAATGGCTTCGCATTAAGAGTAAAGT 165
|||||
DB 428 TGGGTCGGCCAGGCTCCAGGAAGGGTTTGGAATGGCTTCGCATTAAGAGTAAAGT 487
OY 166 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGAT 225
|||||
DB 488 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGAT 547
OY 226 GATTCAACAAAGCATGCTCTATCTGCAAAATGAACAACCTTGAAGCTGAGACACAGCATG 285
|||||
DB 548 GATTCAACAAAGCATGCTCTATCTGCAAAATGAACAACCTTGAAGCTGAGACACAGCATG 607
OY 286 TATTACTGTGTGAG 299
|||||

DB 608 TATTACTGTGTGAG 621
RESULT 13
AF072804 299 bp mRNA linear ROD 13-JUL-1998
LOCUS Mus musculus B.143 anti-DNA immunoglobulin IgM heavy chain variable
DEFINITION region mRNA, partial cds.
ACCESSION AF072804
VERSION AF072804.1 GI:3309238
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 299)
AUTHORS Krishnan,M.R. and Marlon,T.N.
TITLE Comparison of the frequencies of arginines in heavy-chain CDR3 of antibodies expressed in the primary B cell repertoires of autoimmune-prone and normal mice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 299)
AUTHORS Krishnan,M.R. and Marlon,T.N.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1998) Microbiology and Immunology, The University of Tennessee, Memphis, 858 Madison Ave., Memphis, TN 38163, USA
FEATURES
source 1..299
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/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="B.143"
/cell_type="B cell hybridoma generated from LPS-stimulated spleen cells"
<1..>299
/codon_start=3
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/db_xref="GI:3309238"
/translation="KGSLLSCASAGFTFNTAMNVROAPGKLEVARIRSRNNY
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BASE COUNT 90 a 66 c 67 g 76 t
ORIGIN
Query Match 38.2%; Score 141; DB 10; Length 299;
Best Local Similarity 99.5%; Pred. No. 1e-74;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 106 TGGGTCGGCCAGGCTCCAGGAAGGGTTTGGAATGGCTTCGCATTAAGAGTAAAGT 165
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DB 66 TGGGTCGGCCAGGCTCCAGGAAGGGTTTGGAATGGCTTCGCATTAAGAGTAAAGT 125
OY 166 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGAT 225
|||||
DB 126 AATAATTATGCAACATTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGAT 185
OY 226 GATTCAACAAAGCATGCTCTATCTGCAAAATGAACAACCTTGAAGCTGAGACACAGCATG 285
|||||
DB 186 GATTCAACAAAGCATGCTCTATCTGCAAAATGAACAACCTTGAAGCTGAGACACAGCATG 245
OY 286 TATTACTGTGTG 297
|||||
DB 246 TATTACTGTGTG 257
RESULT 14
MDIGMVAO 360 bp mRNA linear ROD 01-APR-1993
LOCUS M.domesticus IgM variable region.
DEFINITION
ACCESSION Z22080
VERSION Z22080.1 GI:288665
KEYWORDS
anti-DNA antibody; IgM gene; IgM variable region; immunoglobulin.

SOURCE Mus musculus domesticus.
ORGANISM Mus musculus domesticus
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Eutheria; Rodentia; Sclerogamathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 360)
JOURNAL Tillingham, D.M., Jou, N., Hill, R.J. and Marion, T.N.
REFERENCE Both IgM and IgG anti-DNA antibody are the products of clonally
AUTHORS selective B cell stimulation in (NZB x NZW)F1 mice
JOURNAL J. Exp. Med. 176 (1992) in press
TITLE 2 (bases 1 to 360)
JOURNAL Marion, T.N.
REFERENCE Direct Submission
AUTHORS Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
JOURNAL Immunology, University of Tennessee, Memphis, 858 Madison Avenue,
Memphis, TN, 38163, USA
FEATURES
source
1..360
/organism="Mus musculus domesticus"
/strain="(NZB x NZW)F1"
/isolate="mouse #17"
/db_xref="taxon:10092"
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/sex="female"
/cell_line="17p.79"
/cell_type="hybridoma"
/tissue_type="spleen"
/dev_stage="somatic variant"
1..360
/gene="IgM"
/gene="IgM"
/function="heavy chain variable region for IgM anti-DNA
antibody; Vh558 family"
/note="17p.79 is clonally related to the IgM hybridoma
17p.80 and the IgG hybridoma 17s.161 in the 17ps-c7
clone"
/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CAA80054.1"
/db_xref="GI:288686"
/translation="EVQLVETGGGLVOPKSLKSCAASGFSEFTNMMNWVROAPGK
LEWVARIRSKSNNTATYVADSVKDRFTISRDSDSMLYLQNNILKTEDTATYTCMRD
YVAFPAWGGGLTVTVA"
BASE COUNT 101 a 74 c 93 g 92 t
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Best Local Similarity 99.5%; Pred. No. 7.1e-73;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 106 TGGTCCGCCAGGCTCCAGAAAGGTTTGAATGGCTCGCATGAAGTAAAGT 165
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DB 106 TGGTCCGCCAGGCTCCAGAAAGGTTTGAATGGCTCGCATGAAGTAAAGT 165
QY 166 AATAATATGCAACATTTTATGCCGATTCACTGAAAGACAGGTTCCACATCCAGAGAT 225
|||||
DB 166 AATAATATGCAACATTTTATGCCGATTCACTGAAAGACAGGTTCCACATCCAGAGAT 225
QY 226 GATTCACAAACGATCTATCTGCAATGAACAACCTGAAAGCTGAGAGACAGCCATG 285
|||||
DB 226 GATTCACAAACGATCTATCTGCAATGAACAACCTGAAAGCTGAGAGACAGCCATG 285
QY 286 TATTACTGT 294
|||||
DB 286 TATTACTGT 294

VERSION AF023222.1 GI:2570570
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Eutheria; Rodentia; Sclerogamathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 242)
JOURNAL Van der Keyl, H., Hsu, C., Tolat, A., Kansil, S., Dalesandro, M.R.,
Dorer, D.R., Caton, A., and Owen, J.A.
REFERENCE Gene family use and somatic mutation in primary and secondary
AUTHORS fluorescein-specific IgM antibody responses
JOURNAL Immunol. Cell Biol. 74 (3), 245-254 (1996)
MEDLINE 96392936
PUBMED 8799724
REFERENCE 2 (bases 1 to 242)
AUTHORS van der Keyl, H., and Owen, J.
JOURNAL Direct Submission
TITLE Submitted (08-SEP-1997) Biology, Haverford College, 370 Lancaster
Ave., Haverford, PA 19041, USA
FEATURES
source
1..242
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/strain="BALB/c"
/db_xref="taxon:10090"
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/clone="185b, family VH10"
1..242
/codon_start=1
/product="anti-fluorescein monoclonal IgM heavy chain"
/protein_id="AA82170.1"
/db_xref="GI:2570571"
/translation="APGKGLEWVARIRSKSNNTATYVADSVKDRFTISRDSDSMLYL
QNNILKTEDTATYTCMRDYVAFPAWGGGLTVTVA"
BASE COUNT 73 a 45 c 63 g 61 t
ORIGIN
Query Match 35.8%; Score 132; DB 10; Length 242;
Best Local Similarity 99.5%; Pred. No. 3.4e-69;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 118 GCTCCAGAAAGGTTTGAATGGCTCGCATGAAGTAAAGTAAATATATATGCA 177
|||||
DB 1 GCTCCAGAAAGGTTTGAATGGCTCGCATGAAGTAAAGTAAATATATATGCA 60
QY 178 ACATTTATGCCGATTCACTGAAAGACAGGTTCCACATCTCCAGAGATTCACAAAGC 237
|||||
DB 61 ACATTTATGCCGATTCACTGAAAGACAGGTTCCACATCTCCAGAGATTCACAAAGC 120
QY 238 ATGCTCTATCTGCAATGAACAACCTGAAAGCTGAGACACAGCCATGTATTACTGTGTG 297
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DB 121 ATGCTCTATCTGCAATGAACAACCTGAAAGCTGAGACACAGCCATGTATTACTGTGTG 180
QY 298 AGA 300
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DB 181 AGA 183

Search completed: November 27, 2002, 06:25:15
Job time : 1473.52 secs

RESULT 15
AF023222 242 bp mRNA linear ROD 30-OCT-1997
LOCUS Mus musculus clone 185b, family VH10 anti-fluorescein monoclonal
DEFINITION IgM heavy chain mRNA, partial cds.
ACCESSION AF023222

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:54:06 : Search time 198.197 Seconds
(without alignments)
4192.745 Million cell updates/sec

Title: US-09-893-615-86

Perfect score: 369
Sequence: 1 GAAGGATGCTGCTGAGTCTCCTCA 369

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	35.8	330	18	AA158261
2	130	35.2	345	18	AA158267
3	110	29.8	1079	21	AA251115
4	96	26.0	96	20	AA105582
5	90	24.4	90	20	AA105579
6	80	21.7	357	17	AA115725
7	80	21.7	1797	17	AA115733
8	76	20.6	359	21	AAA44338
9	69	18.7	69	20	AA105583

10	58	15.7	443	22	AA131378
11	57	15.4	57	20	AA105580
12	57	15.4	57	20	AA105581
13	41	11.1	857	10	AA190301
14	40	10.8	357	22	AA131379
15	38	10.3	375	21	AA140202
16	36	9.8	351	20	AA131382
17	36	9.8	357	17	AA139561
18	36	9.8	440	19	AA122074
19	36	9.8	478	20	AA188433
20	36	9.8	738	15	AA107012
21	36	9.8	1528	5	AA140024
22	36	9.8	1528	5	AA140025
23	36	9.8	1553	16	AA107930
24	35	9.5	42	13	AA102344
25	35	9.5	42	14	AA104176
26	35	9.5	42	17	AA137234
27	35	9.5	42	18	AA112531
28	35	9.5	42	18	AA170515
29	35	9.5	42	18	AA173465
30	35	9.5	42	19	AA138148
31	35	9.5	42	20	AA121887
32	35	9.5	42	20	AA106031
33	35	9.5	48	20	AA131384
34	35	9.5	49	20	AA131379
35	35	9.5	51	22	AA122042
36	35	9.5	52	19	AA118537
37	35	9.5	52	19	AA118573
38	35	9.5	52	19	AA103848
39	35	9.5	52	22	AA121995
40	35	9.5	52	22	AA122024
41	35	9.5	57	20	AA131376
42	35	9.5	57	20	AA131388
43	35	9.5	331	18	AA143738
44	35	9.5	346	18	AA143740
45	35	9.5	357	18	AA158252

ALIGNMENTS

RESULT 1	
ID	AA158261 standard; cDNA: 330 BP.
AC	AA158261:
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DT	22-AUG-1997 (first entry)
XX	
DE	Lead binding MAb 6F5 heavy chain variable region encoding cDNA.
XX	
KW	Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW	pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW	heavy metal; ss.
XX	
OS	Mus musculus.
XX	
FT	key
FT	Location/Qualifiers
FT	1..330
FT	/tag= a
XX	/note= "no stop codon given"
PN	MO9639518-A1.
XX	
PD	12-DEC-1996.
XX	
PF	05-JUN-1996; 96WO-US09258.
XX	
PR	10-OCT-1995; 95US-0541373.
PR	05-JUN-1995; 95US-0462798.
XX	
PA	(BION-) BIONEERASKA INC.
XX	

murine antibody 1D
Anti-Staph (HAY) 9
Anti-Staph (HAY) 9
Insert coding for
Humanised murine a
H. pylori 26 kDa p
MMS561H M. muscul
Variable heavy cha
DNA encoding the h
EST clone GF196.
11-6 binding Inhib
Combined cDNA inse
mRNA encoding gamm
Anti-tobacco mosai
JH specific oligo
Probe specific for
Mouse heavy chain
Probe for mouse he
Mouse immunoglobul
Mouse heavy chain
Probe for the mous
Probe used to isol
Mouse heavy chain
MUSIGHAD mouse Ig
MUSIGHAEI mouse Ig
Mouse Ig V region
Mouse Ig V region
Mouse heavy chain
Mouse heavy chain
Mouse heavy chain
Mouse immunoglobul
Mouse Ig V region
MUSIGHAD mouse pr
MUSIGHACK mouse Ig
Anti-DNA antibody
Anti-DNA antibody
Lead binding MAb 8

PI Lopez O, Murray PJ, Wylie DE;
XX
DR WPI: 1997-043140/04.
DR P-PSDB: AAM01587.
XX
PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as
PT lead cations
XX
PS Claim 1: Page 76: 125pp: English.
XX
CC The present sequence encodes the heavy chain variable region for
CC monoclonal antibody (Mab) 6F5, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from hybridoma cells from
CC mouse spleen cells. The protein can be used for binding heavy metals,
CC such as lead cations. It can be used for detecting, removing, adding
CC or neutralising the heavy metals in biological and inanimate systems.
CC It can be used in e.g. aqueous liquid systems, in biological or
CC environmental systems or in such compositions as perfumes, cosmetics,
CC pharmaceuticals, health care products, skin treatment products,
CC pesticides, herbicides, solvents used in the production of semi-
CC conductor and integrated circuit components and production materials
CC for electronic components.
XX
SQ Sequence 330 BP; 93 A; 73 C; 82 G; 82 T; 0 other;
XX
Query Match 35.8%; Score 132; DB 18; Length 330;
Best Local Similarity 99.5%; Pred. No. 2.2e-58;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 121 CCAGAAAGGTTTGAATGGTCTCGCATAGAACTAAAGTAATATTATGCAACA 180
DB 106 CCAGAAAGGTTTGAATGGTCTCGCATAGAACTAAAGTAATATTATGCAACA 165
QY 181 TTTATGCCGATTCAGTGAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATG 240
DB 166 TATTATGCCGATTCAGTGAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATG 225
QY 241 CTCTATCTGCAAAATGAACTTGAAGAACTGAGACACAGCATGTATTACTGTGTGAGA 300
DB 226 CTCTATCTGCAAAATGAACTTGAAGAACTGAGACACAGCATGTATTACTGTGTGAGA 285
QY 301 CGG 303
DB 286 CGG 288
XX
RESULT 2
AAT58267
ID AAT58267 standard; CDNA: 345 BP.
XX
AC AAT58267;
XX
DT 22-AUG-1997 (first entry)
XX
DE Lead binding Mab 2B4 heavy chain variable region encoding cDNA.
XX
KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..345
FT /tag= a
FT /note= "no stop codon given"
XX
PN WO9639518-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US09258.

XX
PR 10-OCT-1995; 95US-0541373.
PR 05-JUN-1995; 95US-0462798.
XX
PA (BION-) BIONEERASKA INC.
XX
PI Lopez O, Murray PJ, Wylie DE;
XX
DR WPI: 1997-043140/04.
DR P-PSDB: AAM01593.
XX
PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as
PT lead cations
XX
PS Claim 1: Page 88: 125pp: English.
XX
CC The present sequence encodes the heavy chain variable region for
CC monoclonal antibody (Mab) 2B4, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from hybridoma cells from
CC mouse spleen cells. The protein can be used for binding heavy metals,
CC such as lead cations. It can be used for detecting, removing, adding
CC or neutralising the heavy metals in biological and inanimate systems.
CC It can be used in e.g. aqueous liquid systems, in biological or
CC environmental systems or in such compositions as perfumes, cosmetics,
CC pharmaceuticals, health care products, skin treatment products,
CC pesticides, herbicides, solvents used in the production of semi-
CC conductor and integrated circuit components and production materials
CC for electronic components.
XX
SQ Sequence 345 BP; 100 A; 75 C; 87 G; 83 T; 0 other;
XX
Query Match 35.2%; Score 130; DB 18; Length 345;
Best Local Similarity 99.4%; Pred. No. 2.4e-57;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 123 AGAAAGGTTTGAATGGTCTCGCATAGAAAGTAATATTATGCAACATT 182
DB 123 AGAAAGGTTTGAATGGTCTCGCATAGAAAGTAATATTATGCAACATA 182
QY 183 TTATGCCGATTCAGTGAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATCT 242
DB 183 TTATGCCGATTCAGTGAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATCT 242
QY 243 CTATCTGCAAAATGAACTTGAAGAACTGAGACACAGCATGTATTACTGTGTGAGACG 302
DB 243 CTATCTGCAAAATGAACTTGAAGAACTGAGACACAGCATGTATTACTGTGTGAGACG 302
QY 303 G 303
DB 303 G 303
XX
RESULT 3
AAZ51115
ID AAZ51115 standard; DNA: 1079 BP.
XX
AC AAZ51115;
XX
DT 05-JUN-2000 (first entry)
XX
DE Anti-Her2neu single chain antibody gene.
XX
KW Retroviral vector; Spleen Necrosis Virus; SNV;
KW antibody-envelope fusion protein; retroviral envelope protein;
KW gene therapy; antigen binding site; single chain antibody; human;
KW Her2neu cell surface marker; cell specific gene transfer; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 14..1015
FT /tag= a

FT /product- "Anti-Her2neu single chain antibody"
XX
PN WO200009730-A2.
XX
PD 24-FEB-2000.
XX
PF 10-AUG-1999; 99WO-US18141.
XX
PR 17-AUG-1998; 98US-0135121.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Dornburg RC;
XX
DR WPI: 2000-224358/19.
DR P-PSDB; AAT70111.
XX
PT Cell specific gene transfer using retroviral vectors containing
XX antibody-envelope fusion proteins and wild type envelope proteins
XX
PS Example: Fig 8: 45pp; English.
XX
XX The patent discloses a novel retroviral vector, particularly Spleen
CC Necrosis Virus (SNV) vector, having target cell specificity. The vector
CC has a targeting envelope which is a chimeric protein consisting of an
CC antigen binding site of an antibody (e.g. anti-DNP-scfv) or another
CC peptide that binds to a specific cell surface protein, fused to the
CC carboxy terminal part of the retroviral envelope protein. The presence
CC of the wild type envelope protein serves as a helper molecule to
CC improve or supplement a functional membrane fusion domain. The
CC antigen binding site replaces the natural viral receptor binding site.
CC The retroviral vector is used for cell specific gene transfer.
CC especially in gene therapy. The invention overcomes the restricted host
CC range limitation of retroviral vectors. The present sequence is a gene
CC encoding anti-Her2neu single chain antibody (sca). This sequence was used
CC in the construction of plasmid pAV7 which contains a targeting vector
CC comprising the anti-Her2neu sca fused to the
CC SNV-Envelope-TM(transmembrane) coding region.
XX
XX
SO Sequence 1079 BP; 303 A; 253 C; 255 G; 268 T; 0 other:
Query Match 29.8%; Score 110; DB 21; Length 1079;
Best Local Similarity 100.0%; Pred. No. 5.7e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 189 CGATTAGTGAAGACAGGTTCCATCTCCAGAGATGATTCACAAAGCATGCTTATCT 248
DB 631 CGATTAGTGAAGACAGGTTCCATCTCCAGAGATGATTCACAAAGCATGCTTATCT 690
OY 249 GCAATGACCACTGAAACTGAGACAGCAGCATGTTACTGTGTGA 298
DB 691 GCAATGACCACTGAAACTGAGACAGCAGCATGTTACTGTGTGA 740
RESULT 4
AAK05582
ID AAK05582 standard; DNA; 96 BP.
XX
AC AAK05582;
XX
DT 22-APR-1999 (first entry)
XX
DE Anti-Staph (HAY) 96-110 heavy chain variable region encoding DNA.
XX
XX Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM MAb 96-110; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..96
FT CDS /*tag- a

XX
PN WO9857994-A2.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998; 98WO-US12402.
XX
PR 16-JUN-1997; 97US-0049871.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
XX
DR WPI: 1999-095329/08.
DR P-PSDB; AAM94738.
XX
XX
XX New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
XX
PS Claim 17; Fig 12; 150pp; English.
XX
XX The invention relates to a monoclonal antibody (MAb) to lipoteichoic
CC acid of gram positive bacteria, where the MAb is a chimeric
CC immunoglobulin comprising at least part of a human immunoglobulin
CC constant region and at least part of a non-human immunoglobulin variable
CC region having specificity to lipoteichoic acid of gram positive bacteria.
CC The antibodies bind to whole bacteria and enhance phagocytosis and
CC killing of the bacteria and enhance protection from lethal infection. The
CC antibodies or peptides (encoded by a DNA of the variable region of
CC anti-lipoteichoic acid antibody or characterised by amino acids
CC corresponding to one or more of the complementarily determining regions
CC (CDRs) of the variable region of the antibody) can be used for treating
CC or preventing infections caused by gram positive bacteria. They can also
CC be used for the diagnosis of gram positive bacterial infections.
CC Sequences AAK05579-83 represent gene fragments encoding the heavy chain
CC variable regions of the anti-lipoteichoic antibody 96-100.
XX
XX
SO Sequence 96 BP; 33 A; 21 C; 19 G; 23 T; 0 other:
Query Match 26.0%; Score 96; DB 20; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.1e-39;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 205 AGGTCACCATCTCCAGAGATGATTCACAAAGCATGCTTATCTGCAATGACCAACTTG 264
DB 1 AGGTCACCATCTCCAGAGATGATTCACAAAGCATGCTTATCTGCAATGACCAACTTG 60
OY 265 AAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
DB 61 AAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 96
RESULT 5
AAK05579
ID AAK05579 standard; DNA; 90 BP.
XX
AC AAK05579;
XX
DT 22-APR-1999 (first entry)
XX
DE Anti-Staph (HAY) 96-110 heavy chain variable region encoding DNA.
XX
XX Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KM MAb 96-110; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..90
FT CDS /*tag- a

```

PN  MO9857994-A2.
XX
XX  23-DEC-1998.
XX
XX  16-JUN-1998; 98WO-US12402.
PF
XX  16-JUN-1997; 97US-0049871.
PR
XX  (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
XX  Fischer GW, Schuman RF, Stinson JL, Wong H;
XX  WPI: 1999-095329/08.
XX  P-PSDB: AAW94735.
DR
XX
XX  New antibodies to lipoteichoic acid of gram positive bacteria - used
PT  to develop products for the diagnosis, prevention and treatment of
PT  infections caused by gram positive bacteria
XX
XX  Claim 17: Fig 12; 150pp: English.
XX
XX  The invention relates to a monoclonal antibody (Mab) to lipoteichoic
CC  acid of gram positive bacteria, where the Mab is a chimeric
CC  immunoglobulin comprising at least part of a human immunoglobulin
CC  constant region and at least part of a non-human immunoglobulin variable
CC  region having specificity to lipoteichoic acid of gram positive bacteria.
CC  The antibodies bind to whole bacteria and enhance phagocytosis and
CC  killing of the bacteria and enhance protection from lethal infection. The
CC  antibodies or peptides (encoded by a DNA of the variable region of
CC  anti-lipoteichoic acid antibody or characterised by amino acids
CC  corresponding to one or more of the complementarity determining regions
CC  (CDRs) of the variable region of the antibody) can be used for treating
CC  or preventing infections caused by gram positive bacteria. They can also
CC  be used for the diagnosis of gram positive bacterial infections.
CC  Sequences AAX05579-83 represent gene fragments encoding the heavy chain
CC  variable regions of the anti-lipoteichoic antibody 96-100.
XX
XX  Sequence 90 BP; 20 A; 17 C; 28 G; 25 T; 0 other;
SQ
Query Match 24.4%; Score 90; DB 20; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.4e-36;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GAAGTGATGCTGGTGAGCTGTGGAGATTGTGACGACCTAAAGGCTCATTTGAACCTC 60
DB 1 GAAGTGATGCTGGTGAGCTGTGGAGATTGTGACGACCTAAAGGCTCATTTGAACCTC 60
OY 61 TCATGTGCAGCCTCTGGATTCACTTCAAT 90
DB 61 TCATGTGCAGCCTCTGGATTCACTTCAAT 90

RESULT 6
AAT15725
ID AAT15725 standard; CDNA: 357 BP.
XX
XX  AAT15725:
XX
XX  25-JUN-1996 (first entry)
XX
XX  3B1 heavy chain variable region DNA from PCIB4613.
XX
XX  delta endotoxin; Bacillus thuringiensis; western corn rootworm;
KW  MCRM; maize; pesticide; brush border membrane vesicle; monoclonal;
KW  antibody; ss.
XX
XX  Insecta sp.
OS
XX  MO9600783-A1.
XX
XX  11-JAN-1996.
XX
XX  20-JUN-1995; 95WO-IB00497.
PF
```

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XX  28-JUN-1994; 94US-0267641.
PR
XX
XX  (CIBA ) CIBA GEIGY AG.
XX
XX  Carozzi NB, Koziel MG;
XX
XX  WPI: 1996-077494/08.
XX  P-PSDB: AAR90829.
DR
XX
XX  New monoclonal antibodies which bind insect gut proteins - used
PT  partic. with toxin moieties for the control of insect pests. partic.
PT  in plants
XX
XX  Claim 8: Page 50-51; 106pp: English.
XX
XX  AAT15725-35 are DNA mols. encoding a monoclonal antibody or a binding
CC  fragment. Mabs were produced by using insect guts, partic. insect
CC  brush border membranes (BBMs), esp. corn rootworm, as antigen;
CC  immunising a donor animal with the antigen; isolating immunocompetent B
CC  cells from the immunised animal; fusing B cells with a tumour cell line;
CC  isolating the fused cells, culturing them and cloning positive hybrid
CC  cells; and screening the hybrid cells for prodn. of the required Mabs.
CC  The Mabs bind to the gut of a target insect but do not bind to mammalian
CC  BBMs. The DNA sequence can be operably linked to a toxin moiety, esp.
CC  selected from e.g. Bacillus toxins, pseudomonas exotoxin and phytolectin,
CC  etc.. The Abs are useful for control of insect pests, e.g. Coleoptera,
CC  Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref.
CC  applied to a plant, e.g. maize.
XX
XX  Sequence 357 BP; 102 A; 76 C; 91 G; 88 T; 0 other;
SQ
Query Match 21.7%; Score 80; DB 17; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15 GGAGTCTGCTGGAGGATGCTGACGACCTAAAGGCTCATTTGAACCTCATGTGACGCTC 74
DB 15 GGAGTCTGCTGGAGGATGCTGACGACCTAAAGGCTCATTTGAACCTCATGTGACGCTC 74
OY 75 TGGATTCACTTCAATTAAT 94
DB 75 TGGATTCACTTCAATTAAT 94

RESULT 7
AAT15733
ID AAT15733 standard; CDNA: 1797 BP.
XX
XX  AAT15733:
XX
XX  25-JUN-1996 (first entry)
XX
XX  3B1 single chain antibody DNA from PCIB4631.
XX
XX  delta endotoxin; Bacillus thuringiensis; western corn rootworm;
KW  MCRM; maize; pesticide; brush border membrane vesicle; monoclonal;
KW  antibody; ss.
XX
XX  Insecta sp.
OS
XX  MO9600783-A1.
XX
XX  11-JAN-1996.
XX
XX  20-JUN-1995; 95WO-IB00497.
XX
XX  28-JUN-1994; 94US-0267641.
XX
XX  (CIBA ) CIBA GEIGY AG.
XX
XX  Carozzi NB, Koziel MG;
XX
```

DR WPI: 1996-077494/08.
 DR P-PSDB: AAR90837.
 XX
 PT New monoclonal antibodies which bind insect gut proteins - used
 PT partic. with toxin moieties for the control of insect pests, partic.
 PT in plants
 XX
 PS Claim 8: Page 68-72; 106pp; English.
 XX
 CC AA15725-35 are DNA mols. encoding a monoclonal antibody or a binding
 CC fragment. Mabs were produced by using insect guts, partic. insect
 CC brush border membranes (BBMs), esp. corn rootworm, as antigen;
 CC immunising a donor animal with the antigen; isolating immunocompetent B
 CC cells from the immunised animal; fusing B cells with a tumour cell line;
 CC isolating the fused cells, culturing them and cloning positive hybrid
 CC cells; and screening the hybrid cells for prodn. of the required Mabs.
 CC The Mabs bind to the gut of a target insect but do not bind to mammalian
 CC BBMs. The DNA sequence can be operably linked to a toxin moiety, esp.
 CC selected from e.g. Bacillus toxins, Pseudomonas exotoxin and phytolaccin,
 CC etc.. The Abs are useful for control of insect pests, e.g. Coleoptera,
 CC Diptera, Hymenoptera and Lepidoptera. The pesticidal compn. is pref.
 CC applied to a plant, e.g. maize.
 XX
 SQ Sequence 1797 BP; 455 A; 488 C; 452 G; 402 T; 0 other;
 Query Match 21.7%; Score 80; DB 17; Length 1797;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 15 GGAGTGTGTGAGAGATTGGTGCAGCCCTTAAGGCTCATTCGATGTCAGCCTC 74
 DB 477 GGAGTGTGTGAGAGATTGGTGCAGCCCTTAAGGCTCATTCGATGTCAGCCTC 536
 OY 75 TGGATTCACCTTCATTAACCT 94
 DB 537 TGGATTCACCTTCATTAACCT 556

RESULT 8
 AAA44338
 ID AAA44338 standard; cDNA; 359 BP.
 AC AAA44338;
 DT 21-AUG-2000 (first entry)
 DE Human secreted expressed sequence tag SEQ ID NO:913.
 XX
 KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;
 KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
 KW thrombolytic; antiinflammatory; cyostatic; antibacterial; antifungal;
 KW antiviral; antidiabetic; antiparkinsonian; neurotrophic; antiproliferative;
 KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
 KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KW central nervous system disorder; Alzheimer's disease; stroke;
 KW Parkinson's disease; Huntington's disease; coagulation disorder;
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
 KW tumour; infection; depression; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200021991-A1.
 PD 20-APR-2000.
 XX
 XX 15-OCT-1999; 99WO-US24206.
 PF
 PR 15-OCT-1998; 98US-0104436.
 XX

PA (GEMV) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Werberg D, Treacy M, Bowman MR;
 XX
 DR WPI: 2000-317938/27.
 XX
 PT Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (SESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders -
 XX
 PS Claim 1: Page 437-438; 803pp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (SESTs), isolated from human, mouse, chicken and rat
 CC tissue sources. The SESTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cyostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiparkinsonian; anticonvulsant; antiproliferative; neuroprotective;
 CC neurotrophic; antiparkinsonian; antiproliferative; cerebroprotective;
 CC anticonvulsant; and antidepressant. The SESTs can be used for gene
 CC therapy and in vaccines. The SESTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 359 BP; 91 A; 66 C; 93 G; 109 T; 0 other;
 Query Match 20.6%; Score 76; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 2.5e-29;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 106 TGGGTCGCGCAGGCTCCAGGAAGGTTTGGATGCGTTCCTCCATTAACGATAAAGT 165
 DB 219 TGGGTCGCGCAGGCTCCAGGAAGGTTTGGATGCGTTCCTCCATTAACGATAAAGT 278
 OY 166 AATAATTATGCACACAT 181
 DB 279 AATAATTATGCACACAT 294

RESULT 9
 AAX05583
 ID AAX05583 standard; DNA; 69 BP.
 AC AAX05583;
 DT 22-APR-1999 (first entry)
 DE Anti-Staph (HNV) 96-110 heavy chain variable region encoding DNA.
 XX
 KW Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW MAb 96-110; ss.
 XX
 OS Mus sp.
 XX
 PN WO9857994-A2.
 FT Key 1.69 Location/Qualifiers
 FT CDS /*tag= a
 XX

```

XX 23-DEC-1998.
XX
XX 16-JUN-1998; 98MO-US12402.
XX
XX 16-JUN-1997; 97US-0049871.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
XX Flascher GW, Schuman RF, Stinson JL, Wong H;
XX
XX WPI: 1999-095328/08.
XX
XX P-PSDB: AAW94739.
XX
XX New antibodies to lipoteichoic acid of gram positive bacteria - used
XX to develop products for the diagnosis, prevention and treatment of
XX infections caused by gram positive bacteria
XX
XX Claim 17; Fig 12; 150pp; English.
XX
XX The invention relates to a monoclonal antibody (mAb) to lipoteichoic
XX acid of gram positive bacteria, where the mAb is a chimeric
XX immunoglobulin comprising at least part of a human immunoglobulin
XX constant region and at least part of a non-human immunoglobulin variable
XX region having specificity to lipoteichoic acid of gram positive bacteria.
XX The antibodies bind to whole bacteria and enhance phagocytosis and
XX killing of the bacteria and enhance protection from lethal infection. The
XX antibodies or peptides (encoded by a DNA of the variable region of
XX anti-lipoteichoic acid antibody or characterised by amino acids
XX corresponding to one or more of the complementarity determining regions
XX (CDRs) of the variable region of the antibody) can be used for treating
XX or preventing infections caused by gram positive bacteria. They can also
XX be used for the diagnosis of gram positive bacterial infections.
XX Sequences AAX05579-83 represent gene fragments encoding the heavy chain
XX variable regions of the anti-lipoteichoic antibody 96-100.
XX
XX
XX Sequence 69 BP; 14 A; 19 C; 20 G; 16 T; 0 other;
XX
XX Query Match 18.7%; Score 69; DB 20; Length 69;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-25;
XX Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 301 CGGGGGCTTACGAGTACTATGCTATGACACTGCTGCGGTCAGAACCTCACTACC 360
XX |||||||
XX DB 1 CGGGGGCTTACGAGTACTATGCTATGACACTGCTGCGGTCAGAACCTCACTACC 60
XX
XX QY 361 GTCTCTCTCA 369
XX |||||||
XX DB 61 GTCTCTCTCA 69
XX
XX RESULT 10
XX AAD13178
XX ID AAD13178 standard; DNA; 443 BP.
XX
XX AC AAD13178;
XX
XX DT 16-OCT-2001 (first entry)
XX
XX DE Murine antibody 1D9 heavy chain variable region encoding DNA.
XX
XX CC Murine: humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
XX neuroprotective; immunosuppressive; human immunodeficiency virus;
XX HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
XX multiple sclerosis; atherosclerosis; stenosis; allograft rejection;
XX anaphylaxis; malignancy; inflammation; atherosclerosis; asthma;
XX fibrotic disease; angioptosis; acquired immune deficiency syndrome;
XX AIDS; inflammatory glomerulopathy; vascular intervention;
XX neointimal hyperplasia; antibody 1D9 heavy chain variable region;
XX ds.
XX
XX Mus sp.
XX
XX OS

```

```

XX
XX Key Location/Qualifiers
XX CDS 1..443
XX
XX FT /*tag= a
XX FT /product= "Murine antibody 1D9 heavy
XX FT chain variable region"
XX FT /transl_except= (pos:442..443, aa:val)
XX FT /note= "CDS does not include start and stop codon"
XX
XX FT /partial
XX FT 1..57
XX FT sig_peptide
XX FT /*tag= b
XX FT 58..443
XX FT mat_peptide
XX FT /*tag= c
XX FT /product= "Murine mature antibody 1D9 kappa
XX FT light chain variable region"
XX FT 58..411
XX FT misc_feature
XX FT /*tag= d
XX FT /note= "Encodes variable region"
XX FT 412..443
XX FT misc_feature
XX FT /*tag= e
XX FT /note= "Encodes a part of the constant region"
XX
XX PN W0200157226-A1.
XX
XX PD 09-AUG-2001.
XX
XX PD 02-FEB-2001; 2001MO-US03537.
XX
XX PF 03-FEB-2000; 2000US-0497625.
XX
XX PR (MILL-) MILLENNIUM PHARM INC.
XX
XX PA Latosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX
XX P-PSDB: AAE07033.
XX
XX DR WPI: 2001-48888/53.
XX
XX DR P-PSDB: AAE07033.
XX
XX PT Humanised immunoglobulin for treating a CC-chemokine receptor
XX PT 2-mediated disorder in a patient, comprises a binding specificity for
XX PT CCR2, and a non-human antigen binding region and human immunoglobulin
XX PT
XX
XX PS Claim 24; Fig 21; 183pp; English.
XX
XX CC The patent discloses a humanised antibody or its antigen-binding
XX CC fragment, having binding specificity for CC-chemokine receptor 2
XX CC (CCR2), comprising an antigen binding region of non-human origin
XX CC and at least a portion of an immunoglobulin of human origin. The
XX CC humanised antibodies are useful for inhibiting the interaction of
XX CC a cell expressing CCR2. They are useful for inhibiting or treating
XX CC HIV infection. The proteins of the invention are useful for inhibiting
XX CC leukocyte trafficking, for treating CCR2-mediated disorders such as
XX CC inflammatory disorder, autoimmune disorders such as rheumatoid
XX CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
XX CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX CC and in the manufacture of a medicament for treating CCR2 mediated
XX CC disease. They are also useful for treating allergy, anaphylaxis,
XX CC malignancy, chronic and acute inflammation, histamine and IGE-
XX CC mediated allergic reaction, shock, stenosis, allograft rejection,
XX CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX CC immune deficiency syndrome (AIDS), restenosis associated with vascular
XX CC intervention. Including angioplasty and/or stent placement in a mammal.
XX CC Humanised antibodies are also useful for inhibiting narrowing of the
XX CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX CC a vessel in a mammal, preferably associated with vascular intervention.
XX CC The present sequence is a DNA encoding murine antibody 1D9 heavy chain
XX CC variable region.
XX
XX SQ Sequence 443 BP; 117 A; 97 C; 108 G; 121 T; 0 other;
XX
XX Query Match 15.7%; Score 58; DB 22; Length 443;
XX Best Local Similarity 100.0%; Pred. No. 5.4e-20;
XX Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 25 GGAGATTGTCACGCTAAAGGCTGATTGAACCTGTCAGCCTTGATTCA 82
|||||
Db 82 GGAGATTGTCACGCTAAAGGCTGATTGAACCTGTCAGCCTTGATTCA 139

RESULT 11

AA05580 standard; DNA: 57 BP.

AA05580;

22-APR-1999 (first entry)

Anti-Staph (HAY) 96-110 heavy chain variable region encoding DNA.

Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
MAB 96-110; ss.

Mus sp.

Key Location/Qualifiers

FT CDS 1..57

FT CDS /*tag= a

W09857994-A2.

23-DEC-1998.

16-JUN-1998; 98WO-US12402.

16-JUN-1997; 97US-0049871.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Fischer GW, Schuman RF, Stinson JL, Wong H;

WPI: 1999-095329/08.

P-PSDB: AAW94736.

New antibodies to lipoteichoic acid of gram positive bacteria - used
to develop products for the diagnosis, prevention and treatment of
infections caused by gram positive bacteria

Claim 17; Fig 12; 150pp; English.

The invention relates to a monoclonal antibody (Mab) to lipoteichoic
acid of gram positive bacteria, where the Mab is a chimeric
immunoglobulin comprising at least part of a human immunoglobulin
constant region and at least part of a non-human immunoglobulin variable
region having specificity to lipoteichoic acid of gram positive bacteria.
The antibodies bind to whole bacteria and enhance phagocytosis and
killing of the bacteria and enhance protection from lethal infection. The
antibodies or peptides (encoded by a DNA of the variable region of
anti-lipoteichoic acid antibody or characterised by amino acids
corresponding to one or more of the complementarity determining regions
(CDRs) of the variable region of the antibody) can be used for treating
or preventing infections caused by gram positive bacteria. They can also
be used for the diagnosis of gram positive bacterial infections.
Sequences AAX05579-83 represent gene fragments encoding the heavy chain
variable regions of the anti-lipoteichoic antibody 96-100.

Sequence 57 BP; 13 A; 12 C; 19 G; 13 T; 0 other;

Query Match 15.4%; Score 57; DB 20; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.8e-19;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 91 AACTACGCCATGAATTTGGTCCGACGCTCCAGAAAGGTTTGAATGGTTCCT 147
|||||
Db 1 AACTACGCCATGAATTTGGTCCGACGCTCCAGAAAGGTTTGAATGGTTCCT 57

RESULT 12

AA05581 standard; DNA: 57 BP.

AA05581;

22-APR-1999 (first entry)

Anti-Staph (HAY) 96-110 heavy chain variable region encoding DNA.

Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
MAB 96-110; ss.

Mus sp.

Key Location/Qualifiers

FT CDS 1..57

FT CDS /*tag= a

W09857994-A2.

23-DEC-1998.

16-JUN-1998; 98WO-US12402.

16-JUN-1997; 97US-0049871.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Fischer GW, Schuman RF, Stinson JL, Wong H;

WPI: 1999-095329/08.

P-PSDB: AAW94737.

New antibodies to lipoteichoic acid of gram positive bacteria - used
to develop products for the diagnosis, prevention and treatment of
infections caused by gram positive bacteria

Claim 17; Fig 12; 150pp; English.

The invention relates to a monoclonal antibody (Mab) to lipoteichoic
acid of gram positive bacteria, where the Mab is a chimeric
immunoglobulin comprising at least part of a human immunoglobulin
constant region and at least part of a non-human immunoglobulin variable
region having specificity to lipoteichoic acid of gram positive bacteria.
The antibodies bind to whole bacteria and enhance phagocytosis and
killing of the bacteria and enhance protection from lethal infection. The
antibodies or peptides (encoded by a DNA of the variable region of
anti-lipoteichoic acid antibody or characterised by amino acids
corresponding to one or more of the complementarity determining regions
(CDRs) of the variable region of the antibody) can be used for treating
or preventing infections caused by gram positive bacteria. They can also
be used for the diagnosis of gram positive bacterial infections.
Sequences AAX05579-83 represent gene fragments encoding the heavy chain
variable regions of the anti-lipoteichoic antibody 96-100.

Sequence 57 BP; 24 A; 8 C; 10 G; 15 T; 0 other;

Query Match 15.4%; Score 57; DB 20; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.8e-19;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 CGCATGAAGTAAGTAATTAATGCAACATTTATGCCGATTCAGTGAAGAC 204
|||||

Db 1 CGCATGAAGTAAGTAATTAATGCAACATTTATGCCGATTCAGTGAAGAC 57

RESULT 13

AA090301 standard; DNA: 857 BP.

AC AAN90301;
 XX
 DT 01-NOV-1989 (first entry)
 XX
 DE Insert coding for a heavy chain murine variable region.
 XX
 KW Recombinant DNA; chimeric monoclonal antibody; light chain; heavy chain;
 KW variable region; human carcinoembryonic antigen; cell line CE25.
 XX
 FH Key Location/Qualifiers
 FT CDS 322..844
 FT /*tag= a
 FT 370..475
 FT Intron /*tag= b
 XX
 PN EP323806-A.
 XX
 PD 12-JUL-1989.
 XX
 PE 28-DEC-1988; 88EP-0810898.
 XX
 PR 05-JAN-1988; 88GB-0000077.
 XX
 PA (CIBA) CIBA-GEIGY AG.
 XX
 PI Hardman N, Gill LL, de Winter RFJ, Wagner K, Heusser C;
 XX
 DR WPI; 1989-200701/28.
 DR P-PSDB; AAP90480.
 XX
 PT Chimeric monoclonal antibody to human carcinoembryonic antigen
 PT - consisting of variable regions of mouse origin and human constant
 PT regions, for cancer diagnosis and therapy.
 XX
 PS Claim 30; page 37; 53pp; English.
 XX
 CC The recombinant DNA is an insert coding for a heavy chain murine
 CC variable region, which is specific for human carcinoembryonic antigen
 CC and originates from genomic DNA of the cell line CE 25. See also
 CC AAP90480.
 XX
 SO Sequence 857 BP; 225 A; 186 C; 210 G; 236 T; 0 other;
 XX
 Query Match 11.8%; Score 41; DB 10; Length 857;
 Best Local Similarity 100.0%; Pred. No. 3.5e-11;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 329 TGGACTACTGGGTCAGGAAGCACTCACTCACCGTCTCTCA 369
 DB 804 TGGACTACTGGGTCAGGAAGCACTCACTCACCGTCTCTCA 844
 XX
 RESULT 14
 AAD13179
 ID AAD13179 standard; DNA: 357 BP.
 AC AAD13179;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Humanised murine antibody heavy chain 1D9RHA DNA.
 XX
 KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; antibody ID9 heavy chain; 1D9RHA; ds.
 XX
 OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..357
 FT /*tag= a
 FT /product= "humanised murine antibody heavy chain
 FT region, 1D9RHA"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 PN W0200157226-A1.
 XX
 PD 09-AUG-2001.
 XX
 PE 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX
 DR WPI; 2001-488888/53.
 DR P-PSDB; AAE07034.
 XX
 PT Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX
 PS Claim 64; Fig 23; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and arteriosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angiodysplasia and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is a DNA encoding humanised murine antibody heavy
 CC chain region, 1D9RHA. 1D9RHA sequence consists of the complementary
 CC determining regions (CDRs) of the murine ID9 antibody heavy chain
 CC variable (VH) region genetically inserted into the framework regions
 CC (FRs) of the human 4B4/CL antibody VH region.
 XX
 SO Sequence 357 BP; 99 A; 79 C; 95 G; 84 T; 0 other;
 XX
 Query Match 10.8%; Score 40; DB 22; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 106 TGGGTCCGCGAGCTCCAGGAAGGCTTGGAAATGGCTTG 145
 DB 106 TGGGTCCGCGAGCTCCAGGAAGGCTTGGAAATGGCTTG 145
 XX
 RESULT 15
 AAA40202
 ID AAA40202 standard; DNA: 375 BP.


```

XX AC AAA40202:
XX DT 01-NOV-2000 (first entry)
XX DE H. pylori 26 kDa protein-binding antibody heavy chain encoding DNA.
XX DE Acid-resistant microorganism; detection; faecal; intestine; infection;
XX DE monoclonal antibody; heavy chain; ds.
XX KM
XX OS Unidentified.
XX PN WO200026671-A1.
XX PD 11-MAY-2000.
XX PF 29-OCT-1999; 99WO-EP08212.
XX PR 29-OCT-1998; 98EP-0120517.
XX PR 06-NOV-1998; 98EP-0120687.
XX PA (CONN-) CONNEX GMBH.
XX PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
XX PI Ringels A;
XX DR WPI; 2000-365747/31.
XX DR P-PSDB; AAB10022.
XX PS
XX PS Disclosure; Fig 4; 84pp; German.
XX CC This invention describes a novel method for the detection of a mammalian
XX CC infection by an acid-resistant microorganism (A) by treating a faecal
XX CC sample with at least two different monoclonal antibodies (MAb) (or their
XX CC fragments or derivatives) or aptamers (collectively (I)) and detecting
XX CC formation of a complex (C) between (I) and the corresponding antigen of
XX CC (A). The first and second (I) bind to epitopes of different antigens
XX CC (Ag). These epitopes are present, after passage through the intestines,
XX CC in at least some mammals, and have either: (i) their native structure;
XX CC or (ii) a structure against which an antibody is produced by an animal
XX CC infected or immunized with (A), or its extract, lysate, derived protein
XX CC or fragment, or with a synthetic peptide. Practically all mammals display
XX CC at least one of the specified epitopes. The method is used to detect
XX CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
XX CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
XX CC M. tuberculosis, C. jejuni and C. pylori. (i) may also be used
XX CC therapeutically. The method is direct and non-invasive, and provides an
XX CC inexpensive and easily standardizable diagnosis, despite possible
XX CC degradation of antigens during passage through the intestines. This
XX CC sequence encodes the H. pylori 26 kDa protein-binding antibody
XX CC (DMS ACC2355) heavy chain which is used to illustrate the method of the
XX CC invention.
SQ Sequence 375 BP; 102 A; 86 C; 89 G; 98 T; 0 other:
Query Match 10.3%; Score 38; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 263 TGAAGCTGAGACAGCATGATTTACTGTGTGAGA 300
DB 266 TGAAGCTGAGACAGCATGATTTACTGTGTGAGA 303

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

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Post-processing: Listing first 45 summaries

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8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
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19: em_gsa_luv:*
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21: em_gsa_vrt:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	33.1	865	13	B1150936
2	88	23.8	932	12	B1135929
3	61	16.5	359	10	B8843560
4	39	10.6	365	10	AW403942
5	36	9.8	565	12	BG686641
6	35	9.5	552	17	BH319627

7	35	9.5	666	13	BG963642
8	35	9.5	781	13	BG967007
9	35	9.5	861	13	B1455668
10	35	9.5	862	13	B1102617
11	35	9.5	864	10	BE309336
12	35	9.5	1010	14	BQ921928
13	34	9.2	567	14	BQ266826
14	34	9.2	837	13	BG966355
15	34	9.2	963	12	BE578938
16	33	8.9	560	12	BF581663
17	33	8.9	1384	11	AK002875
18	32	8.7	348	10	AW402831
19	32	8.7	361	12	BF844111
20	32	8.7	604	10	BE367979
21	32	8.7	616	12	BF136295
22	32	8.7	639	10	BE371136
23	32	8.7	802	12	BF137216
24	32	8.7	819	13	BG966397
25	32	8.7	839	14	BQ952276
26	32	8.7	883	13	B151077
27	32	8.7	941	12	BF138189
28	31	8.4	676	10	BE369087
29	31	8.4	840	13	BE190298
30	31	8.4	890	12	BG868002
31	31	8.4	987	12	BF577496
32	30	8.1	425	12	BE578521
33	30	8.1	724	12	BF168514
34	30	8.1	851	12	BF663091
35	30	8.1	911	10	BE286958
36	29	7.9	332	12	BF155433
37	29	7.9	650	12	BF579001
38	29	7.9	663	10	BB586011
39	29	7.9	690	13	BG968682
40	29	7.9	718	12	BF136279
41	29	7.9	892	12	BF976010
42	29	7.9	927	12	BF179165
43	29	7.9	928	12	BF531379
44	29	7.9	955	14	BQ947728
45	29	7.9	961	14	BQ711482

ALIGNMENTS

RESULT 1
B1150936
LOCUS 865 bp mRNA linear EST 05-JUL-2001
DEFINITION 602916745F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:5067346 5',
ACCESSION B1150936
VERSION B1150936.1 GI:14610937
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: LNAK1181 row: 1 column: 11
High quality sequence stop: 797.
Location/Qualifiers 1. 865

FEATURES
source

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Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 213 a 229 c 209 g 214 t

ORIGIN

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Best Local Similarity 99.4%; Pred. No. 1.8e-56;
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OY 106 TGGTCCGCCAGCTCCAGAAAGGGTTGGATGGTTGCTGCAGTAAGAAGTAAAGT 165
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DB 215 TGGTCCGCCAGCTCCAGAAAGGGTTGGATGGTTGCTGCAGTAAGAAGTAAAGT 274
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OY 166 AATATTTATGACATTTATGCGATTCAGTAAGACAGTTCACCATCTCCAGAGAT 225
|||||
DB 275 AATATTTATGACATTTATGCGATTCAGTAAGACAGTTCACCATCTCCAGAGAT 334
|||||

OY 226 GATTCACAAAGCATGCTATCTGCAATGAACAATGAAACTGAGAGACAC 278
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DB 335 GATTCACAAAGCATGCTATCTGCAATGAACAATGAAACTGAGAGACAC 387
|||||

RESULT 2
BF135929 932 bp mRNA linear EST 24-OCT-2000
LOCUS 601781259P1 NCI-CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009334 5',
DEFINITION mRNA sequence.
ACCESSION BF135929
VERSION BF135929.1 GI:10974969
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 932)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

FEATURES
Source

BASE COUNT 257 a 244 c 249 g 182 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 213 CATCTCCAGAGATGATTCACAAAGCATGCTATCTGCAATGAACAATGAAACTGAGA 272
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DB 166 CATCTCCAGAGATGATTCACAAAGCATGCTATCTGCAATGAACAATGAAACTGAGA 225
|||||

OY 273 GGACACAGCCATGTTACTGTGTGAGA 300
|||||
DB 226 GGACACAGCCATGTTACTGTGTGAGA 253
|||||

RESULT 3
BB843560 359 bp mRNA linear EST 26-NOV-2001
LOCUS BB843560 RIKEN full-length enriched, 6 days neonate spleen Mus
DEFINITION musculus cDNA clone F430102008 5', mRNA sequence.
ACCESSION BB843560
VERSION BB843560.1 GI:17081927
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 359)
Akimura, T., Arakawa, T., Carninci, P., Furum, M., Hanagaki, T., Ishii
Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K., Ishii
Y., Ito, M., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: <http://genome-gsc.riken.go.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Kondo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagii, K., Fujiwara, S., Inoue, K., Toyawa, Y., Itawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
S., Kawai, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome-gsc.riken.go.jp>) for
further details.
e mouse tissues.
Location/Qualifiers
1. .359
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FEATURES
Source

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/tissue_type="spleen"
/dev_stage="6 days neonate"
/notes="Vector: pSPOR1, Site_1: SalI; Site_2: NotI. This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
Mol Genet 7: 1967-1978."

BASE COUNT      90 a      69 c      91 g      109 t
ORIGIN
Query Match      16.5%; Score 61; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 106 TGGTCCCGCCAGCTCCAGGAAGGTTTGGAATGGCTTCGTCATTAAGTAAGTAAACT 165
      |||||||
Db 229 TGGTCCCGCCAGCTCCAGGAAGGTTTGGAATGGCTTCGTCATTAAGTAAGTAAACT 288

Oy 166 A 166
      |
Db 289 A 289

RESULT 4
LOCUS      AM403942      365 bp      mRNA      linear      EST 16-FEB-2000
DEFINITION UT-HF-BK0-abn-h-04-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
ACCESSION  AM403942
VERSION     AM403942.1 GI:69222910
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            (bases 1 to 365)
REFERENCE   NIH-MGC http://mhc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
AUTHORS     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/dbp/image/image.html
            Seq primer: M13 forward
FEATURES
            source
            1..365
            Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3056887"

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/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/clone_lib="MGC85"
/notes="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      76 a      88 c      108 g      93 t
ORIGIN
Query Match      10.6%; Score 39; DB 10; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 TGTGAGCCTCGATTCACCTTCATATACATACGCGATG 102
      |||||||
Db 126 TGTGAGCCTCGATTCACCTTCATATACATACGCGATG 164

RESULT 5
LOCUS      BG686641      565 bp      mRNA      linear      EST 01-MAY-2001
DEFINITION BG686641 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765555 5',
            mRNA sequence.
ACCESSION  BG686641
VERSION     BG686641.1 GI:13918038
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            (bases 1 to 565)
REFERENCE   NIH-MGC http://mhc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
AUTHORS     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHCMI624 row: J column: 20
            High quality sequence start: 65.
            High quality sequence stop: 565.
FEATURES
            source
            1..565
            Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:4765555"
            /clone_lib="NIH_MGC_48"
            /tissue_type="primary B-cells from tonsils (cell line)"
            /lab_host="DH10B (phage-resistant)"
            /notes="Organ: B-cells; Vector: pOT7; Site_1: XhoI;
            Site_2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
BASE COUNT      118 a      155 c      169 g      123 t
ORIGIN
Query Match      9.8%; Score 36; DB 12; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      196 GTGAAAGACAGGTTCCACCATCTCCAGAGATGATTCA 231
LOCUS   BH319627
Db      306 GTGAAAGACAGGTTCCACCATCTCCAGAGATGATTCA 341

RESULT 6
AUTHORS BH319627
DEFINITION CH230-119P2.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH319627
VERSION   BH319627.1 GI:17250341
KEYWORDS GSS.
SOURCE    Norway rat.
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 552)
AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
          ,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
          Jong,P. and Fraser,C.M.
          Rat BAC End Sequences from Library CHORI-230 EcoRI segment
          Unpublished (1999)
          Other_GSSs: CH230-119P2.TVB
          Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@tigr.org
          Clones are derived from the rat BAC library CHORI-230
          (http://www.chori.org/bacpac/rat230.htm). For BAC library
          availability, please contact Pieter de Jong (pdejong@emil.chi.org).
          Clones may be purchased from BACPAC Resources
          (http://www.chori.org/bacpac/or ering_information.htm). BAC end
          page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
          Plate: 119 row: P column: 2
          Seg primer: SP6
          Class: BAC ends.
FEATURES
  source          Location/Qualifiers
    1..552
    /organism="Rattus norvegicus"
    /strain="BN/SSNhsd/MCW"
    /db_xref="taxon:10116"
    /clone_lib="CH230-119P2"
    /clone_1lb="CHORI-230 Segment 1"
    /sex="Female"
    /cell_type="Brain"
    /note="Vector: PTARBAC2.1; site.1: EcoRI; site.2: EcoRI;
    CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by
    Pieter de Jong"
BASE COUNT      174 a      101 c      116 g      161 t
ORIGIN
Query Match          9.5%; Score 35; DB 17; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      19 TCTGTGTGAGAGATTGTGTCAGCTTAAGGTCATT 53
LOCUS   BH319627
Db      26 TCTGTGTGAGAGATTGTGTCAGCTTAAGGTCATT 60

RESULT 7
AUTHORS BG963642
DEFINITION BG963642
ACCESSION BG963642
VERSION   BG963642.1 GI:14351279

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KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 666)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Email: cgabs-r@mail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHAM10967 row: e column: 12
          High quality sequence stop: 658.
FEATURES
  source          Location/Qualifiers
    1..666
    /organism="Mus musculus"
    /strain="FVB/N"
    /db_xref="taxon:10090"
    /clone_lib="IMAGE:498315"
    /clone_1lb="NCI_CGAP_Co24"
    /lab_host="DH10B (T1 phage-resistant)"
    /note="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
    Site.2: SalI; Cloned unidirectionally. primer: Oligo dT.
    Average insert size 1.6 kb. Constructed by Life
    Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      157 a      186 c      159 g      164 t
ORIGIN
Query Match          9.5%; Score 35; DB 13; Length 666;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      320 ACTATGCTATGACTACTGGGTCAGAGACCTCA 354
LOCUS   BG967007
Db      383 ACTATGCTATGACTACTGGGTCAGAGACCTCA 417

RESULT 8
AUTHORS BG967007
DEFINITION BG967007
ACCESSION BG967007
VERSION   BG967007.1 GI:14354644
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 781)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabs-r@mail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHAM1001 row: n column: 09
          High quality sequence stop: 770.
FEATURES
  source          Location/Qualifiers
    1..781

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:4988744"
/clone_11b="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT 200 a 205 c 194 g 182 t
ORIGIN

Query Match 9.5%; Score 35; DB 13; Length 781;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 ACTATGCTATGACTACTGGGTCAGAACCTCA 354
|||||
Db 404 ACTATGCTATGACTACTGGGTCAGAACCTCA 438
|||||

RESULT 9
BI455668 861 bp mRNA linear EST 21-AUG-2001
LOCUS 603173862F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5253279 5',
DEFINITION mRNA sequence.
ACCESSION BI455668
VERSION BI455668.1 GI:15246324
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 861)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11639 row: 1 column: 16
High quality sequence stop: 780.
Location/Qualifiers
1..861
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image:5253279"
/clone_11b="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 205 a 239 c 211 g 206 t
ORIGIN

Query Match 9.5%; Score 35; DB 13; Length 861;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 ACTATGCTATGACTACTGGGTCAGAACCTCA 354
|||||

Db 432 ACTATGCTATGACTACTGGGTCAGAACCTCA 466
|||||

RESULT 10
B1102617 862 bp mRNA linear EST 26-JUN-2001
LOCUS 602888151F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043444
DEFINITION 5', mRNA sequence.
ACCESSION B1102617
VERSION B1102617.1 GI:14553510
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1119 row: e column: 13
High quality sequence stop: 849.
Location/Qualifiers
1..862
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image:5043444"
/clone_11b="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library. 1"

BASE COUNT 211 a 231 c 209 g 211 t
ORIGIN

Query Match 9.5%; Score 35; DB 13; Length 862;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 ACTATGCTATGACTACTGGGTCAGAACCTCA 354
|||||

Db 380 ACTATGCTATGACTACTGGGTCAGAACCTCA 414
|||||

RESULT 11
BE309336 864 bp mRNA linear EST 26-OCT-2000
LOCUS 601093720F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3488309 5',
DEFINITION mRNA sequence.
ACCESSION BE309336
VERSION BE309336.1 GI:9167366
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 864)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM8527 row: h column: 06
 High quality sequence stop: 645.
 Location/Qualifiers

FEATURES

1. 864

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:3488309"
 /clone_id="NCI_CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 171 a 260 c 222 g 211 t

ORIGIN

Query Match 9.5%; Score 35; DB 10; Length 864;
 Best Local Similarity 100.0%; Pred. No. 4.5e-08;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 320 ACTATGCTATGACTGCGGCTCAGACCTCA 354

Db 366 ACTATGCTATGACTGCGGCTCAGACCTCA 400

RESULT 12

LOCUS

BO921928 1010 bp mRNA linear EST 20-AUG-2002

DEFINITION AGENCOURT_8952829 NCI_CGAP_Co24 Mus musculus CDNA clone

IMAGE:6475284 5', mRNA sequence.

BO921928

BO921928.1 GI:22336959

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

TITLE

AUTHORS

JOURNAL

COMMENT

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1010)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM14013 row: m column: 13
 High quality sequence stop: 608.
 Location/Qualifiers

FEATURES

1. 1010

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:6475284"
 /clone_id="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 241 a 283 c 252 g 231 t 3 others

ORIGIN

Query Match 9.5%; Score 35; DB 14; Length 1010;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 320 ACTATGCTATGACTGCGGCTCAGACCTCA 354

Db 382 ACTATGCTATGACTGCGGCTCAGACCTCA 416

RESULT 13

LOCUS

BO266826 567 bp mRNA linear EST 07-MAY-2002

DEFINITION NISC_ff15c05.y1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:2665800

5', mRNA sequence.

BO266826

BO266826.1 GI:20491891

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

TITLE

AUTHORS

JOURNAL

COMMENT

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 567)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen/Robin Humphreys
 CDNA Library Preparation: Life Technologies
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 MGI:1046572
 Plate: LLM7070 row: F column: 9
 Seq primer: M13Rpl reverse primer (ABI).
 Location/Qualifiers

FEATURES

source

1. 567
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:2665800"
 /clone_id="NCI_CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 144 a 145 c 137 g 141 t

ORIGIN

Query Match 9.2%; Score 34; DB 14; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 321 CTATGCTATGACTGCGGCTCAGACCTCA 354

Db 398 CTATGCTATGACTGCGGCTCAGACCTCA 431

RESULT 14

LOCUS

BG966355 837 bp mRNA linear EST 12-JUN-2001

DEFINITION 602832843F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987379 5',
RNA sequence.
ACCESSION BG966355
VERSION BG966355.1 GI:14353992
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 837)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 692.
Location/Qualifiers
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4987379"
/clone_11b="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
BASE COUNT 201 a 222 c 218 g 196 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 321 CTATGCTATGACTGAGGTCAAGAACTCA 354
|||||
DB 446 CTATGCTATGACTGAGGTCAAGAACTCA 479
RESULT 15
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LOCUS 602095519F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4215533 5',
mRNA sequence.
ACCESSION BF578938
VERSION BF578938.1 GI:11652650
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 963)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM9791 row: e column: 06
High quality sequence start: 4
High quality sequence stop: 624.
Location/Qualifiers
1..963
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4215533"
/clone_11b="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
BASE COUNT 250 a 281 c 251 g 181 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 122 CTATGCTATGACTGAGGTCAAGAACTCA 155
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Job time: 1551.06 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:55:59 ; Search time 41.3581 Seconds
(without alignments)
2736.194 Million cell updates/sec

Title: US-09-893-615-86

Perfect score: 369
Sequence: 1 GAAGTGATCTGCTGTGAGTC.....CCTCACTCACCGTCTCTCA 369

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/lna/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	132	35.8	330	3	US-08-767-128-23
2	130	35.2	345	3	US-08-767-128-35
3	80	21.7	357	1	US-08-442-542-1
4	80	21.7	357	3	US-08-765-469-1
5	80	21.7	1797	1	US-08-442-542-17
6	80	21.7	1797	3	US-08-765-469-17
7	36	9.8	351	2	US-08-752-844-36
8	36	9.8	351	2	US-08-591-196-36
9	36	9.8	738	1	US-08-197-834-6
10	35	9.5	42	1	US-07-834-539A-41
11	35	9.5	42	1	US-08-053-131-49
12	35	9.5	42	1	US-08-645-641-49
13	35	9.5	42	1	US-07-853-408B-49
14	35	9.5	42	1	US-08-096-762-49
15	35	9.5	42	2	US-08-800-353-41
16	35	9.5	42	2	US-08-308-865-49
17	35	9.5	42	4	US-09-042-353-212
18	35	9.5	42	4	US-08-758-417A-60
19	35	9.5	42	5	PCT-US92-06185-41
20	35	9.5	42	5	PCT-US92-10983-49
21	35	9.5	48	2	US-08-752-844-38
22	35	9.5	48	2	US-08-591-196-38
23	35	9.5	49	2	US-08-752-844-33
24	35	9.5	49	2	US-08-591-196-33
25	35	9.5	51	2	US-08-659-567-28
26	35	9.5	57	2	US-08-752-844-30
27	35	9.5	57	2	US-08-752-844-42

ALIGNMENTS

28	35	9.5	57	2	US-08-591-196-30	Sequence 30, Appl
29	35	9.5	57	2	US-08-591-196-42	Sequence 42, Appl
30	35	9.5	346	3	US-08-881-037-13	Sequence 13, Appl
31	35	9.5	357	3	US-08-767-128-5	Sequence 5, Appl
32	35	9.5	360	1	US-08-447-422-14	Sequence 14, Appl
33	35	9.5	360	2	US-08-672-175A-1	Sequence 1, Appl
34	35	9.5	366	3	US-08-881-037-49	Sequence 49, Appl
35	35	9.5	372	3	US-08-767-128-37	Sequence 37, Appl
36	35	9.5	416	1	US-08-253-877C-7	Sequence 7, Appl
37	35	9.5	417	2	US-08-603-024-1	Sequence 1, Appl
38	35	9.5	416	3	US-08-452-164A-7	Sequence 7, Appl
39	35	9.5	420	4	US-08-943-136-3	Sequence 3, Appl
40	35	9.5	420	4	US-08-973-518-3	Sequence 3, Appl
41	35	9.5	711	6	545030-8	Patent No. 545030
42	35	9.5	732	1	US-08-230-843-1	Sequence 1, Appl
43	35	9.5	732	2	US-08-636-936-1	Sequence 1, Appl
44	35	9.5	741	6	545030-10	Patent No. 545030
45	35	9.5	754	1	US-07-958-140-1	Sequence 1, Appl

RESULT 1
US-08-767-128-23
; Sequence 23, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..330
OTHER INFORMATION:
US-08-767-128-23

Query Match 35.8%; Score 132; DB 3; Length 330;
Best Local Similarity 99.5%; Pred. No. 4,4e-61;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 121 CCAGGAAAGGTTTGGATGGTTCGTCATAGAAAGTAATAATTATGCAACA 180
DB 106 CCAGGAAAGGTTTGGATGGTTCGTCATAGAAAGTAATAATTATGCAACA 165
QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAGCATG 240
DB 166 TATTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAGCATG 225
QY 241 CTCTATCTGCAATGAACTTGAAGAACTGAGACACAGCCATGATTAAGTGTGAGA 300
DB 226 CTCTATCTGCAATGAACTTGAAGAACTGAGACACAGCCATGATTAAGTGTGAGA 285
QY 301 CGG 303
DB 286 CGG 288

RESULT 2
US-08-767-128-35
Sequence 35, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DMANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh st
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648,49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..345
OTHER INFORMATION:
US-08-767-128-35

Query Match 35.2%; Score 130; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 5.2e-60;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 123 AGGAAAGGTTTGGATGGTTCGTCATAGAAAGTAATAATTATGCAACATA 182
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DB 183 TTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAGCATGCT 242
QY 243 CTATCTGCAATGAACTTGAAGAACTGAGACACAGCCATGATTAAGTGTGAGACG 302
DB 243 CTATCTGCAATGAACTTGAAGAACTGAGACACAGCCATGATTAAGTGTGAGACG 302
QY 303 G 303
DB 303 G 303

RESULT 3
US-08-442-542-1
Sequence 1, Application US/08442542
Patent No. 5686600
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Kozziel, Michael G.
TITLE OF INVENTION: Antibodies which bind to Insect Gut
TITLE OF INVENTION: Proteins and their use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,542
: FILING DATE: 16-MAY-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/267,641
: FILING DATE: 28-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Spull, W. Murray
: REGISTRATION NUMBER: 32,943
: REFERENCE/DOCKET NUMBER: CGC 1750
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8615
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 357 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..357
: OTHER INFORMATION: /note="3B1 heavy chain variable
: OTHER INFORMATION: region from pcIB4613"
US-08-442-542-1
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Query Match          21.7%; Score 80; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 GGAGCTGTGGAGATTGGTGCACCTAAAGGTCATTGAAACTCTCATGTGCAGCCTC 74
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DB 15 GGAGCTGTGGAGATTGGTGCACCTAAAGGTCATTGAAACTCTCATGTGCAGCCTC 74
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 75 TGGATTCACCTTCATAACT 94
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DB 75 TGGATTCACCTTCATAACT 94
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RESULT 4
US-08-765-469-1
: Sequence 1, Application US/08765469
: Patent No. 6069301
: GENERAL INFORMATION:
: APPLICANT: Carozzi, Nadine B.
: APPLICANT: Kozziel, Michael G.
: TITLE OF INVENTION: Antibodies which bind to Insect Gut
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/765,469
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/267,641
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Spull, W. Murray
: REGISTRATION NUMBER: 32,943
```

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: REFERENCE/DOCKET NUMBER: CGC 1750
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8615
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 357 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..357
: OTHER INFORMATION: /note="3B1 heavy chain variable
: OTHER INFORMATION: region from pcIB4613"
US-08-765-469-1
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Query Match          21.7%; Score 80; DB 3; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 GGAGCTGTGGAGATTGGTGCACCTAAAGGTCATTGAAACTCTCATGTGCAGCCTC 74
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DB 15 GGAGCTGTGGAGATTGGTGCACCTAAAGGTCATTGAAACTCTCATGTGCAGCCTC 74
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 75 TGGATTCACCTTCATAACT 94
    ||||||||||||||||||||
DB 75 TGGATTCACCTTCATAACT 94
    ||||||||||||||||||||
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```

RESULT 5
US-08-442-542-17
: Sequence 17, Application US/08442542
: Patent No. 5686600
: GENERAL INFORMATION:
: APPLICANT: Carozzi, Nadine B.
: APPLICANT: Kozziel, Michael G.
: TITLE OF INVENTION: Antibodies which bind to Insect Gut
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,542
: FILING DATE: 16-MAY-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/267,641
: FILING DATE: 28-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Spull, W. Murray
: REGISTRATION NUMBER: 32,943
: REFERENCE/DOCKET NUMBER: CGC 1750
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8615
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1797 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
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MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1797
OTHER INFORMATION: /note="3B1 single chain antibody"
OTHER INFORMATION: from PCIB4631"
US-08-442-542-17

Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGAGTGTGTGGAGATTGGTGCAGCCTAAGGTCATTGAACCTCATGTGCAGCCTC 74
|||||
DB 477 GGAGTGTGTGGAGATTGGTGCAGCCTAAGGTCATTGAACCTCATGTGCAGCCTC 536
QY 75 TGGATTCACTTCATTAATCT 94
|||||
DB 537 TGGATTCACTTCATTAATCT 556

RESULT 6

US-08-765-469-17
Sequence 17, Application US/08765469
Patent No. 6069301
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which bind to insect gut
TITLE OF INVENTION: Proteins and their use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1797
OTHER INFORMATION: /note="3B1 single chain antibody"
OTHER INFORMATION: from PCIB4631"
US-08-765-469-17

Query Match 21.7%; Score 80; DB 3; Length 1797;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGAGTGTGTGGAGATTGGTGCAGCCTAAGGTCATTGAACCTCATGTGCAGCCTC 74
|||||
DB 477 GGAGTGTGTGGAGATTGGTGCAGCCTAAGGTCATTGAACCTCATGTGCAGCCTC 536
QY 75 TGGATTCACTTCATTAATCT 94
|||||
DB 537 TGGATTCACTTCATTAATCT 556

RESULT 7

US-08-752-844-36
Sequence 36, Application US/08752844
Patent No. 5935821
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Poon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-752-844-36

Query Match 9.8%; Score 36; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 GACTATGCTATGACTGACTGAGGTCAGAGAACTCA 354
|||||
DB 304 GACTATGCTATGACTGACTGAGGTCAGAGAACTCA 339

RESULT 8

US-08-591-196-36
Sequence 36, Application US/08591196
Patent No. 5977316
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Poon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCHIFF, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-591-196-36

Query Match 9.8%; Score 36; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 GACTATGCTATGGACTGCTGGGTCAAGAACTCA 354
|||||
DB 304 GACTATGCTATGGACTGCTGGGTCAAGAACTCA 339

RESULT 9
US-08-197-834-6
Sequence 6, Application US/08197834
Patent No. 5639455
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHITO
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1735 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 028173/1993

FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5639455man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-661-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248955 OPAT UR
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: DNA (synthetic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
US-08-197-834-6

Query Match 9.8%; Score 36; DB 1; Length 738;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 GACTATGCTATGGACTGCTGGGTCAAGAACTCA 354
|||||
DB 688 GACTATGCTATGGACTGCTGGGTCAAGAACTCA 723

RESULT 10
US-07-834-539A-41
Sequence 41, Application US/07834539A
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2600
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539A
FILING DATE: 1992-02-05
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ. ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-834-539A-41

Query Match 9.5%; Score 35; DB 1; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 320 ACTATGCTATGACTACTGGGTCAAGAACCTCA 354
Db 1 ACTATGCTATGACTACTGGGTCAAGAACCTCA 35

RESULT 11

US-08-053-131-49
Sequence 49, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053.131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-053-131-49

Query Match 9.5%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 320 ACTATGCTATGACTACTGGGTCAAGAACCTCA 354
Db 1 ACTATGCTATGACTACTGGGTCAAGAACCTCA 35

RESULT 12

US-08-645-641-49
Sequence 49, Application US/08645641
Patent No. 5719032
GENERAL INFORMATION:

APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-MAY-1996
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-645-641-49

Query Match 9.5%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 320 ACTATGCTATGACTACTGGGTCAAGAACCTCA 354
Db 1 ACTATGCTATGACTACTGGGTCAAGAACCTCA 35

RESULT 13

US-07-853-408B-49
Sequence 49, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:

APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B


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; FILING DATE: 19920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
US-07-853-4088-49

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Pred. No. 2.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 ACTATGCTATGACTACTGGGCTCAAGAACCTCA 354
DB 1 ACTATGCTATGACTACTGGGCTCAAGAACCTCA 35

RESULT 14
US-08-096-762-49
; Sequence 49, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Knourle and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
US-08-096-762-49

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Pred. No. 2.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 ACTATGCTATGACTACTGGGCTCAAGAACCTCA 354
DB 1 ACTATGCTATGACTACTGGGCTCAAGAACCTCA 35

RESULT 15
US-08-800-353-41
; Sequence 41, Application US/08800353
; Patent No. 5874299
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,353
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,539
; FILING DATE: 1992-02-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-800-353-41

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 42;
Pred. No. 2.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 ACTATGCTATGACTACTGGGCTCAAGAACCTCA 354
DB 1 ACTATGCTATGACTACTGGGCTCAAGAACCTCA 35
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Search completed: November 27, 2002, 05:39:23
Job time : 49.3581 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 05:34:00 : Search time 41.3581 Seconds

(without alignments)
3436.030 Million cell updates/sec

Title: US-09-893-615-86

Perfect score: 369
Sequence: 1 GAAGTGATGCTGTGTGAGTC.....CCTCACTACGCTCTCTCA 369

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 341543 seqs, 19255720 residues

Word size : 0

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	101	27.4	466	10	US-09-881-823-15
3	58	15.7	443	10	US-09-840-459-96
4	58	15.7	443	10	US-09-840-459-96
5	40	10.8	357	10	US-09-840-459-97
6	40	10.8	357	10	US-09-840-459-97
7	36	9.8	478	10	US-09-840-459-911
8	35	9.5	51	7	US-10-040-739-911
9	35	9.5	417	7	US-08-779-784-13
10	35	9.5	420	10	US-09-007-093-3
11	35	9.5	466	10	US-09-881-823-11
12	34	9.2	354	10	US-09-949-559-105
13	34	9.2	414	9	US-10-146-305-6
14	33	8.9	736	12	US-10-006-773-12
15	32	8.7	418	10	US-09-753-436-42
16	30	8.1	360	10	US-09-910-059-10
17	30	8.1	765	10	US-09-910-059-10
18	29	7.9	42	9	US-09-252-150-44
19	29	7.9	354	10	US-09-905-243-71

20	29	7.9	396	10	US-09-811-737-12	Sequence 12, Appl
21	29	7.9	396	10	US-09-811-737-13	Sequence 13, Appl
22	29	7.9	420	10	US-09-286-240-3	Sequence 3, Appl
23	29	7.9	782	10	US-09-811-737-21	Sequence 21, Appl
24	29	7.9	782	10	US-09-811-737-22	Sequence 22, Appl
25	28	7.6	372	9	US-09-879-813-87	Sequence 87, Appl
26	28	7.6	454	10	US-09-881-823-3	Sequence 3, Appl
27	28	7.6	518	10	US-09-881-823-17	Sequence 17, Appl
28	27	7.3	351	8	US-08-790-540A-5	Sequence 5, Appl
29	27	7.3	351	8	US-08-791-391A-5	Sequence 5, Appl
30	26	7.0	422	10	US-09-753-436-77	Sequence 77, Appl
31	26	7.0	458	10	US-09-990-205-3	Sequence 3, Appl
32	26	7.0	461	10	US-09-861-294-3	Sequence 3, Appl
33	26	7.0	690	10	US-09-995-693-4	Sequence 4, Appl
34	26	7.0	714	8	US-08-940-544-4	Sequence 4, Appl
35	26	7.0	1598	10	US-09-822-849A-103	Sequence 103, App
36	26	7.0	1617	10	US-09-822-830A-571	Sequence 571, App
37	25	6.8	132	9	US-09-423-800-25	Sequence 25, App
38	25	6.8	308	10	US-09-864-761-27741	Sequence 27741, A
39	25	6.8	311	10	US-09-864-761-31233	Sequence 31233, A
40	25	6.8	335	10	US-09-828-708-111	Sequence 111, App
41	25	6.8	331	8	US-08-790-540A-1	Sequence 1, Appl
42	25	6.8	331	8	US-08-791-391A-1	Sequence 1, Appl
43	25	6.8	351	9	US-10-091-236-7	Sequence 7, Appl
44	25	6.8	354	10	US-09-798-058-1	Sequence 1, Appl
45	25	6.8	397	9	US-10-046-935-2106	Sequence 2106, Ap

ALIGNMENTS

RESULT 1
US-09-893-615-86
Sequence 86, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GI
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FINNEGAN, HENDERSON, FARROW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..369
 SEQUENCE DESCRIPTION: SEQ ID NO: 86:
 US-09-893-615-86

Query Match 100.0%; Score 369; DB 10; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1,1e-188;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAGTATGCTGCTGAGCTGCTGCTGAGAGATTGTCAGACCTAAAGGTCATTGAACCTC 60
 Db 1 GAAGTATGCTGCTGAGCTGCTGCTGAGAGATTGTCAGACCTAAAGGTCATTGAACCTC 60
 Oy 61 TCATGTGAGCCTCTGCAATTCACCTCAATACTAGCCATGAATGGTCCGACAGCT 120
 Db 61 TCATGTGAGCCTCTGCAATTCACCTCAATACTAGCCATGAATGGTCCGACAGCT 120
 Oy 121 CCAGGAAGAGGTTTGAATGGTCTGCTGCAATGAAGTAATAATTATGCAACA 180
 Db 121 CCAGGAAGAGGTTTGAATGGTCTGCTGCAATGAAGTAATAATTATGCAACA 180
 Oy 181 TTTTATGCCGATTGATGATAAAGACAGGTTTCAACCATCTCCAGAGATGATTCACAAAGCATG 240
 Db 181 TTTTATGCCGATTGATGATAAAGACAGGTTTCAACCATCTCCAGAGATGATTCACAAAGCATG 240
 Oy 241 CTCTATGCAATGAACACTTGAATACTGAGACAGCAGCCATGATTAATCTGTGAGA 300
 Db 241 CTCTATGCAATGAACACTTGAATACTGAGACAGCAGCCATGATTAATCTGTGAGA 300
 Oy 301 CGGGGGGCTTCAAGGATGATGATGCTATGAGACTAGCTGAGGGTCAAGAACTCCTACACC 360
 Db 301 CGGGGGGCTTCAAGGATGATGATGCTATGAGACTAGCTGAGGGTCAAGAACTCCTACACC 360
 Oy 361 GTCTCTCTCA 369
 Db 361 GTCTCTCTCA 369

RESULT 2
 US-09-881-823-15
 : Sequence 15, Application US/09881823
 : Patent No. US20020068066A1
 : GENERAL INFORMATION:
 : APPLICANT: SHI, WENYUAN
 : APPLICANT: ANDERSON, MAXWELL
 : APPLICANT: MORRISON, SHERIE
 : APPLICANT: TRINH, RYAN
 : APPLICANT: WIMS, LETITIA
 : APPLICANT: CHEN, LI
 : TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
 : FILE REFERENCE: 22851-032
 : CURRENT APPLICATION NUMBER: US/09/881,823
 : PRIOR FILING DATE: 2001-06-15
 : PRIOR APPLICATION NUMBER: US 07/378,577
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 15
 : LENGTH: 466
 : TYPE: DNA
 : ORGANISM: Murine
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (14)..(442)
 : US-09-881-823-15

Query Match 27.4%; Score 101; DB 10; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1e-44;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 200 AAGACAGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAATGAACA 259

Db 270 AAGACAGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAATGAACA 329
 Oy 260 ACTTGAACCTGAGACACACAGCATGATTAATCTGTGTGAGA 300
 Db 330 ACTTGAACCTGAGACACACAGCATGATTAATCTGTGTGAGA 370

RESULT 3
 US-09-840-459-96
 : Sequence 96, Application US/09840459
 : Patent No. US20020150576A1
 : GENERAL INFORMATION:
 : APPLICANT: Larosa, Gregory J.
 : APPLICANT: Horvath, Christopher
 : APPLICANT: Newman, Walter
 : APPLICANT: Jones, S. Tarran
 : APPLICANT: O'Brien, Siobhan H.
 : APPLICANT: O'Keefe, Theresa
 : TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 : FILE REFERENCE: 1855,1052-012
 : CURRENT APPLICATION NUMBER: US/09/840,459
 : PRIOR FILING DATE: 2001-02-02
 : PRIOR APPLICATION NUMBER: PCT/US01/03537
 : PRIOR FILING DATE: 2001-02-02
 : PRIOR APPLICATION NUMBER: 09/497,625
 : PRIOR FILING DATE: 1999-07-22
 : PRIOR APPLICATION NUMBER: 09/359,193
 : PRIOR FILING DATE: 1998-07-23
 : NUMBER OF SEQ ID NOS: 107
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 96
 : LENGTH: 443
 : TYPE: DNA
 : ORGANISM: Mus musculus
 : US-09-840-459-96

Query Match 15.7%; Score 58; DB 10; Length 443;
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 25 GGAGATTGTGACAGCCTAAAGGCTGATGAACCTCATGCTGACGCTTGATTTCA 82
 Db 82 GGAGATTGTGACAGCCTAAAGGCTGATGAACCTCATGCTGACGCTTGATTTCA 139
 RESULT 4
 US-09-840-459-99/c
 : Sequence 99, Application US/09840459
 : Patent No. US20020150576A1
 : GENERAL INFORMATION:
 : APPLICANT: Larosa, Gregory J.
 : APPLICANT: Horvath, Christopher
 : APPLICANT: Newman, Walter
 : APPLICANT: Jones, S. Tarran
 : APPLICANT: O'Brien, Siobhan H.
 : APPLICANT: O'Keefe, Theresa
 : TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 : FILE REFERENCE: 1855,1052-012
 : CURRENT APPLICATION NUMBER: US/09/840,459
 : PRIOR FILING DATE: 2001-02-02
 : PRIOR APPLICATION NUMBER: PCT/US01/03537
 : PRIOR FILING DATE: 2001-02-02
 : PRIOR APPLICATION NUMBER: 09/497,625
 : PRIOR FILING DATE: 1999-07-22
 : PRIOR APPLICATION NUMBER: 09/359,193
 : PRIOR FILING DATE: 1998-07-23
 : NUMBER OF SEQ ID NOS: 107
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 99
 : LENGTH: 443
 : TYPE: DNA
 : ORGANISM: Mus musculus
 : US-09-840-459-99/c

NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 99
LENGTH: 443
TYPE: DNA
ORGANISM: Mus musculus
US-09-840-459-99

Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 443;
Pred. No. 1.3e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 GGAGGATGTGTCAGCCTCAAGGGCTGTAACCTCTCATGTGCAGCTCTGGATTCA 82
|||||
Db 362 GGAGGATGTGTCAGCCTCAAGGGCTGTAACCTCTCATGTGCAGCCTCTGGATTCA 305

RESULT 5

US-09-840-459-97
Sequence 97, Application US/09840459
Patent No. US20020150576A1

GENERAL INFORMATION:

APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1855.1052-012

CURRENT APPLICATION NUMBER: US/09/840,459

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: PCT/US01/03537

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 97

LENGTH: 357

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized heavy chain

US-09-840-459-97

Query Match
Best Local Similarity 100.0%; Score 40; DB 10; Length 357;
Pred. No. 5.8e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 TGGGTCGCCAGGCTCCAGGAAAGGTTGGATGGCTTG 145
|||||
Db 106 TGGGTCGCCAGGCTCCAGGAAAGGTTGGATGGCTTG 145

RESULT 6

US-09-840-459-103/C

Sequence 103, Application US/09840459

Patent No. US20020150576A1

GENERAL INFORMATION:

APPLICANT: Larosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1855.1052-012

CURRENT APPLICATION NUMBER: US/09/840,459

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: PCT/US01/03537

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 103

LENGTH: 357

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized heavy chain

US-09-840-459-103

Query Match
Best Local Similarity 100.0%; Score 40; DB 10; Length 357;
Pred. No. 5.8e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 TGGGTCGCCAGGCTCCAGGAAAGGTTGGATGGCTTG 145
|||||
Db 252 TGGGTCGCCAGGCTCCAGGAAAGGTTGGATGGCTTG 213

RESULT 7

US-10-040-739-911

Sequence 911, Application US/10040739

Patent No. US20020173635A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

McCoy, John

Lavallee, Edward

Racie, Lisa

Merberg, David

Treacy, Maurice

Spaulding, Ylki

TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS

NUMBER OF SEQUENCES: 1519

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/040,739

FILING DATE: 07-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/036,520

FILING DATE: 03-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 911:

SEQUENCE CHARACTERISTICS:

LENGTH: 478 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 911:
US-10-040-739-911

Query Match 9.8%; Score 36; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 GACTATGCTATGACTACTGGGCTCAGGACCTCA 354
DB 413 GACTATGCTATGACTACTGGGCTCAGGACCTCA 448

RESULT 8
US-08-779-784-13

Sequence 13, Application US/08779784
Patent No. US20020164325A1
GENERAL INFORMATION:

APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-08-779-784-13

Query Match 9.5%; Score 35; DB 7; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 320 ACTATGCTATGACTACTGGGCTCAGGACCTCA 354
DB 2 ACTATGCTATGACTACTGGGCTCAGGACCTCA 36

RESULT 9
US-08-779-784-7

Sequence 7, Application US/08779784
Patent No. US20020164325A1
GENERAL INFORMATION:

APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-779-784-7

Query Match 9.5%; Score 35; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 320 ACTATGCTATGACTACTGGGCTCAGGACCTCA 354
DB 368 ACTATGCTATGACTACTGGGCTCAGGACCTCA 402

RESULT 10
US-09-007-093-3

Sequence 3, Application US/09007093
Patent No. US20020025315A1
GENERAL INFORMATION:

APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E

APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-007-093-3

Query Match
Best Local Similarity 9.5%; Score 35; DB 10; Length 420;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 ACTATGCTATGACTACTGGGTCAGGAACTCA 354
|||||
DB 371 ACTATGCTATGACTACTGGGTCAGGAACTCA 405

RESULT 11
US-09-881-823-11
Sequence 11, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENTUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 466
TYPE: DNA
ORGANISM: Murline
FEATURE:
NAME/KEY: CDS
LOCATION: (11)..(442)

US-09-881-823-11
Query Match
Best Local Similarity 9.5%; Score 35; DB 10; Length 466;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 ACTATGCTATGACTACTGGGTCAGGAACTCA 354
|||||
DB 387 ACTATGCTATGACTACTGGGTCAGGAACTCA 421

RESULT 12
US-09-949-559-105
Sequence 105, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.1
SEQ ID NO 105
LENGTH: 354
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: hTNF40 heavy chain variable domain
NAME/KEY: CDS
LOCATION: (1)..(354)
OTHER INFORMATION:
US-09-949-559-105

Query Match
Best Local Similarity 9.2%; Score 34; DB 10; Length 354;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CTATGCTATGACTACTGGGTCAGGAACTCA 354
|||||
DB 306 CTATGCTATGACTACTGGGTCAGGAACTCA 339

RESULT 13
US-10-146-305-6
Sequence 6, Application US/10146305
Patent No. US20020173035A1
GENERAL INFORMATION:
APPLICANT: YIHAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
FILE REFERENCE: OV17440
CURRENT APPLICATION NUMBER: US/10/146,305
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
LENGTH: 414
TYPE: DNA
ORGANISM: Escherichia coli
US-10-146-305-6

Query Match 9.2%; Score 34; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 9.8e-09;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 321 CTATGCTATGACTCTGGGGTCAGGAACCTCA 354
DB 318 CTATGCTATGACTCTGGGGTCAGGAACCTCA 351

RESULT 14
US-10-006-773-12
Sequence 12, Application US/10006773
Patent No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: Jungmans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti-
FILE REFERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 736
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (14)..(430)
OTHER INFORMATION: 4D4 Heavy chain V region, plus leader
US-10-006-773-12

Query Match 8.9%; Score 33; DB 12; Length 736;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 322 TATGCTATGACTCTGGGGTCAGGAACCTCA 354
DB 383 TATGCTATGACTCTGGGGTCAGGAACCTCA 415

RESULT 15
US-09-753-436-42
Sequence 42, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemary
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-753-436-42

Query Match 8.7%; Score 32; DB 10; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 323 ATGCTATGACTCTGGGGTCAGGAACCTCA 354
DB 371 ATGCTATGACTCTGGGGTCAGGAACCTCA 402

Search completed: November 27, 2002, 07:14:51
Job time : 50.3581 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:19:05 : Search time 43.6911 Seconds
(without alignments)
375.129 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 123
Sequence: 1 EVMLVESGGLVOPKSLK.....SGIDYAMDYWGQGTSLTVSS 123

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	32.5	110	18	AAW01587
2	40	32.5	115	18	AAW01593
3	38	30.9	100	22	AAE06972
4	36	29.3	333	21	AAV70111
5	32	26.0	32	20	AAW94738
6	30	24.4	30	20	AAW94735
7	28	22.8	119	17	AAW90829
8	28	22.8	599	17	AAW90837
9	24	19.5	101	22	AAE06971
10	24	19.5	117	22	AAW09919

11	19.5	117	22	AAE06947	Murine IgD9 antibod
12	19.5	117	23	AAO14978	Mouse heavy chain
13	19.5	148	22	AAE07033	Murine antibody 1D
14	18.7	23	20	AAW94739	Anti-Staph (HAY) 9
15	17.1	117	22	AAU09928	Humanised IgD9 heav
16	17.1	117	22	AAU09929	Humanised IgD9 heav
17	17.1	117	22	AAU09930	Humanised IgD9 heav
18	17.1	117	22	AAE06956	Humanised murine 1
19	17.1	117	22	AAE06957	Humanised murine 1
20	17.1	117	23	AAO14982	Humanised murine h
21	17.1	118	23	AAO14983	Humanised murine h
22	17.1	125	21	AAAB10022	H. pylori 26 kDa p
23	15.4	19	20	AAW94736	Anti-Staph (HAY) 9
24	15.4	19	20	AAW94737	Anti-Staph (HAY) 9
25	14.6	142	14	AAW31534	Human heavy ch
26	14.6	253	23	ABP45326	Human Blys binding
27	13.8	62	16	AAW76969	HSV-neutralising a
28	13.8	117	22	AAU09927	Humanised IgD9 heav
29	13.8	117	22	AAE06954	Humanised murine 1
30	13.8	117	22	AAE06955	Humanised murine 1
31	13.8	117	23	AAO14980	Humanised murine h
32	13.8	117	23	AAO14981	Humanised murine h
33	13.8	119	22	AAE07034	Humanised murine a
34	13.8	250	23	ABP45333	Human Blys binding
35	13.8	494	22	ABW95696	Human protein sequ
36	13.0	114	13	AAW28748	Heavy chain variab
37	13.0	118	13	AAW25412	Heavy chain variab
38	13.0	120	14	AAW30763	Heavy chain variab
39	13.0	120	15	AAW47040	Sequence of the he
40	13.0	121	12	AAW13182	Variable region of
41	13.0	122	14	AAW30772	huxCD3v9, humanise
42	13.0	125	15	AAW56287	Variable heavy cha
43	13.0	137	23	ABW77063	AC885 antibody he
44	13.0	239	23	ABP45871	Human Blys binding
45	13.0	249	23	ABP45806	Human Blys binding

ALIGNMENTS

RESULT 1	AAW01587	standard; Protein; 110 AA.
ID	AAW01587	
AC	AAW01587	
DT	22-AUG-1997	(first entry)
DE	Lead binding Mab 6F5 heavy chain variable region.	
XX	Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide; heavy metal.	
XX	Mus musculus.	
OS	WO9639518-A1.	
PN	12-DEC-1996.	
XX	05-JUN-1996;	96WO-US09258.
PF	10-OCT-1995;	95US-0541373.
PR	05-JUN-1995;	95US-0462798.
PA	(BION-) BIONEERASKA INC.	
XX	Lopez O, Murray PJ, Wylie DE;	
XX	WPI; 1997-043140/04.	
DR	N-PSDB; AAT58261.	
XX	DNA encoding heavy metal binding polypeptide sequences - used for	

PT detecting, removing, adding or neutralising heavy metals, such as
PT lead cations
XX
PS Claim 12: Page 77; 125pp; English.
XX
CC The present sequence represents the heavy chain variable region for
CC monoclonal antibody (MAb) 6F5, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the
CC heavy metals in biological and inanimate systems. It can be used in
CC e.g. aqueous liquid systems, in biological or environmental systems or
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC care products, skin treatment products, pesticides, herbicides,
CC solvents used in the production of semi-conductor and integrated
CC circuit components and production materials for electronic components.
CC The products can provide for applications involving minute amounts of
CC specific heavy metals.
XX
SQ Sequence 110 AA;
XX
Query Match 32.5%; Score 40; DB 18; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.3e-32;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 62 YADSVKDRFTISRDSQSMLYLQNMNLTEDTAMTCVRR 101
DB 57 YADSVKDRFTISRDSQSMLYLQNMNLTEDTAMTCVRR 96
RESULT 2
AAW01593
ID AAW01593 standard; Protein: 115 AA.
XX
XX AAW01593;
XX
DT 22-AUG-1997 (first entry)
XX
DE Lead binding MAb 2B4 heavy chain variable region.
XX
XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.
XX
OS Mus musculus.
XX
PN MO9639518-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US09258.
XX
PR 10-OCT-1995; 95US-0541373.
PR 05-JUN-1995; 95US-0462798.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Murray PJ, Wylie DE;
XX
DR WPI: 1997-043140/04.
DR N-PSDB: AAT58267.
XX
XX DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as
PT lead cations
XX
PS Claim 12: Page 89; 125pp; English.
XX
CC The present sequence represents the heavy chain variable region for
CC monoclonal antibody (MAb) 2B4, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the

CC heavy metals in biological and inanimate systems. It can be used in
CC e.g. aqueous liquid systems, in biological or environmental systems or
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC care products, skin treatment products, pesticides, herbicides,
CC solvents used in the production of semi-conductor and integrated
CC circuit components and production materials for electronic components.
CC The products can provide for applications involving minute amounts of
CC specific heavy metals.
XX
SQ Sequence 115 AA;
XX
Query Match 32.5%; Score 40; DB 18; Length 115;
Best Local Similarity 100.0%; Pred. No. 9.7e-32;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 62 YADSVKDRFTISRDSQSMLYLQNMNLTEDTAMTCVRR 101
DB 62 YADSVKDRFTISRDSQSMLYLQNMNLTEDTAMTCVRR 101
RESULT 3
AAE06972
ID AAE06972 standard; Protein: 100 AA.
XX
XX AAE06972;
XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse germline heavy chain variable (VH) region, MRL-RF24BG.
XX
XX Mouse: humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherosclerosis; atherosclerosis; asthma;
KW anaplasia; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
KW AIDS; inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; VH: heavy chain variable region.
XX
OS Mus sp.
XX
PN WO200157226-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US03537.
PR 03-FEB-2000; 2000US-0497625.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX
DR WPI: 2001-48888/53.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor
PT 2-mediated disorder in a patient, comprises a binding specificity for
PT CCR2, and a non-human antigen binding region and human immunoglobulin
PT -
XX
PS Disclosure, Page 152; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2
CC (CCR2), comprising an antigen binding region of non-human origin
CC and at least a portion of an immunoglobulin of human origin. The
CC humanised antibodies are useful for inhibiting the interaction of
CC a cell expressing CCR2. They are useful for inhibiting or treating
CC HIV infection. The proteins of the invention are useful for inhibiting
CC leukocyte trafficking, for treating CCR2-mediated disorders such as
CC inflammatory disorder, autoimmune disorders such as rheumatoid
CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,

CC especially in gene therapy. The invention overcomes the restricted host

Query Match	26.08;	Score 32;	DB 20;	Length 32;
-------------	--------	-----------	--------	------------

Best Local Similarity 100.0%; Pred. No. 2,6e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 RFTISRDDSSMLYLQNNLKTEDTAMYYCVR 100
Db 1 RFTISRDDSSMLYLQNNLKTEDTAMYYCVR 32

RESULT 6

AAW94735
ID AAW94735 standard; Protein; 30 AA.

XX AAW94735;

DT 22-APR-1999 (first entry)

XX Anti-Staph (HAY) 96-110 heavy chain variable region.

KW Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;

KW Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

XX MAb 96-110.

OS Mus sp.

PN WO9857994-A2.

PD 23-DEC-1998.

PF 16-JUN-1998; 98MO-US12402.

PR 16-JUN-1997; 97US-0049871.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Fischer GW, Schuman RF, Stinson JL, Wong H;

DR WPI; 1999-095329/08.

DR N-PSDB; AAX05579.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used

PT to develop products for the diagnosis, prevention and treatment of

PT infections caused by gram positive bacteria

XX Claim 21: Fig 12; 150pp; English.

XX The invention relates to a monoclonal antibody (MAb) to lipoteichoic

CC acid of gram positive bacteria, where the MAb is a chimeric

CC immunoglobulin comprising at least part of a human immunoglobulin

CC constant region and at least part of a non-human immunoglobulin variable

CC region having specificity to lipoteichoic acid of gram positive bacteria.

CC The antibodies bind to whole bacteria and enhance phagocytosis and

CC killing of the bacteria and enhance protection from lethal infection. The

CC antibodies or peptides (encoded by a DNA of the variable region of

CC anti-lipoteichoic acid antibody or characterised by amino acids

CC corresponding to one or more of the complementarity determining regions

CC (CDRs) of the variable region of the antibody) can be used for treating

CC or preventing infections caused by gram positive bacteria. They can also

CC be used for the diagnosis of gram positive bacterial infections.

CC Sequences AAW94735-39 represent heavy chain variable regions of the

CC anti-lipoteichoic antibody 96-100.

XX Sequence 30 AA;

XX Query Match 24.4%; Score 30; DB 20; Length 30;

XX Best Local Similarity 100.0%; Pred. No. 2,4e-22;

XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVMLVESGGGLVOPKSGSLKSCAASGTFN 30

Db 1 EVMLVESGGGLVOPKSGSLKSCAASGTFN 30

AAR90829
ID AAR90829 standard; Protein; 119 AA.

XX AAR90829;

DT 25-JUN-1996 (first entry)

XX 3B1 heavy chain variable region from PCIB4613.

KW delta endotoxin; Bacillus thuringiensis; western corn rootworm;

KW MCRW; maize; pesticide; brush border membrane vesicle; monoclonal;

XX antibody.

OS Insecta sp.

PN WO9600783-A1.

PD 11-JAN-1996.

PF 20-JUN-1995; 95MO-IB00497.

PR 28-JUN-1994; 94US-0267641.

PA (CIBA) CIBA GEIGY AG.

PI Carozzi NB, Koziel MG;

DR WPI; 1996-077494/08.

DR N-PSDB; AAT15725.

XX New monoclonal antibodies which bind insect gut proteins - used

PT partic. with toxin moieties for the control of insect pests, partic.

PT in plants

XX Claim 8; Page 50-51; 106pp; English.

XX AAR90829-39 are monoclonal antibodies or a binding fragments produced by

CC using insect guts, partic. insect brush border membranes (BBMs), esp.

CC corn rootworm, as antigen; immunising a donor animal with the antigen;

CC isolating immunocompetent B cells from the immunised animal; fusing B

CC cells with a tumour cell line; isolating the fused cells, culturing them

CC and cloning positive hybrid cells; and screening the hybrid cells for

CC prodn. of the regulated Mabs. The Mabs, bind to the gut of a target insect

CC but do not bind to mammalian BBMs. The DNA sequence can be operably

CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,

CC Pseudomonas exotoxin and phytolaccin, etc.. The Abs are useful for

CC control of insect pests, e.g. coleoptera, Diptera, Hymenoptera and

CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.

CC maize.

XX Sequence 119 AA;

XX Query Match 22.8%; Score 28; DB 17; Length 119;

XX Best Local Similarity 100.0%; Pred. No. 7,4e-20;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 AMNVMVROAPGKGLFWARIRKSNVAT 60

Db 33 AMNVMVROAPGKGLFWARIRKSNVAT 60

XX RESULT 8

XX AAR90837

XX ID AAR90837 standard; Protein; 599 AA.

XX AAR90837;

XX 25-JUN-1996 (first entry)

XX 3B1 single chain antibody from PCIB4631.

DE delta endotoxin; Bacillus thuringiensis; western corn rootworm;

KW MCRW; maize; pesticide; brush border membrane vesicle; monoclonal;

KW antibody.
 OS Insecta sp.
 PN WO9600783-A1.
 XX
 PD 11-JAN-1996.
 XX
 PE 20-JUN-1995; 95WO-1B00497.
 XX
 PR 28-JUN-1994; 94US-0267641.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Carozzi NB, Kozziel MG;
 XX
 DR WPI; 1996-077494/08.
 DR N-PSDB; AAT15733.
 XX
 PT New monoclonal antibodies which bind insect gut proteins - used
 PT partic. with toxin moieties for the control of insect pests, partic.
 PT in plants
 PS Claim 8: Page 68-72; 106pp: English.
 XX
 CC AAP80829-39 are monoclonal antibodies or a binding fragments produced by
 CC using insect guts, partic. insect brush border membranes (BBMs), esp.
 CC corn rootworm, as antigen; immunising a donor animal with the antigen;
 CC isolating immunocompetent B cells from the immunised animal; fusing B
 CC cells with a tumour cell line; isolating the fused cells; culturing them
 CC and cloning positive hybrid cells; and screening the hybrid cells for
 CC prodn. of the required MAb. The MAb bind to the gut of a target insect
 CC but do not bind to mammalian BBMs. The DNA sequence can be operably
 CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,
 CC pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for
 CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
 CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
 CC maize.
 XX
 SQ Sequence 599 AA:
 Query Match 22.8%; Score 28; DB 17; Length 599;
 Best Local Similarity 100.0%; Pred. No. 3e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 AMNWYRQARGKGLWYARIRSKSNYYAT 60
 DB 187 AMNWYRQARGKGLWYARIRSKSNYYAT 214
 RESULT 9
 ID AAE06971 standard; Protein: 101 AA.
 AC AAE06971;
 XX
 DT 16-OCT-2001 (first entry)
 DE Murine 1D9 antibody partial heavy chain variable (VH) region.
 XX
 KW Murine: humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; Rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; stenosis; allograft rejection;
 KW anaphylaxis; malignancy; inflammation; restenosis; asthma;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
 KW neonatal hyperplasia; VH; heavy chain variable region.
 XX
 OS Mus sp.
 PN WO200157226-A1.

XX 09-AUG-2001.
 PD
 XX
 PF 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX
 DR WPI; 2001-488888/53.
 XX
 PT Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT
 PS Disclosure: Page 152; 183pp: English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and arteriosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neonatal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is partial heavy chain variable (VH) region of
 CC murine 1D9 antibody.
 XX
 SQ Sequence 101 AA:
 Query Match 19.5%; Score 24; DB 22; Length 101;
 Best Local Similarity 100.0%; Pred. No. 5.8e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LVESGGGLVQPKGSLKSCAASGF 27
 DB 4 LVESGGGLVQPKGSLKSCAASGF 27
 RESULT 10
 ID AAU09919 standard; Protein: 117 AA.
 AC AAU09919;
 XX
 DT 18-JUN-2002 (first entry)
 DE Murine mAb 1D9 heavy chain variable region protein sequence.
 XX
 KW Mouse; mAb 1D9 heavy chain variable region; vasotropic;
 KW antineoplastic; collagen disease; immunosuppressive;
 KW antidiabetic; insulin-dependent diabetes mellitus;
 KW inflammatory bowel disease; ulcerative colitis;
 KW graft rejection; allergic disease; antipsoriatic;
 KW antiarrhythmic; nephrotropic; antichyroid; restenosis;
 KW dermatological; anaphylaxis; cell adhesion inhibitor;
 KW vascular injury; autoimmune disease; immunoglobulin;

KW	complementarity determining region; CDR; CDR1; CDR2;	
KW	atherosclerosis.	
XX		
XX	Mus sp.	
OS		
XX		
XX	Key	Location/Qualifiers
FT	Region	/note= "Part of H1 structure loop"
FT	Region	31..35
FT	Region	/note= "Complementarity determining region 1 (CDR1)"
FT	Region	50..68
FT	Region	/note= "Complementarity determining region 2 (CDR2)"
FT	Region	101..106
FT	Region	/note= "Complementarity determining region 3 (CDR3)"
PN		
XX	WO200170266-A2.	
PD		
XX	27-SEP-2001.	
XX		
XX	15-MAR-2001; 2001WO-US08266.	
PF		
XX	17-MAR-2000; 2000US-0528267.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Horvath CJ, Rao PE;	
XX		
DR	WPI, 2001-607511/69.	
XX		
PT	Inhibiting stenosis or restenosis of a blood vessel following vascular	
PT	injury or angioplasty in a subject by administering agent which	
PT	inhibits recruitment or adhesion of neutrophils, mononuclear cells to	
PT	injury site	
XX		
PS	Claim 30; Fig 16; 108pp: English.	
XX		
CC	The present invention relates to a new method of inhibiting stenosis or	
CC	restenosis of a blood vessel following vascular injury in a subject. The	
CC	new method comprises administering to the subject agents which inhibit	
CC	the adhesion and/or recruitment of neutrophils and mononuclear cells to	
CC	a site of vascular injury by binding CD18 or CCR2. The method of the	
CC	invention inhibits stenosis or restenosis of a blood vessel following	
CC	vascular injury arising from a vascular intervention procedure such as	
CC	vascular by-pass or transplantation surgery. The method is also useful	
CC	for treating a subject having an inflammatory disease or condition	
CC	mediated by neutrophil and mononuclear cell activity e.g. asthma and	
CC	graft versus host disease. Chronic inflammatory diseases of the lung,	
CC	collagen diseases, and insulin-dependent diabetes mellitus can also be	
CC	treated. The method is further useful for treating inflammatory bowel	
CC	diseases, such as ulcerative colitis. Additional diseases or conditions	
CC	include inflammation or allergic diseases and conditions, including	
CC	systemic anaphylaxis of hypersensitivity responses, drug allergies,	
CC	psoriasis and inflammatory dermatoses, autoimmune diseases such as	
CC	arthritis, graft rejection and other diseases including atherosclerosis.	
CC	The present sequence represents the protein sequence of the mouse mAb	
CC	1D9 heavy chain variable region. This sequence contains three CDR's	
CC	that can be used to inhibit stenosis or restenosis.	
XX		
XX	Sequence 117 AA:	
XX		
XX	Query Match 19.5%; Score 24; DB 22; Length 117;	
XX	Best Local Similarity 100.0%; Pred. No. 6,66-16;	
XX	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	4 LVESGGGLVQPKGSLKLSAASGF 27	
DB		
DB	4 LVESGGGLVQPKGSLKLSAASGF 27	
XX		
XX	RESULT 11	
XX	AAE06947	
XX	AAE06947 standard; Protein: 117 AA.	

AC	AAB06947;
XX	
DT	16-OCT-2001 (first entry)
DE	
XX	Murine IgD9 antibody heavy chain variable (VH) region.
KW	Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic
KW	neuroprotective; immunosuppressive; human immunodeficiency virus;
KW	HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW	Inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock
KW	multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW	anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW	fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
KW	AIDS; inflammatory glomerulopathy; vascular intervention; IgD9 antibody;
KM	neointimal hyperplasia; VH; heavy chain variable region.
XX	
OS	Mus sp.
FH	
FH	Key Location/Qualifiers
FT	Region 31..35
FT	/label= Complementarity_determining_region
FT	Region 50..68
FT	/label= Complementarity_determining_region
FT	Region 101..106
FT	/label= Complementarity_determining_region
XX	
PN	WO200157226-A1.
XX	
PD	09-AUG-2001.
XX	
PF	02-FEB-2001; 2001WO-US03537.
XX	
PR	03-FEB-2000; 2000US-0497625.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
PI	Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
DR	WPt: 2001-488888/53.
XX	
PT	Humanized immunoglobulin for treating a CC-chemokine receptor
PT	2-mediated disorder in a patient, comprises a binding specificity for
PT	CCR2, and a non-human antigen binding region and human immunoglobulin
PS	-
XX	
PS	Claim 8; Fig 8; 18pp; English.
CC	The patent discloses a humanised antibody or its antigen-binding
CC	fragment, having binding specificity for CC-chemokine receptor 2
CC	(CCR2), comprising an antigen binding region of non-human origin
CC	and at least a portion of an immunoglobulin of human origin. The
CC	humanised antibodies are useful for inhibiting the interaction of
CC	a cell expressing CCR2. They are useful for inhibiting or creating
CC	Leuk infection. The proteins of the invention are useful for inhibiting
CC	leukocyte trafficking, for treating CCR2-mediated disorders such as
CC	inflammatory disorder, autoimmune disorders such as rheumatoid
CC	arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
CC	and for inhibiting restenosis. They are useful in therapy or diagnosis,
CC	and in the manufacture of a medicament for treating CCR2 mediated
CC	disease. They are also useful for treating allergy, anaphylaxis,
CC	malignancy, chronic and acute inflammation, histamine and Ige-
CC	mediated allergic reaction, shock, stenosis, allograft rejection,
CC	fibrotic disease, asthma, inflammatory glomerulopathies, acquired
CC	immune deficiency syndrome (AIDS), restenosis associated with vascular
CC	intervention, including angioplasty and/or stent placement in a mammal.
CC	Humanised antibodies are also useful for inhibiting narrowing of the
CC	lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
CC	a vessel in a mammal, preferably associated with vascular intervention.
CC	The present sequence is the heavy chain variable (VH) region of
CC	murine IgD9 antibody.
XX	
XX	
Sequence	117 AA:

Query Match 19.5%; Score 24; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.6e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LVESGGGLVQPKGSLKLSCAASGF 27
 |||
 DB 4 LVESGGGLVQPKGSLKLSCAASGF 27

RESULT 12
 AA014978
 ID AA014978 standard: protein; 117 AA.
 XX AA014978;
 AC
 XX 05-SEP-2002 (first entry)
 DT
 DE Mouse heavy chain variable region (mab 1D9).
 XX
 KW Mouse; graft rejection; CC chemokine receptor 2 antagonist;
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
 KW lung transplant; heart-lung transplant; pancreas transplant;
 KW bowel transplant; heart transplant; graft versus host disease;
 KW chronic graft rejection; antibody heavy chain variable region; mab 1D9.
 OS Mus musculus.
 XX US2002042370-A1.
 PM
 XX 11-APR-2002.
 PD
 XX 13-APR-2001; 2001US-0835087.
 PF
 XX 14-APR-2000; 2000US-0549448.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Hancock MW;
 PI
 XX WPI: 2002-351265/38.
 DR
 XX Inhibiting graft rejection, graft versus host disease or chronic
 PT rejection of a transplanted graft, involves administering a CCR2
 PT antagonist -
 XX
 PS Disclosure: Fig 2; 16pp; English.
 XX
 CC The invention comprises a method of inhibiting graft rejection, graft
 CC versus host disease or chronic rejection of a transplanted graft. The
 CC method involves administering an antagonist of CC chemokine receptor 2
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain
 CC complementarily determining regions from various non-human origins). CCR2
 CC is known to be involved in the rejection of transplanted grafts. The
 CC method of the invention is useful for inhibiting graft rejection -
 CC particularly allografts such as kidney, liver, lung, heart-lung,
 CC pancreas, bowel and heart. The method of the invention is also useful for
 CC inhibiting graft versus host disease and for inhibiting chronic rejection
 CC of a transplanted graft. The present amino acid sequence represents a
 CC mouse antibody heavy chain variable region (mab 1D9).
 XX
 SQ Sequence 117 AA:
 Query Match 19.5%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.6e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LVESGGGLVQPKGSLKLSCAASGF 27
 |||
 DB 4 LVESGGGLVQPKGSLKLSCAASGF 27

RESULT 13

AAE07033
 ID AAE07033 standard: Protein; 148 AA.
 XX
 XX AAE07033;
 AC
 XX 16-OCT-2001 (first entry)
 DT
 XX
 DE Murine antibody 1D9 heavy chain variable region.
 XX
 KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; antibody 1D9 heavy chain variable region.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 XX FH 1..19
 XX FT /Label= Signal_peptide
 XX FT 20..148
 XX FT /note= "Murine mature antibody 1D9 kappa
 XX FT light chain variable region"
 XX FT 20..137
 XX FT /Label= Variable_region
 XX FT 138..148
 XX FT /Label= constant_region
 XX FT Misc-difference 148
 XX FT /note= "Encoded by GI"
 XX
 XX WO200157226-A1.
 XX
 XX 09-AUG-2001.
 XX
 XX 02-FEB-2001; 2001WO-US03537.
 XX
 XX 03-FEB-2000; 2000US-0497625.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX WPI: 2001-488888/53.
 XX N-PSDB: AMD13178.
 DR
 XX Humanised immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX
 PS Disclosure: Fig 21; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular

CC Intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is murine antibody 1D9 heavy chain variable region.
 XX
 SQ Sequence 148 AA;
 Query Match 19.5%; Score 24; DB 22; Length 148;
 Best Local Similarity 100.0%; Pred. No. 8, 1e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 LVESGGLVOPKSGSLKSCASGF 27
 ID 23 LVESGGLVOPKSGSLKSCASGF 46
 XX
 RESULT 14
 ID AAW94739 standard; Protein: 23 AA.
 XX
 AC AAW94739;
 XX
 DT 22-APR-1999 (first entry)
 DE Anti-Staph (HAY) 96-110 heavy chain variable region.
 XX
 KM Monoclonal antibody; Mab: lipoteichoic acid; gram positive; bacteria;
 KM immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KM MAb 96-110.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 1..12
 FT /note= "complementarity determining region (CDR)"
 XX
 PN WO9857994-A2.
 PD 23-DEC-1998.
 XX
 PF 16-JUN-1998; 98WO-US12402.
 XX
 PR 16-JUN-1997; 97US-0049871.
 XX
 PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX
 PI Fischer GW, Schuman RF, Stinson JL, Wong H;
 DR WPI; 1999-095329/08.
 DR N-PSDB; AAX05583.
 XX
 PT New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX
 PS Claim 21; Fig 12; 150pp; English.
 XX
 CC The invention relates to a monoclonal antibody (MAB) to lipoteichoic
 CC acid of gram positive bacteria, where the MAB is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94735-39 represent heavy chain variable regions of the
 CC anti-lipoteichoic antibody 96-100.

XX
 SQ Sequence 23 AA;
 Query Match 18.7%; Score 23; DB 20; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1, 6e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 101 RGASGIDYAMDYWGQSTLTYS 123
 ID 1 RGASGIDYAMDYWGQSTLTYS 23
 XX
 RESULT 15
 ID AAU09928 standard; Protein: 117 AA.
 XX
 AC AAU09928;
 XX
 DT 18-JUN-2002 (first entry)
 DE Humanised 1D9 heavy chain variable region, 1D9RHB protein sequence.
 XX
 DE Human; mouse; 4B4/CL heavy chain variable region; vasotropic;
 KW antiinflammatory; collagen disease; immunosuppressive;
 KW antidiabetic; insulin-dependent diabetes mellitus;
 KW inflammatory bowel disease; ulcerative colitis; 1D9RHB;
 KW graft rejection; allergic disease; antipsoriatic;
 KW antiarthritic; nephrotropic; antithyroid; restenosis;
 KW dermatological; anaphylaxis; cell adhesion inhibitor;
 KW vascular injury; autoimmune disease; immunoglobulin;
 KW complementarity determining region; CDR; CD18; CCR2;
 KW atherosclerosis; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 OS Chimeric - Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 27..30
 FT /note= "Part of H1 structure loop"
 FT Misc-difference 28
 FT /note= "Substitution of Thr residue normally present
 FT in human 4B4/CL sequence (AAU09926) by Ser
 FT residue normally present in mouse mab 1D9 heavy
 FT chain sequence (AAU09919)."
 FT Misc-difference 30
 FT /note= "Substitution of Ser residue normally present
 FT in human 4B4/CL sequence (AAU09926) by Asn
 FT residue normally present in mouse mab 1D9 heavy
 FT chain sequence (AAU09919)."
 FT Region 31..35
 FT /note= "Complementarity determining region 1 (CDR1),
 FT grafted from mouse mab 1D9 heavy chain
 FT sequence (AAU09919)."
 FT Region 50..68
 FT /note= "Complementarity determining region 2 (CDR2),
 FT grafted from mouse mab 1D9 heavy chain
 FT sequence (AAU09919)."
 FT Region 101..108
 FT /note= "Complementarity determining region 3 (CDR3),
 FT grafted from mouse mab 1D9 heavy chain
 FT sequence (AAU09919)."
 PN WO200170266-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 15-MAR-2001; 2001WO-US08266.
 PF
 PR 17-MAR-2000; 2000US-0528267.
 XX

PA (MILL-) MILLENNIUM PHARM INC.

XX
XX
PI Horvath CJ, Rao PE;

XX
XX
DR WPI: 2001-607511/69.

XX
XX
PT Inhibiting stenosis or restenosis of a blood vessel following vascular
PT injury or angioplasty in a subject by administering agent which
PT inhibits recruitment or adhesion of neutrophils, mononuclear cells to
PT injury site

PS Claim 32: Fig 18; 108pp; English.

XX
XX
CC The present invention relates to a new method of inhibiting stenosis or
CC restenosis of a blood vessel following vascular injury in a subject. The
CC new method comprises administering to the subject agents which inhibit
CC the adhesion and/or recruitment of neutrophils and mononuclear cells to
CC a site of vascular injury by binding CD18 or CCR2. The method of the
CC invention inhibits stenosis or restenosis of a blood vessel following
CC vascular injury arising from a vascular intervention procedure such as
CC vascular by-pass or transplantation surgery. The method is also useful
CC for treating a subject having an inflammatory disease or condition
CC mediated by neutrophil and mononuclear cell activity e.g. asthma and
CC graft versus host disease. Chronic inflammatory diseases of the lung,
CC collagen diseases, and insulin-dependent diabetes mellitus can also be
CC treated. The method is further useful for treating inflammatory bowel
CC diseases, such as ulcerative colitis. Additional diseases or conditions
CC include inflammatory or allergic diseases and conditions, including
CC systemic anaphylaxis of hypersensitivity responses, drug allergies,
CC psoriasis and inflammatory dermatoses, autoimmune diseases such as
CC arthritis, graft rejection and other diseases including atherosclerosis.
CC This sequence represents the variable region of one of several humanised
CC 1D9 heavy chains (AAU09927-AAU09930). These heavy chains were used in
CC the invention for the production of anti-CCR2 antibody or antigen-binding
CC fragment.

XX
SQ Sequence 117 AA:

Query Match 17.1%; Score 21; DB 22; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.1e-13;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 YAMNMVROAPGKGLEWVARIR 52

DB 32 YAMNMVROAPGKGLEWVARIR 52

Search completed: November 27, 2002, 07:27:59
Job time : 45.6911 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:25:20 ; Search time 18.5212 Seconds
(without alignments)
638.431 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 123

Sequence: 1 EVMLESGLVGPCKSLK.....SGIDYAMDYMGQTSLFVSS 123

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	31.7	119	2	A27630 Ig heavy chain pre
2	39	31.7	141	2	I25213 Ig heavy chain pre
3	38	30.9	100	2	S26462 Ig heavy chain v r
4	37	30.1	110	2	PH1091 Ig heavy chain v r
5	35	28.5	137	2	S42467 Ig heavy chain v r
6	28	22.8	110	2	PH1092 Ig heavy chain v r
7	28	22.8	121	2	A41940 Ig heavy chain v r
8	25	20.3	101	2	B42575 Ig heavy chain v r
9	20	16.3	110	2	PH1093 Ig heavy chain v r
10	18	14.6	118	2	S00700 Ig heavy chain v r
11	17	13.8	120	2	E49590 Ig heavy chain v r
12	16	13.0	105	2	S38488 Ig heavy chain v r
13	16	13.0	139	2	S31678 Ig heavy chain v r
14	15	12.2	34	2	S20777 Ig heavy chain v r
15	15	12.2	95	2	S46469 Ig heavy chain v r
16	15	12.2	98	2	PH0874 Ig heavy chain v r
17	15	12.2	98	2	S26891 Ig heavy chain v r
18	15	12.2	98	2	S26940 Ig heavy chain v r
19	15	12.2	98	2	S26894 Ig heavy chain v r
20	15	12.2	110	2	S36282 Ig heavy chain v r
21	15	12.2	112	2	S25572 Ig heavy chain v r
22	15	12.2	113	2	S25573 Ig heavy chain v r
23	15	12.2	116	2	S21979 Ig heavy chain v r
24	15	12.2	116	2	S17080 Ig heavy chain v r
25	15	12.2	117	2	S34012 Ig heavy chain v r
26	15	12.2	117	2	S21980 Ig heavy chain v r
27	15	12.2	119	2	PH1290 Ig heavy chain pre
28	15	12.2	119	2	PH1292 Ig heavy chain pre
29	15	12.2	121	2	H36005 Ig heavy chain v r

30	15	12.2	123	2	S26794 Ig heavy chain v r
31	15	12.2	123	2	S34009 Ig heavy chain v r
32	15	12.2	127	2	PT0369 Ig gamma chain pre
33	15	12.2	127	2	S19878 Ig heavy chain v r
34	15	12.2	133	2	PH1286 Ig heavy chain pre
35	15	12.2	133	2	PH1287 Ig heavy chain pre
36	15	12.2	141	2	S31669 Ig heavy chain v r
37	15	12.2	143	2	S23624 Ig heavy chain v r
38	15	12.2	144	2	PH1285 Ig heavy chain pre
39	15	12.2	145	2	I47203 Ig heavy chain pre
40	14	11.4	40	2	S33406 Ig heavy chain v r
41	14	11.4	40	2	S33410 Ig heavy chain v r
42	14	11.4	83	2	C25913 Ig heavy chain v r
43	14	11.4	94	2	PL0120 Ig heavy chain v r
44	14	11.4	94	2	S14580 Ig heavy chain v r
45	14	11.4	96	2	PH0873 Ig heavy chain v r

ALIGNMENTS

RESULT 1
A27630

Ig heavy chain precursor V-10 region (MRL-DNA4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 23-Jul-1999

C:Accession: A27630

R:Kotler, R.

J. Immunol. 140, 4031-4034, 1988

A:Title: A new murine Ig V-H gene family.

A:Reference number: A27630; MUID:88229103; PMID:3131427

A:Accession: A27630

A:Molecule type: DNA

A:Residues: 1-119 <KOR>

A:Cross-references: GB:M21470; NID:g196220; PIDN:AAA38634.1; PID:g196221; GB:M20825

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:34-119/Domain: Immunoglobulin homology <IMM>

Query Match 31.7%; Score 39; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.5e-32;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 YADSVKDRFTISRDSQSMLYLQNMNLTREPTAMYYCVR 100

DB 81 YADSVKDRFTISRDSQSMLYLQNMNLTREPTAMYYCVR 119

RESULT 2

Ig heavy chain precursor V region (MRL4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999

C:Accession: I32513

R:Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization a

A:Reference number: A94689; MUID:88331394; PMID:3136286

A:Accession: I32513

A:Molecule type: DNA

A:Residues: 1-141 <KOR>

A:Cross-references: GB:M20829; NID:g196951; PIDN:AAA38634.1; PID:g196952

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:34-119/Domain: Immunoglobulin homology <IMM>

Query Match 31.7%; Score 39; DB 2; Length 141;

Best Local Similarity 100.0%; Pred. No. 4e-32;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 YADSVKDRFTISRDSQSMLYLQNMNLTREPTAMYYCVR 100

DB 81 YADSVKDRFTISRDSQSMLYLQNMNLTREPTAMYYCVR 119

RESULT 3

S26462

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_rev150n 06-Jan-1995 #text_change 08-Sep-1997

C:Accession: S26462

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26462

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-100 <KAV>

A:Cross-references: EMBL:X59104; NID:951920; PID:951921

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 30.9%; Score 38; DB 2; Length 100;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 YADSVKDRFTISRDSQSMYLOMNNLKTEDTAMVYCV 99

DB 54 YADSVKDRFTISRDSQSMYLOMNNLKTEDTAMVYCV 91

RESULT 4

PH1091

Ig heavy chain V region (clone p17.79) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_rev150n 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1091

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1091

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-110 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 30.1%; Score 37; DB 2; Length 110;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 YADSVKDRFTISRDSQSMYLOMNNLKTEDTAMVYCV 98

DB 62 YADSVKDRFTISRDSQSMYLOMNNLKTEDTAMVYCV 98

RESULT 5

S42467

Ig heavy chain V region precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_rev150n 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S42467

R:Shlyanov, P.A.; Bspalov, I.A.; Terletska, H.N.; Deyev, S.M.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42466

A:Accession: S42467

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137 <SHI>

A:Cross-references: EMBL:X78107; NID:9460798; PID:CA54997.1; PID:9460799

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 28.5%; Score 35; DB 2; Length 137;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 SVKDRFTISRDSQSMYLOMNNLKTEDTAMVYCV 99

DB 84 SVKDRFTISRDSQSMYLOMNNLKTEDTAMVYCV 118

RESULT 6

PH1092

Ig heavy chain V region (clone p17.80) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_rev150n 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1092

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1092

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-110 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 22.8%; Score 28; DB 2; Length 110;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 YADSVKDRFTISRDSQSMYLOMNNLK 89

DB 62 YADSVKDRFTISRDSQSMYLOMNNLK 89

RESULT 7

A41940

Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)

N:Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region

C:Species: Mus musculus (house mouse)

C:Date: 04-Mar-1993 #sequence_rev150n 18-Nov-1994 #text_change 07-May-1999

C:Accession: A41940; PLO201

R:Heiron, J.N.; He, X.W.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Vos

Proteins 11, 159-175, 1991

A:Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional

A:Reference number: A41940; MUID:92086633; PMID:1749770

A:Accession: A41940

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-121 <HER>

A>Note: sequence extracted from NCBI backbone (NCBIP:70715)

R:Smith, R.G.; Voss Jr., E.W.

Mol. Immunol. 27, 463-470, 1990

A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies fro

A:Reference number: PLO198; MUID:90309768; PMID:2114528

A:Accession: PLO201

A:Molecule type: mRNA

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:50-68/Region: complementarity-determining 2

F:101-110/Region: complementarity-determining 3

F:101-106/Region: D region

F:107-115/Region: JH region

Query Match

Best Local Similarity 22.8%; Score 28; DB 2; Length 121;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 AMNVRAPGKGLGVARRSRKSNRYAT 60
 ||||||||||||||||||||||||||||
 Db 33 AMNVRAPGKGLGVARRSRKSNRYAT 60

RESULT 8

B42575

Ig heavy chain V region (anti-angiotensin II) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: B42575

R:Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.

Science 257, 528-531, 1992

A:Title: Recognition of angiotensin II: antibodies at different levels of an idiotypic r

A:Reference number: A42575; MUID:92342952; PMID:1636087

A:Accession: B42575

A:Molecule type: mRNA

A:Residues: 1-101 <GAR>

A:Cross-references: GB:5A0679; NID:9252098; PIDN:AAB22669.1; PID:9252099

A:Experimental source: BALB/c mice, myeloma cell line NS-1

A:Note: sequence extracted from NCBI backbone (NCBI:109337, NCBI:109338)

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: Immunoglobulin

F:7-92/Domain: Immunoglobulin homology <IMM>

Query Match 20.3%; Score 25; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 YADSVKDRFTSRDQSMLYLOM 86
 ||||||||||||||||||||||||

Db 54 YADSVKDRFTSRDQSMLYLOM 78

RESULT 9

PH1093

Ig heavy chain V region (clone S17.161) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1093

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1093

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-110 <TIL>

A:Experimental source: B cell, strain (NZB x NZW)F1

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-100/Domain: Immunoglobulin homology <IMM>

Query Match 16.3%; Score 20; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.3e-13;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GGGVQPKGSLKSCASGF 27
 ||||||||||||||||||||

Db 8 GGGVQPKGSLKSCASGF 27

RESULT 10

S00700

Ig heavy chain V region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: S00700

R:Yamawaki-Kataoka, Y.; Honjo, T.

Nucleic Acids Res. 15, 5888, 1987

A:Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy ch

A:Reference number: S00700; MUID:87289054; PMID:3112743

A:Accession: S00700

A:Molecule type: DNA

A:Residues: 1-118 <YAM>

A:Cross-references: EMBL:Y00380; NID:964810; PIDN:CAAB6452.1; PID:964811

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Introns: 15/3

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 14.6%; Score 18; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 8.4e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 LYLQNNLKTEDTAMVYC 98
 ||||||||||||||||||||

Db 98 LYLQNNLKTEDTAMVYC 115

RESULT 11

E49590

Ig heavy chain V region (ACHSV1, clone 2) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C:Accession: E49590

R:Burton, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.; Burton, D.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 355-359, 1994

A:Title: Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents

A:Reference number: A49590; MUID:94105168; PMID:8278393

A:Accession: E49590

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-120 <BUR>

A:Experimental source: bone marrow lymphocytes

A:Note: sequence extracted from NCBI backbone (NCBI:141854)

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:11-94/Domain: Immunoglobulin homology <IMM>

Query Match 13.8%; Score 17; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 8.9e-10;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 YAMNVRAPGKGLGV 48
 ||||||||||||||||||||

Db 28 YAMNVRAPGKGLGV 44

RESULT 12

S38488

Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38488

R:Marks, J.D.; Ouehand, W.H.; Bye, J.M.; Finern, R.; Corick, B.D.; Voak, D.; Thorpe

submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from

A:Reference number: S38488

A:Accession: S38488

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <MAR>

A:Cross-references: EMBL:Z23026; NID:9414023; PIDN:CAAB64561.1; PID:9414024

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 13.0%; Score 16; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 8.4e-09;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 MNWVROAPGKLEWV 48
|||||
DB 33 MNWVROAPGKLEWV 48

RESULT 13

S31678
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31678
R:Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31678
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CU>
A:Cross-references: EMBL:214169; NID:g31003; PIDN:CAA78538.1; PID:g31004
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:31-116/Domain: Immunoglobulin homology <IMM>

Query Match 13.0%; Score 16; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKLEWARI 51
|||||
DB 52 WVRQAPGKLEWARI 67

RESULT 14

S46469
Ig heavy chain V region (DA-5) - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S46469
R:COOK, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Win
Nature Genet. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46469
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-34 <COO>
A:Cross-references: EMBL:229981; NID:g505463; PIDN:CAA82871.1; PID:g1335180
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 12.2%; Score 15; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 MNWVROAPGKLEWV 48
|||||
DB 7 MNWVROAPGKLEWV 21

RESULT 15

S20777
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20777
R:Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Description: Analysis of human cord blood Ig heavy chain Iga and Igg repertoire.
A:Reference number: S20764
A:Accession: S20777
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-95 <MOR>
A:Cross-references: EMBL:211947; NID:g33886; PIDN:CAA78004.1; PID:g33887
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 12.2%; Score 15; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 MNWVROAPGKLEWV 48
|||||
DB 9 MNWVROAPGKLEWV 23

Search completed: November 27, 2002, 07:31:21
Job time : 19.5212 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:23:05 ; Search time 11.8726 Seconds
(without alignments)
429.695 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 123

Sequence: 1 EVMLVESGGGLVQPKGSLK.....SGIDYAMDYWGQGTSLTVSS 123

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	11.4	97	1 HV56_MOUSE	P18527 mus musculu
2	14	11.4	98	1 HV57_MOUSE	P18528 mus musculu
3	14	11.4	114	1 HV3B_HUMAN	P01763 homo sapien
4	14	11.4	116	1 HV3T_HUMAN	P01781 homo sapien
5	14	11.4	117	1 HV3O_HUMAN	P01776 homo sapien
6	14	11.4	117	1 HV53_MOUSE	P18524 mus musculu
7	14	11.4	117	1 HV54_MOUSE	P18525 mus musculu
8	14	11.4	119	1 HV3I_HUMAN	P01770 homo sapien
9	14	11.4	119	1 HV3M_HUMAN	P01774 homo sapien
10	14	11.4	119	1 HV3N_HUMAN	P01775 homo sapien
11	14	11.4	121	1 HV3J_HUMAN	P01771 homo sapien
12	14	11.4	126	1 HV3K_HUMAN	P01772 homo sapien
13	14	11.4	142	1 HV01_RAT	P01605 rattus norv
14	13	10.6	115	1 HV3S_HUMAN	P01780 homo sapien
15	13	10.6	116	1 HV3Q_HUMAN	P01778 homo sapien
16	13	10.6	116	1 HV3R_HUMAN	P01779 homo sapien
17	13	10.6	117	1 HV03_CARAU	P19180 carassius a
18	13	10.6	117	1 HV3C_HUMAN	P01764 homo sapien
19	13	10.6	118	1 HV3Y_HUMAN	P80419 homo sapien
20	13	10.6	119	1 HV3P_HUMAN	P01777 homo sapien
21	13	10.6	124	1 HV1D_HUMAN	P01760 homo sapien
22	13	10.6	136	1 HV2C_RABIT	P01829 oryctolagus
23	13	10.6	116	1 HV1A_RABIT	P01826 oryctolagus
24	12	9.8	116	1 HV36_MOUSE	P01806 mus musculu
25	12	9.8	117	1 HV2B_RABIT	P01828 oryctolagus
26	12	9.8	117	1 HV41_MOUSE	P01811 mus musculu
27	12	9.8	117	1 HV42_MOUSE	P01812 mus musculu
28	12	9.8	117	1 HV55_MOUSE	P18526 mus musculu
29	12	9.8	119	1 HV37_MOUSE	P01807 mus musculu
30	12	9.8	119	1 HV38_MOUSE	P01808 mus musculu
31	12	9.8	119	1 HV40_MOUSE	P01810 mus musculu
32	11	8.9	116	1 HV01_HETFR	P03983 heterodontu
33	11	8.9	117	1 HV17_MOUSE	P01786 mus musculu

ALIGNMENTS

34	11	8.9	120	1 HV3E_HUMAN	P01766 homo sapien
35	11	8.9	122	1 HV20_MOUSE	P01789 mus musculu
36	11	8.9	122	1 HV21_MOUSE	P01790 mus musculu
37	11	8.9	123	1 HV18_MOUSE	P01787 mus musculu
38	11	8.9	123	1 HV19_MOUSE	P01788 mus musculu
39	11	8.9	123	1 HV22_MOUSE	P01791 mus musculu
40	11	8.9	123	1 HV23_MOUSE	P01792 mus musculu
41	11	8.9	123	1 HV24_MOUSE	P01793 mus musculu
42	11	8.9	123	1 HV25_MOUSE	P01794 mus musculu
43	11	8.9	136	1 HV16_MOUSE	P01783 mus musculu
44	10	8.1	114	1 HV01_CANFA	P01784 canis fam11
45	10	8.1	115	1 HV3D_HUMAN	P01765 homo sapien

RESULT 1

HV56_MOUSE	STANDARD:	PRT:	97 AA.
AC P18527;			
DT 01-NOV-1990 (Rel. 16, Created)			
DT 01-NOV-1990 (Rel. 16, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE Ig heavy chain V region 914.			
OS Mus musculus (Mouse)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_Taxid=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=BALB/CJ;			
RX MEDLINE=89279149; PubMed=2499654;			
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;			
RT "Early onset of somatic mutation in immunoglobulin VH genes during			
RT the primary immune response."			
RL J. Exp. Med. 169:2007-2019(1989).			
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.			
DR PIR: J0504; HYMS91.			
DR HSSP: P01810; 2FB3.			
DR InterPro: IPR003006; Ig_MHC.			
DR InterPro: IPR003596; Ig_V.			
DR Pfam: PF00047; Ig_V.			
DR SMART: SM00406; IGV: 1.			
KM Immunoglobulin V region.			
FT NON_TER			
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FE5DA893 CRC64;			
Query Match	11.4%;	Score 14;	DB 1; Length 97;
Best local Similarity	100.0%;	Pred. NO. 1.8e-07;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY 16 GSILKSCASGFTF 29			
DB 16 GSILKSCASGFTF 29			
RESULT 2			
HV57_MOUSE	STANDARD:	PRT:	98 AA.
ID HV57_MOUSE			
AC P18528;			
DT 01-NOV-1990 (Rel. 16, Created)			
DT 01-NOV-1990 (Rel. 16, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE Ig heavy chain V region 6.96.			
OS Mus musculus (Mouse)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_Taxid=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=BALB/CJ;			
RX MEDLINE=89279149; PubMed=2499654;			

RA Levy N.S., Mallatiero U.V., Lebeque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCCLANE005: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.
DR PIR: J10501: HWS96.
DR HSSP: P01772: 2PB4.
DR InterPro: IPR003506: Ig_MHC.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR SMART: SM00406: IGV_1.
KW Immunoglobulin V region.
FT NON_TER 98
SQ SEQUENCE 98 AA: 11007 MW: B8644F792F8F95B CRC64:

Query Match 11.4%; Score 14; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GSLKISCAASGFTF 29
Db 16 GSLKISCAASGFTF 29
|||||

RESULT 3
HV3B_HUMAN STANDARD; PRT; 114 AA.
ID HV3B_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -I- MISCCLANE005: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR: A02046: M3HUMF.
DR HSSP: P01772: 2PB4.
DR InterPro: IPR003506: Ig_MHC.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR SMART: SM00406: IGV_1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT NON_TER 114
SQ SEQUENCE 114 AA: 12256 MW: D88294FB418A07B7 CRC64:

Query Match 11.4%; Score 14; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 MNWVROAPGKLEW 47
Db 34 MNWVROAPGKLEW 47
|||||

RESULT 4
HV3T_HUMAN STANDARD; PRT; 116 AA.
ID HV3T_HUMAN
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V-II region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
type), subgroup H III. Architecture of the complete IgM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -I- MISCCLANE005: THIS KU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR: A02064: M3HUGL.
DR HSSP: P01772: 2PB4.
DR InterPro: IPR003506: Ig_MHC.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR SMART: SM00406: IGV_1.
KW Immunoglobulin V region.
FT NON_TER 116
SQ SEQUENCE 116 AA: 12730 MW: 2C67CA9AAMAA1282 CRC64:

Query Match 11.4%; Score 14; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKLEWVA 49
Db 36 WVRQAPGKLEWVA 49
|||||

RESULT 5
HV3O_HUMAN STANDARD; PRT; 117 AA.
ID HV3O_HUMAN
AC P01776;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region WAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kenne J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
of the VH3 subgroup: definitive identification of four heavy chain
hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -I- MISCCLANE005: THIS CHAIN WAS ISOLATED FROM AN UG1 MYELOMA
PROTEIN.
DR PIR: A02059: G1HUMS.
DR HSSP: P01772: 2PB4.
DR InterPro: IPR003506: Ig_MHC.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR SMART: SM00406: IGV_1.
KW Immunoglobulin V region.
FT NON_TER 117
SQ SEQUENCE 117 AA: 13091 MW: 201DEF0E1E53D9BF CRC64:

Query Match 11.4%; Score 14; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKLEMYA 49
 DB 36 WVRQAPGKLEMYA 49

RESULT 6

HV53_MOUSE
 ID HV53_MOUSE STANDARD; PRT; 117 AA.

AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain v region RF precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/CJ;
 MEDLINE-89279149; PubMed-2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR HSSP; J0503; HVMSRF.

DR HSSP; P01810; 2FBJ.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

KW Immunoglobulin V region; Hybridoma; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.

FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

SO SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 11.4%; Score 14; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GSKLSCAASGTF 29
 DB 35 GSKLSCAASGTF 48

RESULT 7

HV54_MOUSE
 ID HV54_MOUSE STANDARD; PRT; 117 AA.

AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain v region 5-84 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/CJ;
 MEDLINE-89279149; PubMed-2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR; J0503; HVMS84.

DR HSSP; P01810; 2FBJ.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.

FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

SO SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 11.4%; Score 14; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GSKLSCAASGTF 29
 DB 35 GSKLSCAASGTF 48

RESULT 8

HV31_HUMAN
 ID HV31_HUMAN STANDARD; PRT; 119 AA.

AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region NIE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RC MEDLINE-77070269; PubMed-826475;

RA Ponslingl H., Hilschmann N.;

RT "The rule of antibody structure. The primary structure of a

monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The

chymotryptic peptides of the H-chain, alignment of the tryptic

peptides and discussion of the complete structure.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

RN [2]

RP DISULFIDE BOND.

RC MEDLINE-77070267; PubMed-1002129;

RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal

IgG1 immunoglobulin (myeloma protein NIE). I: Purification and

characterization of the protein, the L- and H-chains, the

cyanogen bromide cleavage products, and the disulfide bridges.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976)

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA

PROTEIN.

DR PIR; A02053; GIHUNI.

DR HSSP; P01772; 2FBJ.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

KW Immunoglobulin V region.

FT MOD_RES 1 1

FT DISULFID 22 96 PYRROLIDONE CARBOXYLIC ACID.

FT NON_TER 119 119

FT SEQUENCE 119 AA; 13242 MW; C96935A655E165B CH 54;

Query Match 11.4%; Score 14; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKGLEWYA 49
DB 36 WVRQAPGKGLEWYA 49

RESULT 9

HV3M_HUMAN STANDARD; PRT; 119 AA.
ID HV3M_HUMAN
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-III region F0M.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M
RT anti-gamma globulins.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A02057; M3H0PM.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT VARIANT 54
FT N -> D (PROBABLY DUE TO DEAMINATION
FT DURING ISOLATION).
FT /FTID=VAR_003966.
SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCB2610 CRC64;

Query Match 11.4%; Score 14; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKGLEWYA 49
DB 36 WVRQAPGKGLEWYA 49

RESULT 10

HV3N_HUMAN STANDARD; PRT; 119 AA.
ID HV3N_HUMAN
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-III region LAY.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M
RT anti-gamma globulins.";
SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCB2610 CRC64;

Query Match 11.4%; Score 14; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A02058; M3H0LY.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 119
SQ SEQUENCE 119 AA; 12858 MW; D6338098794DCFE5 CRC64;

Query Match 11.4%; Score 14; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKGLEWYA 49
DB 36 WVRQAPGKGLEWYA 49

RESULT 11

HV3J_HUMAN STANDARD; PRT; 121 AA.
ID HV3J_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-III region HIL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=79124695; PubMed=420800;
RX Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RA "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG H11.";
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR: A02054; G1H0HL.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 11.4%; Score 14; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKGLEWYA 49
DB 36 WVRQAPGKGLEWYA 49

RESULT 12

HV3K_HUMAN STANDARD; PRT; 126 AA.
ID HV3K_HUMAN
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-III region KOL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
SQ SEQUENCE 126 AA; 13566 MW; 480FC53610EF5DAB CRC64;

OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marquart M., Delsenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule kol and its antigen-binding fragment at 3.0 A
 and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 DR PIR: A02055; G1HUKL.
 DR PDB: 2FB4; 12-JUL-89.
 DR PDB: 2IG2; 12-JUL-89.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Igv; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT MOD_RES 1 1
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT STRAND 29 31
 FT HELIX 34 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 58 60
 FT TURN 62 67
 FT STRAND 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 99
 FT TURN 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 113
 FT STRAND 120 124
 FT NON_TER 126 126
 SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;
 Query Match 11.4%; Score 14; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 36 WYRQAPGKGLEWVA 49
 DB 36 WYRQAPGKGLEWVA 49
 RESULT 13
 HV01_RAT STANDARD; PRT; 142 AA.
 AC P01805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region IR2 precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Petersson U., Engstrom A., Karlsson L., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E.";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 CC -I- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
 IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/MSL RATS.
 DR PIR: A02075; EVRTR2.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Igv; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 142
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 16024 MW; DE29BECFE745DF3B CRC64;
 Query Match 11.4%; Score 14; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 36 WYRQAPGKGLEWVA 49
 DB 55 WYRQAPGKGLEWVA 68
 RESULT 14
 HV35_HUMAN STANDARD; PRT; 115 AA.
 ID HV35_HUMAN
 AC P01780;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region JON.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74142702; PubMed=4522793;
 RA Capra J.D., Kehoe J.M.;
 RT "Variable region sequences of five human immunoglobulin heavy chains
 of the VH3 subgroup: definitive identification of four heavy chain
 hypervariable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG3 MYELOMA
 PROTEIN.
 CC PIR: A02063; G3HUNJ.
 DR HSSP: P01772; 2FBA.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Igv; 1.
 KW Immunoglobulin V region.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12563 MW; 68B66B531C12514 CRC64;
 Query Match 10.6%; Score 13; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 36 WYRQAPGKGLEWVA 48
 DB 36 WYRQAPGKGLEWVA 48
 RESULT 15
 HV30_HUMAN

```

ID HV30_HUMAN STANDARD; PRT; 116 AA.
AC P01778;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region ZAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.W.;
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup: definitive identification of four heavy chain
RT hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGAI MYELOMA
CC PROTEIN.
DR PIR: A02061; A1H0ZP.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12582 MW; 892F8C217CEC9865 CRC64;

Query Match 10.6%; Score 13; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. NO. 2.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKGLWV 48
DB 36 WVRQAPGKGLWV 48

```

Search completed: November 27, 2002, 07:28:47
 Job time : 12.8726 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:24:25 ; Search time 34.668 Seconds
(without alignments)
731.044 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 123
Sequence: 1 EVMVSGGLVQPKGSLKL.....SGIDYAMDYMGQTSITVSS 123

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 segs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

SPTREMBL_21:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mhc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.todent:*

12: sp.virus:*

13: sp.vertebrate:*

14: sp.unclassified:*

15: sp.virus:*

16: sp.bacteriap:*

17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	13.8	494	Q96K68	Q96K68 homo sapien
2	17	13.8	597	Q96B89	Q96B89 homo sapien
3	15	12.2	118	Q9UL91	Q9UL91 homo sapien
4	15	12.2	471	Q8TC77	Q8TC77 homo sapien
5	14	11.4	95	Q9UL86	Q9UL86 homo sapien
6	14	11.4	113	Q9UL90	Q9UL90 homo sapien
7	14	11.4	116	Q9UL93	Q9UL93 homo sapien
8	14	11.4	119	Q920E7	Q920E7 mus musculu
9	14	11.4	122	Q9UL84	Q9UL84 homo sapien
10	14	11.4	437	Q9RIA4	Q9RIA4 mus musculu
11	14	11.4	487	Q99KA4	Q99KA4 mus musculu
12	14	11.4	613	Q8WUK1	Q8WUK1 homo sapien
13	13	10.6	104	Q9UL87	Q9UL87 homo sapien
14	13	10.6	112	Q9HCC1	Q9HCC1 homo sapien
15	13	10.6	112	Q9UGP3	Q9UGP3 homo sapien
16	13	10.6	118	Q9UL72	Q9UL72 homo sapien

17	13	10.6	121	4	Q9UL71	Q9UL71 homo sapien
18	13	10.6	131	4	Q9UL88	Q9UL88 homo sapien
19	13	10.6	573	4	Q8WU38	Q8WU38 homo sapien
20	12	9.8	124	6	Q9N0W6	Q9N0W6 oryctolagus
21	12	9.8	124	6	Q9N0W4	Q9N0W4 oryctolagus
22	12	9.8	143	11	Q92AR0	Q92AR0 mus musculu
23	12	9.8	145	11	Q92AR4	Q92AR4 mus musculu
24	12	9.8	146	11	Q92AR3	Q92AR3 mus musculu
25	12	9.8	298	11	Q9QYF0	Q9QYF0 mus musculu
26	11	8.9	15	11	Q9QV16	Q9QV16 ratu sp.
27	11	8.9	110	11	Q9JL77	Q9JL77 mus musculu
28	11	8.9	117	11	Q9QXE9	Q9QXE9 mus musculu
29	11	8.9	121	11	Q99NC4	Q99NC4 mus musculu
30	11	8.9	145	11	Q92AR1	Q92AR1 mus musculu
31	11	8.9	145	11	Q92AR9	Q92AR9 mus musculu
32	11	8.9	145	11	Q92AR6	Q92AR6 mus musculu
33	11	8.9	145	11	Q92AR7	Q92AR7 mus musculu
34	11	8.9	426	11	Q9DCD9	Q9DCD9 mus musculu
35	11	8.9	469	11	Q8R3V9	Q8R3V9 mus musculu
36	11	8.9	473	11	Q91Z05	Q91Z05 mus musculu
37	11	8.9	484	11	Q9JLA6	Q9JLA6 mus musculu
38	11	8.9	484	11	Q8VEA0	Q8VEA0 mus musculu
39	10	8.1	142	11	Q92AQ1	Q92AQ1 mus musculu
40	10	8.1	147	4	Q9Y509	Q9Y509 homo sapien
41	10	8.1	150	4	Q9Y298	Q9Y298 homo sapien
42	10	8.1	482	11	Q91X82	Q91X82 mus musculu
43	10	8.1	486	11	Q91Z07	Q91Z07 mus musculu
44	9	7.3	64	11	Q61750	Q61750 mus musculu
45	9	7.3	119	5	Q9GY22	Q9GY22 schistosoma

ALIGNMENTS

RESULT 1

ID Q96K68 PRELIMINARY: PRT: 494 AA.

AC Q96K68: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA.

DE Homo sapiens (Human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY GLAND;

RA Itogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Watanabe S., Kimura K., Murekami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Ninomiya K., Iwayanagi T.;

RT "NEO human cDNA sequencing project."

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK027379; BAB55072.1; -

DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig_4.

DR PROSITE: PS00290; Ig_MHC; UNKNOWN.1.

SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AE5AE4C0E CkC64;

Query Match 13.8%; Score 17; DB 4; Length 494;

Best local similarity 100.0%; Pred. No. 4.6e-05;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 65.0 kDa protein.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-CELL;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC015760; AHH5760.1;
 DR InterPro: IPR003006; Iq_MHC.
 DR Pfam: PF00047; Iq_5.
 DR PROSITE: PS00290; Iq_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 13.8%; Score 17; DB 4; Length 597;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 YAMNVRQAPGKLEWV 48
 DB 51 YAMNVRQAPGKLEWV 67

RESULT 3

Q9UL91 PRELIMINARY; PRT; 118 AA.
 AC Q9UL91;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Beiney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035023; AAD56259.1;
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003596; Iq_v.
 DR Pfam: PF00047; Iq_1.
 DR SMART: SM00406; IqV_1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 12.2%; Score 15; DB 4; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 MNWVRQAPGKLEWV 48
 DB 34 MNWVRQAPGKLEWV 48

RESULT 4

Q8TC77 PRELIMINARY; PRT; 471 AA.
 AC Q8TC77;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 51.8 kDa protein.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC024289; AAH24289.1;
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 12.2%; Score 15; DB 4; Length 471;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 MNWVRQAPGKLEWV 48
 DB 53 MNWVRQAPGKLEWV 67

RESULT 5

Q9ULB6 PRELIMINARY; PRT; 95 AA.
 AC Q9ULB6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Immunoglobulin heavy chain (Fragment).
 GN VH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tange Y., Kayano H.;
 RT "Human VH gene sequence";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB035268; BAA87067.1;
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003596; Iq_v.
 DR Pfam: PF00047; Iq_1.
 DR SMART: SM00406; IqV_1.
 FT NON_TER 1
 FT NON_TER 95
 SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D1D22574A CRC64;

Query Match 11.4%; Score 14; DB 4; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 WVRQAPGKLEWVA 49
 DB 35 WVRQAPGKLEWVA 48

RESULT 6

Q9UL90 PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DE Myosin-reactive immunoglobulin heavy chain variable region
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCB1_TaxID-9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035024; AAD56260.1; -.
DR HSSP: P01772; 2F84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match
Best Local Similarity 11.4%; Score 14; DB 4; Length 113;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLGVYA 49
DB 36 WVRQAPGKGLGVYA 49

RESULT 7
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID-9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035021; AAD56257.1; -.
DR HSSP: P01772; 2F84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match
Best Local Similarity 11.4%; Score 14; DB 4; Length 116;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLGVYA 49
DB 35 WVRQAPGKGLGVYA 48

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RESULT 8
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Pterin-mimicking anti-Idiotope heavy chain variable region
DE (Fragment).
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID-10090;
[1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horvath O., Colton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307937; AAL09421.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match
Best Local Similarity 11.4%; Score 14; DB 11; Length 119;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GSKLSCAASGTF 29
DB 16 GSKLSCAASGTF 29

RESULT 9
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID-9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035030; AAD56266.1; -.
DR HSSP: P01772; 2F84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 360540A1366545B8 CRC64;

Query Match
Best Local Similarity 11.4%; Score 14; DB 4; Length 122;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLGVYA 49

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Db 36 WVRQAPGKGLEWVA 49

RESULT 10

Q9RLA4
ID Q9RLA4 PRELIMINARY; PRT; 437 AA.
AC Q9RLA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Gamma heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -
DR HSSP; P01842; 7FAB.
DR MCD; MGI:96446; Igh-4.
DR InterPro: IPR003600; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; IG_1like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT SEQUENCE 437 AA; 48142 MW; 5C3A7BB3E7D697C CRC64;

Query Match 11.4%; Score 14; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GSKLSCAASGTF 29
Db 15 GSKLSCAASGTF 28

RESULT 11

Q99KA4
ID Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -
DR HSSP; P01810; 2FBJ.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003600; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IG; 3.

DR SMART; SM00406; IG; 1.
DR SMART; SM00410; IG_1like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 11.4%; Score 14; DB 11; Length 487;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GSKLSCAASGTF 29
Db 35 GSKLSCAASGTF 48

RESULT 12

Q8WUK1
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TONSIL;
RA Strausberg R.;
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 11.4%; Score 14; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLEWVA 49
Db 55 WVRQAPGKGLEWVA 68

RESULT 13

Q9UL87
ID Q9UL87 PRELIMINARY; PRT; 104 AA.
AC Q9UL87;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Betney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal


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RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035027; AAD56263.1; -.
DR HSSP: P01810; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match
Best Local Similarity 100.0%; Score 13; DB 4; Length 104;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLEWV 48
DB 15 WVRQAPGKGLEWV 27

RESULT 14
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment specific for native lysozyme: Isolation from a
RT human synthetic phage display library and characterization."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBD databases.
DR EMBL: AB049915; BAB16829.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR SMART: SM00410; Ig_Like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match
Best Local Similarity 100.6%; Score 13; DB 4; Length 112;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLEWV 48
DB 36 WVRQAPGKGLEWV 48

RESULT 15
Q9UGP3 PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN IGH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zafirovopoulos A., Kandiloglou M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RT "Induction of somatic mutations in human B cells by in vitro
RT immunization."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AJ132560; CAB65078.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;

Query Match
Best Local Similarity 100.6%; Score 13; DB 4; Length 112;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLEWV 48
DB 19 WVRQAPGKGLEWV 31

Search completed: November 27, 2002, 07:30:26
Job time : 36.918 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:26:06 : Search time 17.0965 Seconds
(without alignments)
211.682 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 123

Sequence: 1 EVMLVSGSGGLVQPKGSLKL.....SGIDYAMDYWGQSTLTVSS 123

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued_Patents_AA: *
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2: /cgnt2_6/ptodata/1/1aa/5B.COMB.pep: *
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4: /cgnt2_6/ptodata/1/1aa/6B.COMB.pep: *
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6: /cgnt2_6/ptodata/1/1aa/backfillseq1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	32.5	110	US-08-767-128-24	Sequence 24, Appl
2	40	32.5	115	US-08-767-128-36	Sequence 36, Appl
3	28	22.8	119	US-08-442-542-2	Sequence 2, Appl
4	28	22.8	119	US-08-765-469-2	Sequence 2, Appl
5	28	22.8	599	US-08-442-542-18	Sequence 18, Appl
6	28	22.8	599	US-08-765-469-18	Sequence 18, Appl
7	17	13.8	20	US-08-050-113-1	Sequence 1, Appl
8	17	13.8	113	US-08-428-197-46	Sequence 46, Appl
9	17	13.8	113	PCT-US93-10555-46	Sequence 46, Appl
10	16	13.0	120	US-07-934-373C-2	Sequence 2, Appl
11	16	13.0	120	US-07-934-373C-42	Sequence 42, Appl
12	16	13.0	120	US-07-934-373C-44	Sequence 44, Appl
13	16	13.0	120	US-07-934-373C-48	Sequence 48, Appl
14	16	13.0	120	US-08-437-642B-2	Sequence 2, Appl
15	16	13.0	120	US-08-437-642B-42	Sequence 42, Appl
16	16	13.0	120	US-08-437-642B-44	Sequence 44, Appl
17	16	13.0	120	US-08-146-206C-2	Sequence 2, Appl
18	16	13.0	120	PCT-US93-07832-2	Sequence 2, Appl
19	16	13.0	122	US-07-934-373C-20	Sequence 20, Appl
20	16	13.0	122	US-07-934-373C-45	Sequence 45, Appl
21	16	13.0	122	US-08-437-642B-20	Sequence 20, Appl
22	16	13.0	122	US-08-437-642B-45	Sequence 45, Appl
23	16	13.0	122	US-08-146-206C-20	Sequence 20, Appl
24	16	13.0	122	US-08-146-206C-26	Sequence 26, Appl
25	16	13.0	122	PCT-US93-07832-20	Sequence 20, Appl
26	16	13.0	449	US-09-679-397-2	Sequence 2, Appl
27	16	13.0	449	US-09-680-148-2	Sequence 2, Appl

28	16	13.0	461	2	US-08-463-587A-26	Sequence 26, Appl
29	16	13.0	461	2	US-08-463-667A-4	Sequence 4, Appl
30	16	13.0	461	3	US-08-923-854-26	Sequence 26, Appl
31	16	13.0	461	5	PCT-US91-09133-27	Sequence 27, Appl
32	15	12.2	98	1	US-08-211-202-116	Sequence 116, App
33	15	12.2	98	2	US-08-665-202-31	Sequence 31, Appl
34	15	12.2	111	1	US-08-379-057-32	Sequence 32, Appl
35	15	12.2	111	1	US-08-211-202-134	Sequence 134, Appl
36	15	12.2	112	1	US-08-211-202-133	Sequence 133, App
37	15	12.2	116	2	US-08-428-197-10	Sequence 10, Appl
38	15	12.2	116	2	US-09-027-449-50	Sequence 50, Appl
39	15	12.2	116	3	US-09-184-658-48	Sequence 48, Appl
40	15	12.2	116	3	US-08-804-444A-50	Sequence 50, Appl
41	15	12.2	116	4	US-09-026-985-50	Sequence 50, Appl
42	15	12.2	116	4	US-09-121-952A-50	Sequence 50, Appl
43	15	12.2	116	4	US-09-234-340A-50	Sequence 50, Appl
44	15	12.2	116	5	PCT-US93-10555-10	Sequence 10, Appl
45	15	12.2	117	3	US-08-545-809A-107	Sequence 107, App

ALIGNMENTS

RESULT 1
US-08-767-128-24
Sequence 24, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767, 128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541, 373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462, 798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35, 093
REFERENCE/DOCKET NUMBER: 8648, 49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 24:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 110 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
US-08-767-128-24

Query Match      32.5%; Score 40; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 YADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCVRR 101
Db 57 YADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCVRR 96

RESULT 2
US-08-767-128-36
: Sequence 36, Application US/08767128
: Patent No. 6111079
: GENERAL INFORMATION:
: APPLICANT: WYLIE, DWANE E.
: APPLICANT: LOPEZ, OSVALDO
: APPLICANT: MURRAY, PETER JOSEPH
: APPLICANT: GOEBEL, PETER
: TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
: TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant, Gould, Smith, Edell, Meltzer & Schmidt
: STREET: 3100 No. 6111079west Center, 90 South seventh St
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/767,128
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/09258
: FILING DATE: 05-JUN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/541,373
: FILING DATE: 10-OCT-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/462,798
: FILING DATE: 05-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Carter, Charles G.
: REGISTRATION NUMBER: 35,093
: REFERENCE/DOCKET NUMBER: 8648.49USF1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612/371-5278
: TELEFAX: 612/332-9081
: TELEX:
: INFORMATION FOR SEQ. ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 115 amino acids
```

```

: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
US-08-767-128-36

Query Match      32.5%; Score 40; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-30;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 YADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCVRR 101
Db 62 YADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCVRR 101

RESULT 3
US-08-442-542-2
: Sequence 2, Application US/08442542
: Patent No. 5686600
: GENERAL INFORMATION:
: APPLICANT: Carozzi, Nadine B.
: APPLICANT: Koziel, Michael G.
: TITLE OF INVENTION: Antibodies which Bind to Insect Gut
: TITLE OF INVENTION: Proteins and their use
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,542
: FILING DATE: 16-MAY-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/267,641
: FILING DATE: 28-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Spull, W. Murray
: REGISTRATION NUMBER: 32,943
: REFERENCE/DOCKET NUMBER: CGC 1750
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8615
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ. ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 119 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-442-542-2

Query Match      22.8%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 AMNWVRQAPGKGLWVARIKSNYYAT 60
Db 33 AMNWVRQAPGKGLWVARIKSNYYAT 60

RESULT 4
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US-08-765-469-2
; Sequence 2, Application US/08765469
; Patent No. 6069301
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/267,641
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-469-2

Query Match 22.8%; Score 28; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AMNWVRQAPGKGLEWVARIRSKSNYYAT 60
|||||
DB 33 AMNWVRQAPGKGLEWVARIRSKSNYYAT 60

RESULT 5
US-08-442-542-18
; Sequence 18, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-442-542-18

Query Match 22.8%; Score 28; DB 1; Length 599;
Best Local Similarity 100.0%; Pred. No. 1.2e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AMNWVRQAPGKGLEWVARIRSKSNYYAT 60
|||||
DB 187 AMNWVRQAPGKGLEWVARIRSKSNYYAT 214

RESULT 6
US-08-765-469-18
; Sequence 18, Application US/08765469
; Patent No. 6069301
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/267,641
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-765-469-18
Query Match      22.8%; Score 28; DB 3; Length 599;
Best Local Similarity 100.0%; Pred. No. 1.2e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AMNVROAPGKGLVWIRIRSKSNYYAT 60
   |||||
Db 187 AMNVROAPGKGLVWIRIRSKSNYYAT 214

RESULT 7
US-08-050-113-1
; Sequence 1, Application US/08050113
; Patent No. 5514554
; GENERAL INFORMATION:
; APPLICANT: Bacus, Sarah S
; APPLICANT: Yarden, Yosef
; APPLICANT: Sela, Michael
; TITLE OF INVENTION: Methods and Compositions for Cancer
; TITLE OF INVENTION: Therapy and for Prognosticating Responses to Cancer
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton, Dickinson &
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,113
; FILING DATE: 07-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hightet, David W
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: P-2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 847 5317
; TELEFAX: 201 848 9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-050-113-1

Query Match      13.8%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVESGGGLVQPKGSLKL 20
   |||||
Db 4 LVESGGGLVQPKGSLKL 20

RESULT 8
US-08-428-197-46
; Sequence 46, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
```

```
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US93/10555
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-428-197-46

Query Match      13.8%; Score 17; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AMNVROAPGKGLVW 49
   |||||
Db 33 AMNVROAPGKGLVW 49

RESULT 9
PCT-US93-10555-46
; Sequence 46, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
```

ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10555-46

Query Match 13.8%; Score 17; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 33 AMNVROAPGKGLEWVA 49
|||||
Db 33 AMNVROAPGKGLEWVA 49

RESULT 10
US-07-934-373C-2
Sequence 2, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934, 373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-2

Query Match 13.0%; Score 16; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 WVRQAPGKGLEWVARI 51
|||||
Db 36 WVRQAPGKGLEWVARI 51

RESULT 11
US-07-934-373C-42
Sequence 42, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934, 373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-42

Query Match 13.0%; Score 16; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 WVRQAPGKGLEWVARI 51
|||||
Db 36 WVRQAPGKGLEWVARI 51

RESULT 12
US-07-934-373C-44
Sequence 44, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WYRQAPGKGLEWVARI 51
Db 36 WYRQAPGKGLEWVARI 51

RESULT 15

US-08-437-642B-42
; Sequence 42, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437.642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709p2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-42

Query Match 13.0%; Score 16; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WYRQAPGKGLEWVARI 51
Db 36 WYRQAPGKGLEWVARI 51

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Job time : 18.0965 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:28:06 ; Search time 11.3977 Seconds
(without alignments)
171.849 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 123

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 102317

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*

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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*

12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*

13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	38	30.9	100	10	US-09-840-459-35
3	33	26.8	143	10	US-09-881-823-16
4	24	19.5	101	10	US-09-840-459-34
5	24	19.5	117	10	US-09-835-087-8
6	24	19.5	117	10	US-09-809-739-12
7	24	19.5	117	10	US-09-840-459-10
8	24	19.5	148	10	US-09-840-459-100
9	21	17.1	117	10	US-09-835-087-12
10	21	17.1	117	10	US-09-835-087-13
11	21	17.1	117	10	US-09-809-739-22
12	21	17.1	117	10	US-09-809-739-23
13	21	17.1	117	10	US-09-840-459-19
14	21	17.1	117	10	US-09-840-459-20
15	17	13.8	116	10	US-09-828-708-12
16	17	13.8	117	10	US-09-835-087-10
17	17	13.8	117	10	US-09-835-087-11
18	17	13.8	117	10	US-09-809-739-20
19	17	13.8	117	10	US-09-809-739-21

20	17	13.8	117	10	US-09-840-459-17	Sequence 17, Appl
21	17	13.8	117	10	US-09-840-459-18	Sequence 18, Appl
22	17	13.8	119	10	US-09-840-459-104	Sequence 104, Appl
23	16	13.0	120	10	US-09-971-543-11	Sequence 11, Appl
24	16	13.0	252	10	US-09-971-543-1	Sequence 1, Appl
25	15	12.2	98	12	US-10-066-895-4	Sequence 4, Appl
26	15	12.2	103	10	US-09-864-761-47355	Sequence 47355, A
27	15	12.2	115	10	US-09-974-449-2	Sequence 2, Appl
28	15	12.2	118	10	US-09-056-160B-108	Sequence 108, Appl
29	15	12.2	118	10	US-09-056-160B-112	Sequence 112, Appl
30	15	12.2	118	10	US-09-056-160B-116	Sequence 116, Appl
31	15	12.2	118	10	US-09-056-160B-118	Sequence 118, Appl
32	15	12.2	123	10	US-09-056-160B-7	Sequence 7, Appl
33	15	12.2	123	10	US-09-056-160B-14	Sequence 14, Appl
34	15	12.2	123	10	US-09-056-160B-127	Sequence 127, Appl
35	15	12.2	128	10	US-09-850-165-81	Sequence 81, Appl
36	15	12.2	128	10	US-09-850-165-110	Sequence 110, Appl
37	15	12.2	218	10	US-09-974-449-35	Sequence 35, Appl
38	14	11.4	14	10	US-09-253-794-33	Sequence 33, Appl
39	14	11.4	14	10	US-09-828-708-64	Sequence 64, Appl
40	14	11.4	87	10	US-09-840-459-53	Sequence 53, Appl
41	14	11.4	88	10	US-09-840-459-51	Sequence 51, Appl
42	14	11.4	89	10	US-09-840-459-48	Sequence 48, Appl
43	14	11.4	89	10	US-09-840-459-49	Sequence 49, Appl
44	14	11.4	98	10	US-09-840-459-38	Sequence 38, Appl
45	14	11.4	98	10	US-09-840-459-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1

US-09-893-615-87

; Sequence 87, Application US/09893615

; Patent No. US20020082395A1

; GENERAL INFORMATION:

; APPLICANT: Fischer, Gerald W.

; Schuman, Richard F.

; Wong, Hing

; Stinson, Jeffrey L.

; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND

; CHEMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR

; POSITIVE BACTERIA

; NUMBER OF SEQUENCES: 89

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

; CITY: Washington

; STATE: DC

; STREET: 1300 I Street, NW

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/893,615

; FILING DATE: 29-Jun-2001

; ATTORNEY/AGENT INFORMATION:

; NAME: Elnaudi, Carol P.

; REGISTRATION NUMBER: 32,220

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 87:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 123 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-09-893-615-87
Query Match      100.0%; Score 123; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.5e-103; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;

QY 1 EYMLVESGGGLVQPKGSLKSLCAASGFTFNAYAMNVRQAPGKGLVWVARIRSKSNYYAT 60
DQ 1 EYMLVESGGGLVQPKGSLKSLCAASGFTFNAYAMNVRQAPGKGLVWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCYVRRGASGIDYAMDYWGQTSLT 120
DQ 61 FYADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCYVRRGASGIDYAMDYWGQTSLT 120
QY 121 VSS 123
DQ 121 VSS 123

RESULT 2
US-09-840-459-35
; Sequence 35, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-35

Query Match      30.9%; Score 38; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 YADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCV 99
DQ 62 YADSVKDRFTISRDSQSMLYLQMNMLKTEDTAMYYCV 99

RESULT 3
US-09-881-823-16
; Sequence 16, Application US/09881823
; Patent No. US2002008066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
```

```
;
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-16

Query Match      26.8%; Score 33; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.2e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 DRFTISRDSQSMLYLQMNMLKTEDTAMYYCV 100
DQ 87 DRFTISRDSQSMLYLQMNMLKTEDTAMYYCV 119

RESULT 4
US-09-840-459-34
; Sequence 34, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-34

Query Match      19.5%; Score 24; DB 10; Length 101;
Best Local Similarity 100.0%; Pred. No. 7.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVESGGGLVQPKGSLKSLCAASGF 27
DQ 4 LVESGGGLVQPKGSLKSLCAASGF 27

RESULT 5
US-09-835-087-8
; Sequence 8, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
```

```
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
US-09-835-087-8

Query Match          19.5%; Score 24; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVESGGGLVQPKGSLKLSCAASGF 27
   |||||
Db 4 LVESGGGLVQPKGSLKLSCAASGF 27

RESULT 6
US-09-809-739-12
; Sequence 12, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
; NAME/KEY: SITE
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
; NAME/KEY: SITE
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (50)...(68)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-12

Query Match          19.5%; Score 24; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVESGGGLVQPKGSLKLSCAASGF 27
   |||||
Db 4 LVESGGGLVQPKGSLKLSCAASGF 27

RESULT 7
US-09-840-459-10
; Sequence 10, Application US/09840459
; Patent No. US20020150576A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-10

Query Match          19.5%; Score 24; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVESGGGLVQPKGSLKLSCAASGF 27
   |||||
Db 4 LVESGGGLVQPKGSLKLSCAASGF 27

RESULT 8
US-09-840-459-100
; Sequence 100, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-100

Query Match          19.5%; Score 24; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 LVESGGGLVQPKGSLKLSAASGF 27
Db 23 LVESGGGLVQPKGSLKLSAASGF 46

RESULT 9

US-09-835-087-12
; Sequence 12, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-12

Query Match 17.1%; Score 21; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 YAMNWRQAPKGLWVARIR 52
Db 32 YAMNWRQAPKGLWVARIR 52

RESULT 10

US-09-835-087-13
; Sequence 13, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-13

Query Match 17.1%; Score 21; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 YAMNWRQAPKGLWVARIR 52
Db 32 YAMNWRQAPKGLWVARIR 52

RESULT 11

US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. US20020106369A1

; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-22

Query Match 17.1%; Score 21; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 YAMNWRQAPKGLWVARIR 52
Db 32 YAMNWRQAPKGLWVARIR 52

RESULT 12

US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23

Query Match 17.1%; Score 21; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 YAMNWRQAPKGLWVARIR 52
Db 32 YAMNWRQAPKGLWVARIR 52

RESULT 13

US-09-840-459-19
; Sequence 19, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa

RESULT 14
US-09-840-459-20
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-19

Query Match 17.1%; Score 21; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 YAMNVRQAPGKGLEWVARIR 52
DB 32 YAMNVRQAPGKGLEWVARIR 52

RESULT 14
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Slobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-20

Query Match 17.1%; Score 21; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 YAMNVRQAPGKGLEWVARIR 52
DB 32 YAMNVRQAPGKGLEWVARIR 52

RESULT 15
US-09-828-708-12
; Sequence 12, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their part
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005U1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-12

Query Match 13.8%; Score 17; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 YAMNVRQAPGKGLEWV 48
DB 25 YAMNVRQAPGKGLEWV 41

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Job time : 12.3977 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 04:43:17 ; Search time 1253.48 Seconds
(without alignments) 7383.171 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318

Sequence: 1 CAAATGTTCTCTCCAGTC.....GGACCATGCTGGAAATAGA 318

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

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2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	199	62.6	318	10	AF178619	AF178619 Mus muscu
2	172	54.1	318	6	AR096196	AR096196 Sequence
3	172	54.1	318	6	AR210595	AR210595 Sequence
4	172	54.1	321	6	AR096128	AR096128 Sequence
5	172	54.1	321	6	AR210527	AR210527 Sequence
6	172	54.1	335	6	AR096195	AR096195 Sequence
7	172	54.1	335	6	AR210594	AR210594 Sequence
8	161	50.6	318	10	AF178620	AF178620 Mus muscu
9	147	46.2	767	10	MMU231219	AF231219 Mus muscu
10	146	45.9	327	10	AF087025	AF087025 Mus muscu
11	142	44.7	300	10	AF137624	AF137624 Mus muscu
12	142	44.7	300	10	AF137625	AF137625 Mus muscu
13	142	44.7	312	10	S48339	S48339 Ig V kappa
14	141	44.3	302	10	MUSIGKAF	M4153 Mus musculu
15	140	44.0	1370	10	MUSIGKAAR	K01641 Mouse Ig ka
16	139	43.7	272	10	AF139247	AF139247 Mus muscu
17	138	43.4	300	10	MUSIGKAFI	M4157 Mus musculu
18	135	42.5	293	10	AF206030	AF206030 Mus muscu
19	135	42.5	360	10	AF029237	AF029237 Mus muscu
20	134	42.1	321	10	MMIG013	X58586 Mouse hybri
21	131	41.2	318	6	AX256247	AX256247 Sequence
22	131	41.2	318	12	AF277092	AF277092 Synthetic
23	131	41.2	765	6	AX057984	AX057984 Sequence
24	131	41.2	1239	6	AX057945	AX057945 Sequence
25	131	41.2	1280	6	AX057947	AX057947 Sequence
26	125	39.3	403	6	I09200	I09200 Sequence 40
27	125	39.3	403	10	MUSIGKCNA	MI7954 Mouse Ig re
28	124	39.0	307	10	AF139231	AF139231 Mus muscu
29	120	37.7	386	6	A20585	A20585 A5B7 human1
30	120	37.7	705	6	A83197	A83197 Sequence 17
31	120	37.7	705	6	A8182927	A8182927 Sequence
32	120	37.7	732	6	A51863	A51863 Sequence 27
33	120	37.7	732	6	A83237	A83237 Sequence 57
34	120	37.7	732	6	AR085831	AR085831 Sequence
35	120	37.7	732	6	AR182961	AR182961 Sequence
36	120	37.7	1590	6	AX000421	AX000421 Sequence
37	120	37.7	1590	6	AX000422	AX000422 Sequence
38	120	37.7	3217	6	A83232	A83232 Sequence 52
39	120	37.7	3217	6	AR182956	AR182956 Sequence
40	117	36.8	403	6	I08812	I08812 Sequence 14
41	113	35.5	350	10	AY058906	AY058906 Mus muscu
42	109	34.3	264	10	MMU37887	U37887 Mus musculu
43	109	34.3	309	10	MMIGVKP4	X06517 Mouse Ig ac
44	107	33.6	435	6	A17967	A17967 Variable re
45	98	30.8	741	12	AY049714	AY049714 Synthetic

ALIGNMENTS

RESULT 1
AF178619
LOCUS AF178619
DEFINITION Mus musculus 8-3 immunoglobulin light chain variable region mRNA,
partial cds.
ACCESSION AF178619
VERSION AF178619.1 GI:5853221
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
REFERENCE
AUTHORS Putterman,C., Deocharan,B. and Diamond,B.
TITLE Molecular analysis of the autoantibody response in peptide-induced

QY	112	AAGCCAGGATCCTCCCCAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC	171
Db	112 <td>AAGCCAGGATCCTCCCCAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC</td> <td>171</td>	AAGCCAGGATCCTCCCCAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC	171
QY	172 <td>CCTGCTCGCTTCAGTGGCAGTGCGTCTGGGACCTCTTACTCTCTACAATCAGCAGAGTG</td> <td>231</td>	CCTGCTCGCTTCAGTGGCAGTGCGTCTGGGACCTCTTACTCTCTACAATCAGCAGAGTG	231
Db	172 <td>CCTGCTCGCTTCAGTGGCAGTGCGTCTGGGACCTCTTACTCTCTACAATCAGCAGAGTG</td> <td>231</td>	CCTGCTCGCTTCAGTGGCAGTGCGTCTGGGACCTCTTACTCTCTACAATCAGCAGAGTG	231
QY	232 <td>GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA</td> <td>274</td>	GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA	274
Db	232 <td>GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA</td> <td>274</td>	GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA	274

RESULT 4

AR096128

LOCUS AR096128 321 bp DNA Linear. PAT 08-SEP-2000

DEFINITION Sequence 6 from patent US 6005091.

ACCESSION AR096128

VERSION AR096128.1 GI:10024649

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 321)
AUTHORS Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev.,
Gross, M. Stuart., Nichols, A. John., Padlan, E. Augustin.,
Patel, A. Haribhai., and Sylvester, D. Robert.
TITLE Nucleic acids encoding immunoglobulin domains
JOURNAL Patent: US 6005091-A 6 21-DEC-1999;
FEATURES Location/Qualifiers
source 1. .321
BASE COUNT 78 a 92 c 79 g 72 t
ORIGIN

Query Match 54.1%; Score 172; DB 6; Length 321;
Best Local Similarity 99.6%; Pred. No. 6.2e-94;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
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Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
|||||
QY 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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Db 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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QY 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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Db 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||

RESULT 5
AR210527
LOCUS AR210527 321 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6391299.
ACCESSION AR210527
VERSION AR210527.1 GI:21513278
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 321)
AUTHORS Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev.,
Gross, M. Stuart., Nichols, A. John., Padlan, E. Augustin.,
Patel, A. Haribhai., and Sylvester, D. Robert.
TITLE Anti-factor IX/IXa antibodies
JOURNAL Patent: US 6391299-A 6 21-MAY-2002;
FEATURES Location/Qualifiers
source 1. .321
BASE COUNT 78 a 92 c 79 g 72 t
ORIGIN

Query Match 54.1%; Score 172; DB 6; Length 321;
Best Local Similarity 99.6%; Pred. No. 6.2e-94;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
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Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
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QY 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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Db 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
|||||
QY 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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Db 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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REFERENCE 1 (bases 1 to 321)
AUTHORS Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev.,
Gross, M. Stuart., Nichols, A. John., Padlan, E. Augustin.,
Patel, A. Haribhai., and Sylvester, D. Robert.
TITLE Anti-factor IX/IXa antibodies
JOURNAL Patent: US 6391299-A 6 21-MAY-2002;
FEATURES Location/Qualifiers
source 1. .321
BASE COUNT 78 a 92 c 79 g 72 t
ORIGIN

Query Match 54.1%; Score 172; DB 6; Length 321;
Best Local Similarity 99.6%; Pred. No. 6.2e-94;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
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Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
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QY 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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Db 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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QY 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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Db 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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RESULT 6
AR096195
LOCUS AR096195 335 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 102 from patent US 6005091.
ACCESSION AR096195
VERSION AR096195.1 GI:10024780
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 335)
AUTHORS Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev.,
Gross, M. Stuart., Nichols, A. John., Padlan, E. Augustin.,
Patel, A. Haribhai., and Sylvester, D. Robert.
TITLE Nucleic acids encoding immunoglobulin domains
JOURNAL Patent: US 6005091-A 102 21-DEC-1999;
FEATURES Location/Qualifiers
source 1. .335
BASE COUNT 80 a 97 c 85 g 73 t
ORIGIN

Query Match 54.1%; Score 172; DB 6; Length 335;
Best Local Similarity 99.6%; Pred. No. 6.2e-94;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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Db 112 AAGCCAGGATCCCTCCCCCAACCTGGATTCTGCCACATCCCAACCTGGCTTCTGGAGTC 171
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QY 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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Db 172 CTGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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RESULT 7
AR210594
LOCUS AR210594 335 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 102 from patent US 6391299.
ACCESSION AR210594
VERSION AR210594.1 GI:21513362
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 335)
AUTHORS Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev.,
Gross, M. Stuart., Nichols, A. John., Padlan, E. Augustin.,
Patel, A. Haribhai., and Sylvester, D. Robert.
TITLE Anti-factor IX/IXa antibodies
JOURNAL Patent: US 6391299-A 102 21-MAY-2002;
FEATURES Location/Qualifiers
source 1. .335
BASE COUNT 80 a 97 c 85 g 73 t
ORIGIN

Query Match 54.1%; Score 172; DB 6; Length 335;
Best Local Similarity 99.6%; Pred. No. 6.2e-94;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCAGCTGGTACCAGCAG 111
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Db 52  AGGTCACATGACCTTGGAGGCCACCTCAAGTGTAAATACATGACCTGGTACCAGCAG 111
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Qy 112  AAGCCAGGATCCTCCCAAAACCTCGATTTCTGCCACATCCAACTGGCTTCTGGAGTC 171
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Db 112  AAGCCAGGATCCTCCCAAAACCTCGATTTATGCCACATCCAACTGGCTTCTGGAGTC 171
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Qy 172  CCTGCTCGCTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
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Db 172  CCTGCTCGCTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTCAATCAGCAGAGTG 231
|||||
Qy 232  GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGAGTA 274
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Db 232  GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGAGTA 274
|||||

RESULT 8
AF178620
LOCUS      AF178620          318 bp      mRNA      linear      ROD 22-MAY-2000
DEFINITION Mus musculus 39-9 immunoglobulin light chain variable region mRNA,
partial cds.
ACCESSION AF178620
VERSION    AF178620.1  GI:5853223
KEYWORDS   Mus musculus.
SOURCE     Mus musculus.
ORGANISM   Mus musculus.
REFERENCE 1 (bases 1 to 318)
AUTHORS   Puterman,C., Deocharan,B. and Diamond,B.
TITLE     Molecular analysis of the autoantibody response in peptide-induced
autoimmunity
JOURNAL   J. Immunol. 164 (5), 2542-2549 (2000)
MEDLINE   20143847
PUBMED    10679092
REFERENCE 2 (bases 1 to 318)
AUTHORS   Puterman,C., Deocharan,B. and Diamond,B.
TITLE     Direct Submission
JOURNAL   Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
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         /strain="BALB/c"
         /db_xref="taxon:10090"
         /cell_line="39-9"
         /cell_type="hybridoma"
         /note="from peptide-immunized mouse"
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         /note="IgM kappa; anti-peptide antibody"
         /codon_start=1
         /product="immunoglobulin light chain variable region"
         /protein_id="AAB54373.1"
         /db_xref="GI:5853224"
         /translation="GIVLFSPAILSPGKVTWTCRASSSVYMLWYQKPGSSPK
PWYATSNLNSAGVPARFSGSGSYSLTISRVEADAATYYCOQSSNPPTGGGTK
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BASE COUNT 75 a 89 c 81 g 73 t
ORIGIN
Query Match 50.68; Score 161; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.6e-87;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144  TGGCACATCCCAACCTGGCTCTGGAGTCCCTCGCTTCAGTGGCAGTGGCTCTGGGAC 203
|||||
Db 144  TGGCACATCCCAACCTGGCTCTGGAGTCCCTCGCTTCAGTGGCAGTGGCTCTGGGAC 203
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Qy 204  CTCCTTACTCTCAACATCAGCAGAGTGAGGCTCAAGATGCTGCCACTTATTACTGCCA 263
|||||
Db 204  CTCCTTACTCTCAACATCAGCAGAGTGAGGCTCAAGATGCTGCCACTTATTACTGCCA 263
|||||
Qy 264  GCAGTGGAGTAGTAACCCACCCAGCTTCGGAGGGGGACCA 304
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Db 264  GCAGTGGAGTAGTAACCCACCCAGCTTCGGAGGGGGACCA 304
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RESULT 9
MMU231219
LOCUS      MMU231219          767 bp      DNA      linear      ROD 02-AUG-1999
DEFINITION Mus musculus IgVκ am4 gene.
ACCESSION AJ231219
VERSION    AJ231219.1  GI:5304999
KEYWORDS   IgVκ gene; immunoglobulin; kappa light chain; variable region.
SOURCE     Mus musculus.
ORGANISM   Mus musculus.
REFERENCE 1 (bases 1 to 767)
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Schaeble,K.F., Thiebe,R., Bensch,A., Brensing-Kneppers,J., Heim,V.,
Kirschbaum,T., Lamm,R., Ohnrich,M., Pourrajabi,S.,
Roessenthaler,F., Schwendinger,J., Wichelhaus,D. and Zocher
Zachau,H.G.
TITLE     Characteristics of the immunoglobulin Vκappa genes, pseudogenes,
relics and orphans in the mouse genome
JOURNAL   Eur. J. Immunol. 29 (7), 2082-2086 (1999)
MEDLINE   99354924
PUBMED    10427970
REFERENCE 2 (bases 1 to 767)
AUTHORS   Kirschbaum,T.
TITLE     Direct Submission
JOURNAL   Submitted (23-DEC-1998) T. Kirschbaum, Adolf-Butenandt-Institut
fuer, Physiologische Chemie, Schillerstr. 44, D-80336 Muenchen, FRG
FEATURES
     source
     1. 767
         /organism="Mus musculus"
         /strain="C57BL/6"
         /db_xref="taxon:10090"
         /chromosome="6"
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         /haplotype="c"
         /tissue_type="liver"
         /clone_lib="mouse cosmid library"
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         /gene="am4"
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         /product="immunoglobulin light chain variable region"
         /protein_id="CAB46133.1"
         /db_xref="GI:5305000"
         /translation="MDFQVQIFSELLISASVIMSGOIVLSQSPAILSPGKVTMT
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DAATYYCOQSSNP"
         join(<175..223,402..>703)
         /gene="am4"
         /product="variable region of immunoglobulin kappa light
chain"
         175..223
         /gene="am4"
         /number=1
         224..401
         /gene="am4"
         /number=1
         402..703
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         705..711
         /gene="am4"
         /note="heptamer recombination signal"
         724..732

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/Note="nonamer recombination signal"
BASE COUNT      210 a      180 c      149 g      228 t
ORIGIN
Query Match      46.2%; Score 147; DB 10; Length 767;
Best Local Similarity 99.5%; Pred. No. 1.4e-78;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 90 TTACATGCACTGGTACCAGCAGAGGATCCTCCGCCAAACCCCTGGATTCTGCCAC 149
|||||
Db 508 TTACATGCACTGGTACCAGCAGAGGATCCTCCGCCAAACCCCTGGATTCTGCCAC 567
|||||

QY 150 ATCCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
|||||
Db 568 ATCCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 627
|||||

QY 210 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
|||||
Db 628 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 687
|||||

QY 270 GAGTAGTAACCCACCCAC 287
|||||
Db 688 GAGTAGTAACCCACCCAC 705
|||||

RESULT 10
LOCUS AF087025 327 bp DNA linear ROD 01-OCT-1998
DEFINITION Mus musculus hybrid 2-2H11 immunoglobulin light chain gene, partial
sequence.
ACCESSION AF087025
VERSION AF087025.1 GI:3676751
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 327)
AUTHORS Retter,M.W. and Nemazee,D.
TITLE Receptor editing occurs frequently during normal B cell development
JOURNAL J. Exp. Med. (1998) In press
REFERENCE 2 (bases 1 to 327)
AUTHORS Retter,M.W. and Nemazee,D.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1998) Pediatrics K1023, National Jewish Medical
and Research Center, 1400 Jackson Street, Denver, CO 80206, USA
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/strain="B10.D2 x Jkappa deficient)f1"
/db_xref="taxon:10090"
/rearranged
/Note="hybrid 2-2H11"
<1..327
misc_feature
/Note="productively rearranged immunoglobulin light chain
silenced by RS-IRSI rearrangement; Vk4/5, Jk5"
BASE COUNT      75 a      95 c      84 g      73 t
ORIGIN
Query Match      45.9%; Score 146; DB 10; Length 327;
Best Local Similarity 99.5%; Pred. No. 6.2e-78;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 90 TTACATGCACTGGTACCAGCAGAGGATCCTCCGCCAAACCCCTGGATTCTGCCAC 149
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QY 150 ATCCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
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Db 150 ATCCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
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QY 210 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
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Db 210 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
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QY 270 GAGTAGTAACCCACCCAC 282
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Db 252 GAGTAGTAACCCAC 264
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RESULT 12
LOCUS AF137625 300 bp mRNA linear ROD 03-JUN-1999
DEFINITION Mus musculus clone HV3PH4E2 anti-I-fluorescein immunoglobulin light
chain mRNA, partial cds.
ACCESSION AF137624
VERSION AF137624.1 GI:4972854
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 300)
AUTHORS van der Keyl,H., Gellad,Z.F. and Owen,J.A.
TITLE Disparity in the kinetics of onset of hypermutation in
immunoglobulin heavy and light chains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 300)
AUTHORS van der Keyl,H., Gellad,Z.F. and Owen,J.A.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1999) Biology, Haverford College, 370 Lancaster
Avenue, Haverford, PA 19041-1392, USA
FEATURES
Location/Qualifiers
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/strain="Balb/c"
/db_xref="taxon:10090"
/clone="HV3P3G10"
/cell_type="hybridoma"
<1..300
/Note="from primary IgM antibody"
/codon_start=1
/product="anti-I-fluorescein immunoglobulin light chain"
/protein_id="AAD34819.1"
/db_xref="GI:4972855"
/translation="SPAILASPGKEKVTMTCRASSVSVMHWYQKPGSSPKPIYAT
SNLASGVPARFSGSGSTSYSLTISRVEADNATYYCOOWSSNPWTFGGTKLEIK"
BASE COUNT      73 a      84 c      77 g      66 t
ORIGIN
Query Match      44.7%; Score 142; DB 10; Length 300;
Best Local Similarity 99.5%; Pred. No. 1.8e-75;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 90 TTACATGCACTGGTACCAGCAGAGGATCCTCCGCCAAACCCCTGGATTCTGCCAC 149
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Db 72 TTACATGCACTGGTACCAGCAGAGGATCCTCCGCCAAACCCCTGGATTCTGCCAC 131
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QY 150 ATCCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
|||||
Db 132 ATCCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 191
|||||

QY 210 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
|||||
Db 192 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 251
|||||

QY 270 GAGTAGTAACCCAC 282
|||||
Db 252 GAGTAGTAACCCAC 264
|||||

RESULT 12
LOCUS AF137625 300 bp mRNA linear ROD 03-JUN-1999
DEFINITION Mus musculus clone HV3PH4E2 anti-I-fluorescein immunoglobulin light
```

```

chain mRNA, partial cds.
ACCESSION AF137625
VERSION AF137625.1 GI:4972856
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 300)
AUTHORS van der Keyl, H., Gellad, Z.F. and Owen, J.A.
TITLE Disparity in the kinetics of onset of hypermutation in immunoglobulin heavy and light chains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 300)
AUTHORS van der Keyl, H., Gellad, Z.F. and Owen, J.A.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1999) Biology, Haverford College, 370 Lancaster Avenue, Haverford, PA 19041-1392, USA
FEATURES
    source 1..300
        /organism="Mus musculus"
        /strain="Balb/c"
        /db_xref="taxon:10090"
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        <1..>300
        /note="from primary IgM antibody"
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        /db_xref="GI:4972857"
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BASE COUNT 71 a 85 c 78 g 66 t
ORIGIN
    Query Match 44.7%; Score 142; DB 10; Length 300;
    Best Local Similarity 99.5%; Pred. No. 1.8e-75;
    Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 90 TTACATGCACTGGTGTACAGCAGAGGCGAGGATCTCTCCCAAAACCCCTGGATTCTTGCAC 149
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 75 TTACATGCACTGGTGTACAGCAGAGGCGAGGATCTCTCCCAAAACCCCTGGATTCTTGCAC 134
QY 150 ATCCAACTGGCTTCTGAGTCCCTGCTGCTTCAGTGGCAGTGGGTCTGGACCTCTTA 209
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 135 ATCCAACTGGCTTCTGAGTCCCTGCTGCTTCAGTGGCAGTGGGTCTGGACCTCTTA 194
QY 210 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 195 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 254
QY 270 GAGTAGTAACCCA 282
    |||||||||||||||
Db 255 GAGTAGTAACCCA 267

RESULT 13
S48339
LOCUS S48339 312 bp mRNA linear ROD 08-MAY-1993
DEFINITION Ig V kappa -anti-idiotypic Fab [mice, mRNA Partial, 312 nt].
ACCESSION S48339
VERSION S48339.1 GI:257749
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 312)
AUTHORS Kasai, Y., Herlyn, D., Sperlagh, M., Maruyama, H., Matsushita, S. and
    Linnebach, A.J.
TITLE Monoclonal cloning of murine monoclonal anti-idiotypic Fab
JOURNAL J. Immunol. Methods 155 (1), 77-89 (1992)

```

```

MEDLINE 93017981
PUBMED 1383347
REMARK GenBank staff at the National Library of Medicine created this
        entry [NCBI gibbsq 118382] from the original journal article.
        This sequence comes from Fig. 5.
FEATURES
    source 1..312
        /organism="Mus sp."
        /db_xref="taxon:10095"
    gene 1..312
        /partial
        /gene="Ig V kappa>"
        /note="anti-idiotypic Fab"
    CDS 1..312
        /partial
        /gene="Ig V kappa>"
        /note="anti-idiotypic Fab; This sequence comes from Fig.
        5"
        /codon_start=1
        /protein_id="AAB23708.1"
        /db_xref="GI:257750"
        /translation="VMTQSPAILASPGKEVTMTCRASSSVSYMHVYQKPGSSPKPW
        IYATSNLASGVPAFSGSGSTSYSLTISRVEADANTYTCQWSSNPWTFGGTKLE
        IK"
BASE COUNT 76 a 88 c 80 g 68 t
ORIGIN
    Query Match 44.7%; Score 142; DB 10; Length 312;
    Best Local Similarity 99.5%; Pred. No. 1.8e-75;
    Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 90 TTACATGCACTGGTGTACAGCAGAGGCGAGGATCTCTCCCAAAACCCCTGGATTCTTGCAC 149
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 84 TTACATGCACTGGTGTACAGCAGAGGCGAGGATCTCTCCCAAAACCCCTGGATTCTTGCAC 143
QY 150 ATCCAACTGGCTTCTGAGTCCCTGCTGCTTCAGTGGCAGTGGGTCTGGACCTCTTA 209
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 144 ATCCAACTGGCTTCTGAGTCCCTGCTGCTTCAGTGGCAGTGGGTCTGGACCTCTTA 203
QY 210 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 204 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 263
QY 270 GAGTAGTAACCCA 282
    |||||||||||||||
Db 264 GAGTAGTAACCCA 276

RESULT 14
MUSIGKAPE
LOCUS Mus musculus Mouse Ig active kappa-chain mRNA V-region.
DEFINITION M64153
ACCESSION M64153.1 GI:196690
VERSION M64153.1
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
        processed gene.
SOURCE Mus musculus.
ORGANISM Mus musculus.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 302)
AUTHORS Caton, A.J., Stark, S.E., Kavalier, J., Staudt, L.M., Schwartz, D. and
    Gerhard, W.
TITLE Many variable region genes are utilized in the antibody response of
    BALB/c mice to the influenza virus A/PR/8/34 hemagglutinin
JOURNAL J. Immunol. 147 (5), 1675-1686 (1991)
MEDLINE 91349593
PUBMED 1908881
COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.
FEATURES
    source 1..302
        /organism="Mus musculus"
        /strain="BALB/c"

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CDs

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/cell_type="B-cell hybridoma"
<1..3302
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/product="immunoglobulin kappa-chain Vk-1"
/protein_id="AAB02375.1"
/db_xref="GI:196691"
/translation="QIVLSQSPAILSSPGEKVTMTCRASSSVSYMHVYQOKPGSSPK
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BASE COUNT 69 a 87 c 77 g 69 t
ORIGIN

Query Match 44.3%; Score 141; DB 10; Length 302;
Best Local Similarity 99.5%; Pred. No. 7.5e-75;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 90 TTACATGCACCTGGTACACGAGAGCCAGGATCCTCCCCAAACCCCTGGATTTCGCCAC 149
Db 90 TTACATGCACCTGGTACACGAGAGCCAGGATCCTCCCCAAACCCCTGGATTTCGCCAC 149

Qy 150 ATCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGCTCGGACCTCTTA 209
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Qy 210 CTCCTCACAATCAGCAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
Db 210 CTCCTCACAATCAGCAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269

Qy 270 GAGTAGTAACCC 281
Db 270 GAGTAGTAACCC 281

RESULT 15
MUSIGKAAR 1370 bp DNA linear ROD 27-APR-1993
LOCUS Mouse Ig kappa active V-region from 702/3 cells.
DEFINITION K01641
ACCESSION K01641
VERSION K01641.1 GI:196460
KEYWORDS C-region; V-region; Immunoglobulin light chain; immunoglobulin-kappa.
SOURCE Mouse 702/3 cell DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1370)
AUTHORS Parslow,T.G., Blair,D.L., Murphy,W.J. and Granner,D.K.
TITLE Structure of the 5' ends of immunoglobulin genes: a novel conserved sequence
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (9), 2650-2654 (1984)
MEDLINE 84194064
PUBMED 6425835
COMMENT Corrections to the sequence were sent by Dr. Richard E. Manroe and Dr. Tristram G. Parslow on Dec. 9, 1991.
FEATURES
source 1..1370
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/db_xref="taxon:10090"
join(776..824,1003..1337)
/partial
/note="Ig kappa chain variable region"
/codon_start=1
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DAATYYCQWSSNPRTFGGKTLEIK"
<776..824
/note="Ig kappa chain variable region"
/number=1
825..1002

CDs

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/cell_type="B-cell hybridoma"
<1..3302
/codon_start=1
/product="immunoglobulin kappa-chain Vk-1"
/protein_id="AAB02375.1"
/db_xref="GI:196691"
/translation="QIVLSQSPAILSSPGEKVTMTCRASSSVSYMHVYQOKPGSSPK
PWIAYSNLSAGVPARFSGSGTSLTISRVEADAATYYCQWSSNPYTFGGGT"

BASE COUNT 69 a 87 c 77 g 69 t
ORIGIN

exon

/note="kappa cds intron"
1003..>1337
/note="Ig kappa chain variable region"
/number=2
1338..>1369
/note="kappa cds intron J-C"
404 a 273 c 253 g 440 t

BASE COUNT 404 a 273 c 253 g 440 t
ORIGIN

Query Match 44.0%; Score 140; DB 10; Length 1370;
Best Local Similarity 100.0%; Pred. No. 2.9e-74;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 TGCCACATCCAACTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGAC 203
Db 1163 TGCCACATCCAACTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGAC 1222

Qy 204 CTCCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 263
Db 1223 CTCCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 1282

Qy 264 GCAGTGGAGTAGTAACCCAC 283
Db 1283 GCAGTGGAGTAGTAACCCAC 1302

Search completed: November 27, 2002, 06:25:23
Job time : 1264.48 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:54:06 : Search time 170.803 Seconds
(without alignments)
4192.745 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318

Sequence: 1 CAATATGTTCTCTCCAGTC.....GGACCATCTCGAATAAAGA 318

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	54.1	318	18 AAT79900	Anti-Factor IX MAB
2	172	54.1	318	24 ABK24005	Mouse-human light
3	172	54.1	321	18 AAT77377	Mouse anti-human F
4	172	54.1	321	24 ABK23937	Murine BC2 light c
5	172	54.1	335	18 AAT79899	Anti-Factor IX MAB
6	172	54.1	335	24 ABK24004	Murine BC2 light c
7	141	44.3	449	21 AAA43472	Mouse secreted exp
8	131	41.2	318	24 AAS97128	Anti-NGK2D hybrido
9	131	41.2	765	22 AAC86590	DNA encoding a fus

10	131	41.2	1239	22 AAC86563	DNA encoding a fus
11	131	41.2	1280	22 AAC86564	Anti-CD20 single c
12	130	40.9	1925	21 AAA15019	DNA encoding a CD-
13	125	39.3	403	8 AAN70972	2H7 VL sequence in
14	125	39.3	403	10 AAN91147	2H7 Vh sequence.
15	125	39.3	404	20 AAV82358	Mouse antibody 2H7
16	125	39.3	404	22 AAH22071	2H7 light chain va
17	125	39.3	426	18 AAT36317	2H7 antibody light
18	125	39.3	426	18 AAT70869	2H7 light chain va
19	125	39.3	426	18 AAT51043	Coding sequence fo
20	125	39.3	426	19 AAV03927	Mouse 2H7 antibody
21	125	39.3	426	19 AAV18558	Mouse 2H7 antibody
22	125	39.3	426	19 AAV18594	Mouse 2H7 antibody
23	120	37.7	387	13 AAQ20983	Encodes Variable r
24	120	37.7	387	13 AAQ27350	Encodes A5B7 antib
25	120	37.7	705	20 AAV72047	Plasmid PNG3/A5B7V
26	120	37.7	732	17 AAT42508	Murine A5B57 Light
27	120	37.7	732	20 AAV72081	Plasmid pPE14/A5B7
28	120	37.7	1590	20 AAX24806	A5B7 F(ab')2 codin
29	120	37.7	3217	20 AAV72076	IRES-based A5B7 ch
30	107	33.6	435	12 AAQ15115	IL-2 chimeric anti
31	107	33.6	435	14 AAQ36613	Anti-IL2R-alpha an
32	96	30.2	96	20 AAX05587	Anti-Staph (HAY) 9
33	94	29.6	765	22 AAC86591	DNA encoding a fus
34	90	28.3	292	11 AAQ06213	VK domain of antib
35	90	28.3	292	17 AAT63502	Monoclonal antibod
36	90	28.3	292	17 AAT36662	Monoclonal antibod
37	90	28.3	292	20 AAZ23370	Mouse antibody MAK
38	90	28.3	292	21 AAZ88541	Mouse monoclonal a
39	72	22.6	321	13 AAQ25668	Sequence of the an
40	71	22.3	306	11 AAQ06228	VK domain of antib
41	71	22.3	306	17 AAT63506	Monoclonal antibod
42	71	22.3	306	17 AAT36660	Monoclonal antibod
43	71	22.3	309	14 AAT45948	MAB BW 2128 light
44	71	22.3	331	18 AAT73613	CDNA encoding ligh
45	71	22.3	384	17 AAT15539	Mouse 5C7.29 monoc

ALIGNMENTS

RESULT 1

AAT79900
ID AAT79900 standard; CDNA; 318 BP.

XX AAT79900;

XX 27-DEC-1997 (first entry)

DT Anti-Factor IX MAB chimeric light chain CDNA.

DE Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;

KW chimeric antibody; antibody engineering; light chain; ss.

XX Chimeric Mus musculus.

OS Chimeric Homo sapiens.

XX Chimeric synthetic.

PN WO9726010-A1.

XX 24-JUL-1997.

XX 17-JAN-1997; 97WO-US00759.

XX 24-OCT-1996; 96US-0029119.

XX 17-JAN-1996; 96US-0010108.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX Blackburn MN, Church WR, Feuerstein GZ, Gross MS;

PI Nichols AJ, Padlan EA, Patel AH, Sylvester DR;

XX

```

DR WPI: 1997-385117/35.
XX P-PSDB; AAW24532.
PT Inhibiting thrombosis with self-limiting antibody to coagulation
PT factor - avoids uncontrolled bleeding by providing only partial
PT inhibition
XX
PS Example 7; Page 128; 150pp; English.
XX
CC This cDNA sequence encodes a mouse-human chimeric antibody
CC light chain (AAW24532) in which the variable region is derived
CC from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see
CC AAW79899) and human sequences from the immunoglobulin Rf-TS3/CL
CC framework. It was obtained by PCR amplification (see AAT79897-98)
CC of BC2 cDNA and insertion of the PCR product into p9HZHC 1-3 cDNA
CC (see AAT77374). Claimed anti-Factor IX chimeric antibodies are
CC useful in the treatment of thrombosis.
XX
SQ Sequence 318 BP; 79 A; 91 C; 78 G; 70 T; 0 other;
Query Match 54.1%; Score 172; DB 18; Length 318;
Best Local Similarity 99.6%; Pred. No. 4.7e-75;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGGTCACATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
DB 52 AAGGTCACATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
QY 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCAACTGGCTTCGGAGTC 171
DB 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCAACTGGCTTCGGAGTC 171
QY 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
DB 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCACCTATTATTACTGCCAGCAGTGGAGTA 274
DB 232 GAGGCTGAAGATGCTGCACCTATTATTACTGCCAGCAGTGGAGTA 274
RESULT 2
ABK24005
ID ABK24005 standard; cDNA; 318 BP.
XX
AC ABK24005;
XX
DT 09-APR-2002 (first entry)
XX
DE Mouse-human light chain DNA.
XX
KW Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
KW thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss;
KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KW vasotropic; cardiant; PCR primer; anti-respiratory syncytial virus;
KW heavy chain variable region; light chain variable region.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN WO200187339-A1.
XX
PD 22-NOV-2001.
XX
PF 05-OCT-2000; 2000WO-US27438.
XX
PR 15-MAY-2000; 2000US-0571434.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
XX
DR WPI: 2002-082944/11.

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DR P-PSDB; AAU81002.
XX
PT Treating post-thromboembolic induced ischaemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator
XX
PS Example 7; Page 154-155; 163pp; English.
XX
CC The invention relates to a method for treating an animal
CC post-thromboembolic induced ischaemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thromboembolic induced
CC ischaemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating
CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
CC stroke in an animal, and for reducing a required dose of a thrombolytic
CC agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding
CC antibodies and PCR primers used in the method of the invention.
XX
SQ Sequence 318 BP; 79 A; 91 C; 78 G; 70 T; 0 other;
Query Match 54.1%; Score 172; DB 24; Length 318;
Best Local Similarity 99.6%; Pred. No. 4.7e-75;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGGTCACATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
DB 52 AAGGTCACATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
QY 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCAACTGGCTTCGGAGTC 171
DB 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCAACTGGCTTCGGAGTC 171
QY 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
DB 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCACCTATTATTACTGCCAGCAGTGGAGTA 274
DB 232 GAGGCTGAAGATGCTGCACCTATTATTACTGCCAGCAGTGGAGTA 274
RESULT 3
AAT77377
ID AAT77377 standard; cDNA; 321 BP.
XX
AC AAT77377;
XX
DT 26-DEC-1997 (first entry)
XX
DE Mouse anti-human Factor IX antibody BC2 light chain cDNA.
XX
KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
KW humanised antibody; antibody engineering; light chain; CDR;
KW complementarity determining region; myocardial infarction;
KW angina; atrial fibrillation; stroke; kidney damage;
KW pulmonary embolism; deep vein thrombosis; coronary angioplasty;
KW disseminated intravascular coagulation; artificial organ; sepsis;
KW shunt; prosthesis; ss.
XX
OS Mus musculus.
XX
PN WO9736010-A1.
XX
PD 24-JUL-1997.
XX
PR 17-JAN-1997; 97WO-US00759.
XX
PR 24-OCT-1996; 96US-0029119.
XX
PR 17-JAN-1996; 96US-0010108.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
DR (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

```

XX PI Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
PI Nichols AJ, Padian EA, Patel AH, Sylvester DR;
XX DR WPI; 1997-385117/35.
DR P-PSDB; AAW24520.
XX PT Inhibiting thrombosis with self-limiting antibody to coagulation
PT factor - avoids uncontrolled bleeding by providing only partial
PT inhibition
XX PS Example 5; Page 64; 150pp; English.
XX CC This cDNA sequence encodes the light chain variable region (see
CC AAW24520) of mouse anti-human Factor IX monoclonal antibody BC2.
CC Claimed humanised antibodies (see AAW24510-18) contain CDRs (see
CC AAW24504-09) of BC2 heavy and light chains inserted into framework
CC regions of selected human antibody sequences. They have self-
CC limiting neutralising activity, and are useful as anticoagulant
CC agents in treatment of thrombosis associated with myocardial
CC infarction, unstable angina, atrial fibrillation, stroke, renal
CC damage, pulmonary embolism, deep vein thrombosis, percutaneous
CC transluminal coronary angioplasty, disseminated intravascular
CC coagulation, sepsis, or artificial organs, shunts or prostheses
CC (claimed). Also claimed are chimeric antibodies (see AAT79900), and
CC Fab and Fab'2 fragments. The claimed antibodies do not cause
CC uncontrolled bleeding (contrast heparin and warfarin) since they
CC provide only partial inhibition of coagulation.
XX SQ Sequence 321 BP; 78 A; 92 C; 79 G; 72 T; 0 other;
Query Match 54.1%; Score 172; DB 18; Length 321;
Best Local Similarity 99.6%; Pred. No. 4.7e-75;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACTGGTACCAGCAG 111
Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACTGGTACCAGCAG 111
QY 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
Db 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
QY 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Db 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
RESULT 4
ABK23937
ID ABK23937 standard; cDNA; 321 BP.
XX AC ABK23937;
XX DT 09-APR-2002 (first entry)
XX DE Murine BC2 light chain variable region cDNA.
XX KW Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
KW Thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss;
KW Thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KW Vasoactive; cardiant; PCR primer; anti-respiratory syncytial virus;
KW heavy chain variable region; light chain variable region.
XX OS Mus sp.
XX PN WO200187339-A1.
XX PD 22-NOV-2001.

XX PF 05-OCT-2000; 2000WO-US27438.
XX PR 15-MAY-2000; 2000US-0571434.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
XX WPI; 2002-082944/11.
DR P-PSDB; AAU80976.
XX PT Treating post-thromboembolic induced ischaemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator
XX PS Example 5; Page 94; 163pp; English.
XX CC The invention relates to a method for treating an animal
CC post-thromboembolic induced ischaemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thromboembolic induced
CC ischaemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating
CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
CC stroke in an animal, and for reducing a required dose of a thrombolytic
CC agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding
CC antibodies and PCR primers used in the method of the invention.
XX SQ Sequence 321 BP; 78 A; 92 C; 79 G; 72 T; 0 other;
Query Match 54.1%; Score 172; DB 24; Length 321;
Best Local Similarity 99.6%; Pred. No. 4.7e-75;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACTGGTACCAGCAG 111
Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACTGGTACCAGCAG 111
QY 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
Db 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
QY 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Db 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
RESULT 5
AAT79899
ID AAT79899 standard; cDNA; 335 BP.
XX AC AAT79899;
XX DT 27-DEC-1997 (first entry)
XX DE Anti-Factor IX MAb BC2 light chain PCR product.
XX KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
KW chimeric antibody; antibody engineering; light chain; ss.
XX OS Chimeric Mus musculus.
XX OS Chimeric synthetic.
XX PN WO9726010-A1.
XX PD 24-JUL-1997.
XX PD 17-JAN-1997; 97WO-US00759.

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XX 24-OCT-1996; 96US-0029119.
PR 17-JAN-1996; 96US-0010108.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
XX Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
PI Nichols AJ, Padlan EA, Patel AH, Sylvestre DR;
XX
XX WPI: 1997-385117/35.
DR P-PSDB: AAW24531.
XX
XX Inhibiting thrombosis with self-limiting antibody to coagulation
PT factor - avoids uncontrolled bleeding by providing only partial
PT inhibition
XX
XX Example 7; Page 126; 150pp; English.
PS
XX This cDNA sequence was obtained by PCR amplification (see AAT79897
CC and AAT79898) of the light chain variable region (see also AAT77377)
CC of mouse anti-human factor IX monoclonal antibody BC2 cDNA. The
CC amplification resulted in the addition of ScaI, NariI ends to the
CC VL region. The PCR product was ligated into ScaI, NariI-digested
CC F9ZHC 1-3 (see AAT77374) and digested with ScaI, NariI to produce a
CC mouse-human chimeric light chain F9ZHC (see AAT79900, AAW24532).
CC Claimed anti-Factor IX chimeric antibodies are useful in the
CC treatment of thrombosis.
XX
XX Sequence 335 BP; 80 A; 97 C; 85 G; 73 T; 0 other;
SQ
Query Match 54.1%; Score 172; DB 18; Length 335;
Best Local Similarity 99.6%; Pred. No. 4.6e-75;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGTCAACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCTGTGTACACGAG 111
DB 52 AAGTCAACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCTGTGTACACGAG 111
QY 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCCAACCTGGCTTCTGGAGTC 171
DB 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCCAACCTGGCTTCTGGAGTC 171
QY 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
DB 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
RESULT 6
ABK24004
ID ABK24004 standard; cDNA; 335 BP.
XX
XX AC ABK24004;
XX
XX 09-APR-2002 (first entry)
XX
XX Murine BC2 light chain modified variable region DNA.
DE
XX Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
XX thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss;
XX thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
XX vasotrophic; cardiant; PCR primer; anti-respiratory syncytial virus;
XX heavy chain variable region; light chain variable region.
XX
XX Mus sp.
XX Synthetic.
XX
XX PN WO200187339-A1.
XX
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PD 22-NOV-2001.
XX
XX 05-OCT-2000; 2000WO-US27438.
XX
XX 15-MAY-2000; 2000US-0571434.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA
XX Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
PI
XX WPI: 2002-082944/11.
DR P-PSDB: AAU81001.
XX
XX Treating post-thromboembolic induced ischaemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator
XX
XX Example 7; Page 152-153; 163pp; English.
PS
XX The invention relates to a method for treating an animal
CC post-thromboembolic induced ischaemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thromboembolic induced
CC ischaemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating thromboembolic
CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
CC stroke in an animal, and for reducing a required dose of a thrombolytic
CC agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding
CC antibodies and PCR primers used in the method of the invention.
XX
XX Sequence 335 BP; 80 A; 97 C; 85 G; 73 T; 0 other;
SQ
Query Match 54.1%; Score 172; DB 24; Length 335;
Best Local Similarity 99.6%; Pred. No. 4.6e-75;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGTCAACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCTGTGTACACGAG 111
DB 52 AAGTCAACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCTGTGTACACGAG 111
QY 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCCAACCTGGCTTCTGGAGTC 171
DB 112 AAGCCAGGATCTCTCCCAACCTGGATTTCGCCACATCCCAACCTGGCTTCTGGAGTC 171
QY 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
DB 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
RESULT 7
AAA43472
ID AAA43472 standard; cDNA; 449 BP.
XX
XX AC AAA43472;
XX
XX 21-AUG-2000 (first entry)
XX
XX Mouse secreted expressed sequence tag SEQ ID NO:47.
DE
XX Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
XX expressed sequence tag; EST; probe; chemotactic; proliferative;
XX immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
XX thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
XX antiviral; antidiabetic; antiasthmatic; vulnery; antiparkinsonian;
XX antidiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
XX cerebroprotective; anticonvulsant; antidepressant; gene therapy;
XX vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
XX insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
XX lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
```

KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW tumour; infection; depression; psoriasis; ss.
XX
OS Mus musculus.
XX
PN WO200021991-A1.
XX
PD 20-APR-2000.
XX
XX 15-OCT-1999; 99WO-US24206.
PF
XX 15-OCT-1998; 98US-0104436.
PR
XX (GENY) GENETICS INST INC.
PA
XX Jacobs K, McCoy JM, LaValle ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
XX WPI; 2000-317938/27.
DR
XX Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (SESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
XX
XX Claim 1; Page 214; 803pp; English.
PS
XX AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC sequence tags (SESTs), isolated from human, mouse, chicken and rat
CC tissue sources. The SESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC antischmatic; vulnary; antitumor; osteopathic; neuroprotective;
CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 449 BP; 110 A; 124 C; 107 G; 108 T; 0 other;
Query Match 44.3%; Score 141; DB 21; Length 449;
Best Local Similarity 99.5%; Pred. No. 9.4e-60;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 90 TTACATGCACTGGTACCAGCAGAGCCAGGATCTCCGCCAACCCCTGGATTTGCCCAC 149
Db 179 TTACATGCACTGGTACCAGCAGAGCCAGGATCTCCGCCAACCCCTGGATTTGCCCAC 238
QY 150 ATCCAACTGGCTCTGGAGTCCCTCGCTTACGTCGCTGGTCTGGACCTCTTA 209
Db 239 ATCCAACTGGCTCTGGAGTCCCTCGCTTACGTCGCTGGTCTGGACCTCTTA 298
QY 210 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
Db 299 CTCTCTCAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 358
QY 270 GAGTAGTAACCC 281
Db 359 GAGTAGTAACCC 370

RESULT 8
AAS97128
ID AAS97128 standard; cDNA; 318 BP.
XX
XX AAS97128;
AC
XX 26-FEB-2002 (first entry)
DT
XX
DE Anti-NGK2D hybridoma 6H7E7 variable light chain DNA.
XX
XX Human; NGK2D; NGK2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; ss;
KW sarcoma; leukemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
KW helminth; cytostatic; antimicrobial; immunomodulatory; lln2D10; 6H7E7;
KW 8G7C10; 6E5A7; PCR primer.
XX
XX Homo sapiens.
OS
XX
XX WO200171005-A2.
PN
XX 27-SEP-2001.
PD
XX 26-MAR-2001; 2001WO-EP03414.
PF
XX 24-MAR-2000; 2000EP-0106467.
PR
XX (KUFE/) KUFER P.
PA
XX Kufer P, Riethmuller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX
XX WPI; 2002-055119/07.
DR P-PSDB; AAU72833.
XX
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NGK2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
PS
XX Example 3; Fig 16; 114pp; English.
XX
XX The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NGK2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. The sequences represent the NGK2D receptor DNA, DNA
CC encoding the polypeptides of the invention and PCR primers used to
CC amplify the DNA sequences.
XX
SQ Sequence 318 BP; 76 A; 92 C; 80 G; 70 T; 0 other;
Query Match 41.2%; Score 131; DB 24; Length 318;
Best Local Similarity 99.5%; Pred. No. 8.2e-55;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 90 TTACATGCACTGGTACCAGCAGAGCCAGGATCTCCGCCAACCCCTGGATTTGCCCAC 149
Db 90 TTACATGCACTGGTACCAGCAGAGCCAGGATCTCCGCCAACCCCTGGATTTGCCCAC 149

QY 150 ATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
|||||
Db 150 ATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
|||||
QY 210 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
|||||
Db 210 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
|||||
QY 270 GA 271
||
Db 270 GA 271
||
RESULT 9
AAC86590
ID AAC86590 standard; DNA; 765 BP.
XX
AC AAC86590;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding a fusion of a single chain antibody and streptavidin.
XX
KW Streptavidin; tumour cell; cancer; adenocarcinoma;
KW hematological malignancy; ss.
XX
OS Synthetic.
OS Streptomyces avidinii.
OS Unidentified.
XX
PN WO200075333-A1.
XX
XX 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-US15595.
XX
XX 07-JUN-1999; 99US-0137900.
PR 03-DEC-1999; 99US-0168976.
XX
XX (NEOR-) NEORX CORP.
XX
XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
PI WPI; 2001-091213/10.
XX
DR New vector constructs for expressing genomic streptavidin fusion
XX proteins which are useful for targeting tumour cells associated with
PT cancer, e.g. adenocarcinomas -
PT
XX Example 5; Page 95; 100pp; English.
XX
PS The present sequence encodes a fusion of an anti-CD20 single chain
XX antibody and streptavidin. The fusion protein is expressed using
CC vectors of the invention. The specification describes vector constructs
CC for expressing streptavidin fusion proteins. The vector comprises a
CC nucleic acid encoding streptavidin or its functional variant operatively
CC linked to a promoter, and a cloning site for insertion of a second
CC nucleic acid sequence encoding a polypeptide to be fused with
CC streptavidin, interposed between the promoter and the first nucleic
CC acid sequence. Alternatively, the vector construct comprises a nucleic
CC acid, operatively linked to a promoter, encoding a polypeptide to be
CC fused with streptavidin, and a cloning site for insertion of a second
CC nucleic acid encoding at least 129 amino acids of streptavidin or its
CC functional variant. The fusion proteins are useful for targeting tumour
CC cells, particularly tumour cells associated with cancer,
CC e.g. adenocarcinomas or hematological malignancies. The vector construct
CC is useful for expressing of streptavidin fusion proteins. In particular,
CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
CC target site within a mammalian host.
XX
SQ Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;

Query Match 41.2%; Score 131; DB 22; Length 765;
Best Local Similarity 99.5%; Pred. No. 8e-55;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 90 TTACATGCACCTGGTACCAGCAGAGCCAGGATCCTCCCCAAACCCCTGGATTTCTGCCAC 149
|||||
Db 537 TTACATGCACCTGGTACCAGCAGAGCCAGGATCCTCCCCAAACCCCTGGATTTATGCCAC 596
|||||
QY 150 ATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209
|||||
Db 597 ATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 656
|||||
QY 210 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
|||||
Db 657 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 716
|||||
QY 270 GA 271
||
Db 717 GA 718
||
RESULT 10
AAC86563
ID AAC86563 standard; DNA; 1239 BP.
XX
AC AAC86563;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding a fusion of anti-CD20 single chain antibody/streptavidin.
XX
KW Streptavidin; tumour cell; cancer; adenocarcinoma;
KW hematological malignancy; ss.
XX
OS Synthetic.
OS Streptomyces avidinii.
OS Homo sapiens.
XX
PN WO200075333-A1.
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-US15595.
XX
XX 07-JUN-1999; 99US-0137900.
PR 03-DEC-1999; 99US-0168976.
XX
XX (NEOR-) NEORX CORP.
XX
XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
PI WPI; 2001-091213/10.
XX
DR P-PSDB; AAB30694.
XX
PT New vector constructs for expressing genomic streptavidin fusion
XX proteins which are useful for targeting tumour cells associated with
PT cancer, e.g. adenocarcinomas -
XX
XX Example 2; Fig 11A; 100pp; English.
XX
PS The present sequence encodes a fusion of an anti-CD20 single chain
CC antibody (B9E9) streptavidin. The fusion protein is expressed using
CC vectors of the invention. The specification describes vector constructs
CC for expressing streptavidin fusion proteins. The vector comprises a
CC nucleic acid encoding streptavidin or its functional variant operatively
CC linked to a promoter, and a cloning site for insertion of a second
CC nucleic acid sequence encoding a polypeptide to be fused with
CC streptavidin, interposed between the promoter and the first nucleic
CC acid sequence. Alternatively, the vector construct comprises a nucleic
CC acid, operatively linked to a promoter, encoding a polypeptide to be
CC fused with streptavidin, and a cloning site for insertion of a second
CC nucleic acid encoding at least 129 amino acids of streptavidin or its
CC functional variant. The fusion proteins are useful for targeting tumour
CC cells, particularly tumour cells associated with cancer,
CC e.g. adenocarcinomas or hematological malignancies. The vector construct
CC is useful for expressing of streptavidin fusion proteins. In particular,
CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
CC target site within a mammalian host.
XX
SQ Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;

CC functional variant. The fusion proteins are useful for targeting tumour
CC cells, particularly tumour cells associated with cancer,
CC e.g. adenocarcinomas or hematological malignancies. The vector construct
CC is useful for expressing of streptavidin fusion proteins. In particular,
CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
CC target site within a mammalian host.

XX Sequence 1239 BP; 270 A; 392 C; 356 G; 221 T; 0 other;

Query Match 41.2%; Score 131; DB 22; Length 1239;
Best Local Similarity 99.5%; Pred. No. 7.8e-55;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 90 TTACATGCACCTGGTACACAGCAGAGCCAGGATCCCTCCCAACCCCTGGATTTCGCCAC 149

DB 90 TTACATGCACCTGGTACACAGCAGAGCCAGGATCCCTCCCAACCCCTGGATTTCGCCAC 149

OY 150 ATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209

DB 150 ATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209

OY 210 CTCCTCACAATCAGCAGAGTGGAGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269

DB 210 CTCCTCACAATCAGCAGAGTGGAGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269

OY 270 GA 271

DB 270 GA 271

RESULT 11

AAC86564

ID AAC86564 standard; DNA; 1280 BP.

XX AAC86564;

XX 02-APR-2001 (first entry)

XX Anti-CD20 single chain antibody/streptavidin fusion protein cassette.

XX Streptavidin; tumour cell; cancer; adenocarcinoma;

XX hematological malignancy; ss.

XX Synthetic.

XX Streptomyces avidinii.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 3..1274

XX /*tag= a

XX /product= "anti-CD20 scFv and streptavidin fusion"

XX WO200075333-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15595.

XX 07-JUN-1999; 99US-0137900.

XX 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

XX WPI; 2001-091213/10.

XX P-PSDB; AAB30695.

XX New vector constructs for expressing genomic streptavidin fusion

XX proteins which are useful for targeting tumour cells associated with

XX cancer, e.g. adenocarcinomas .

PS Example 2; Fig 11C; 100pp; English.

XX The present sequence encodes a fusion of an anti-CD20 single chain
XX antibody (B9E9) streptavidin. The fusion protein is expressed using
XX vectors of the invention. The specification describes vector constructs
XX for expressing streptavidin fusion proteins. The vector comprises a
XX nucleic acid encoding streptavidin or its functional variant operatively
XX linked to a promoter, and a cloning site for insertion of a second
XX nucleic acid sequence encoding a polypeptide to be fused with
XX streptavidin, interposed between the promoter and the first nucleic
XX acid sequence. Alternatively, the vector construct comprises a nucleic
XX acid, operatively linked to a promoter, encoding a polypeptide to be
XX fused with streptavidin, and a cloning site for insertion of a second
XX nucleic acid encoding at least 129 amino acids of streptavidin or its
XX functional variant. The fusion proteins are useful for targeting tumour
XX cells, particularly tumour cells associated with cancer, the vector construct
XX e.g. adenocarcinomas or hematological malignancies. The vector construct
XX is useful for expressing of streptavidin fusion proteins. In particular,
XX these are useful as tools for medical diagnostics and therapeutic
XX purposes, e.g. for detecting the presence or absence of, or treating, a
XX target site within a mammalian host.

SQ Sequence 1280 BP; 267 A; 397 C; 388 G; 228 T; 0 other;

Query Match 41.2%; Score 131; DB 22; Length 1280;

Best Local Similarity 99.5%; Pred. No. 7.8e-55;

Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 90 TTACATGCACCTGGTACACAGCAGAGCCAGGATCCCTCCCAACCCCTGGATTTCGCCAC 149

DB 545 TTACATGCACCTGGTACACAGCAGAGCCAGGATCCCTCCCAACCCCTGGATTTCGCCAC 604

OY 150 ATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209

DB 605 ATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 664

OY 210 CTCCTCACAATCAGCAGAGTGGAGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269

DB 665 CTCCTCACAATCAGCAGAGTGGAGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 724

OY 270 GA 271

DB 725 GA 726

RESULT 12

AAA15019

ID AAA15019 standard; DNA; 1925 BP.

XX AAA15019;

XX 21-AUG-2000 (first entry)

XX DNA encoding a CD-20 specific chimeric receptor.

XX CD20-specific receptor; CD-20 specific redirected T cell; leukemia;

XX CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;

XX stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; ss.

XX Synthetic.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 27..1928

XX /*tag= a

XX WO200023573-A2.

XX 27-APR-2000.

XX 20-OCT-1999; 99WO-US24484.

XX 20-OCT-1998; 98US-0105014.

```
XX (CITY ) CITY OF HOPE.
XX PA
XX Raubitschek A, Jensen MC, Wu AM;
XX
XX WPI; 2000-339676/29.
XX P-PSDB; AAY84965.
XX
XX Genetically engineered CD20-specific redirected T cells useful for
XX treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+
XX acute or chronic leukemia, and autoimmune disease -
XX
XX Example 1; Page 50-53; 58pp; English.
XX
XX The present sequence encodes a synthetic CD20-specific chimeric
XX receptor. The specification describes CD-20 specific redirected T cells
XX which express and bear on the cell surface membrane a CD20-chimeric
XX receptor comprising an intracellular signalling domain, a transmembrane
XX domain and an extracellular domain, the extracellular domain comprising
XX a CD20-specific receptor. The genetically engineered CD20-specific
XX redirected T cells are useful for treating a CD20+ malignancy, such
XX as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a
XX human patient having previously undergone myeloablative chemotherapy and
XX stem cell rescue. The genetically engineered CD20-specific redirected
XX T cells are also useful for abrogating an untoward B cell function, such
XX as autoimmune disease (lupus or rheumatoid arthritis) in a patient.
XX
XX Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;
XX
XX Query Match 40.9%; Score 130; DB 21; Length 1925;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-54;
XX Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 144 TGGCACATCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
XX |
XX Db 230 TGGCACATCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 289
XX |
XX QY 204 CTCTTACTCTCTCACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 263
XX |
XX Db 290 CTCTTACTCTCTCACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 349
XX |
XX QY 264 GCAGTGGAGT 273
XX |
XX Db 350 GCAGTGGAGT 359
XX |
XX
XX RESULT 13
XX ID AAN70972 standard; cDNA; 403 BP.
XX AC
XX AC AAN70972;
XX
XX 03-OCT-2002 (updated)
XX DT 09-APR-1991 (first entry)
XX
XX 2H7 VL sequence in which the VK gene contains JK5 sequences.
XX
XX Chimeric antibody; Anti-cancer antibody; ss.
XX
XX Chimeric - Homo sapiens.
XX OS Chimeric - Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 20..86
XX /*tag= a
XX /label=leader peptide
XX CDS 67..138
XX /*tag= b
XX /label=FR1
XX CDS 139..165
XX /*tag= c
XX /label=CDR1
XX CDS 166..210
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FT /label=FR2
FT 211..231
FT /*tag= e
FT /label=CDR2
FT 232..327
FT /*tag= f
FT /label=FR3
FT 328..354
FT /*tag= g
FT /label=CDR3
FT 355..403
FT /*tag= h
FT /label=FR4
FT 349..403
FT /*tag= i
FT /label=JK5
XX
XX W08702671-A.
XX
XX 07-MAY-1987.
XX
XX 27-OCT-1986; 86WO-US02269.
XX
XX 01-NOV-1985; 85US-0793980.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX (ROBI/) ROBINSON R R.
XX
XX Robinson RR, Liu AY, Horwitz AH, Wall R;
XX
XX WPI; 1987-136004/19.
XX P-PSDB; AAP70628.
XX
XX Prodn. of immunoglobulin chains and molecules - is by recombinant
XX DNA procedures, with chimeric antibodies etc. related to cancer
XX specific antigens.
XX
XX Example; Fig 22; 126pp; English.
XX
XX The patentors claim a chimeric antibody molecule comprising 2 light
XX chains and 2 heavy chains, each comprising a constant human region
XX and a variable non-human region. Coding sequences for the Ig chains
XX are also claimed. The invention provides consensus sequences of
XX light and heavy chain J regions useful in the design of
XX oligonucleotides (UIGs) for use as primers or probes for cloning
XX immunoglobulinlight or heavy chain mRNAs or genes. Depending on the
XX nature of design of a particular UIG, it may be capable of
XX hybridizing to all Ig mRNAs or genes containing a single specific J
XX sequence. UIG denotes universal immunoglobulin gene.
XX (Updated on 03-OCT-2002 to add missing OS field.)
XX
XX Sequence 403 BP; 100 A; 112 C; 93 G; 98 T; 0 other;
XX
XX Query Match 39.3%; Score 125; DB 8; Length 403;
XX Best Local Similarity 100.0%; Pred. No. 7.5e-52;
XX Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 149 CATCCAACCTGGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTT 208
XX |
XX Db 234 CATCCAACCTGGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTT 293
XX |
XX QY 209 ACTTCTCTCAATCAGCAGAGTGGAGCTCAAGCTGCTGCACCTTATTACTGCCAGCAGT 268
XX |
XX Db 294 ACTTCTCTCAATCAGCAGAGTGGAGCTCAAGCTGCTGCACCTTATTACTGCCAGCAGT 353
XX |
XX QY 269 GGAGT 273
XX |
XX Db 354 GGAGT 358
XX |
XX
XX RESULT 14
XX AAN91147
```


ID AAN91147 standard; DNA; 403 BP.
XX AC AAN91147;
XX DT 06-JUL-1990 (first entry)
XX DE 2H7 Vh sequence.
XX KW Antibodies; passive immunisation; pH3-6a; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT CDS 20..403
XX FT misc_feature 320..352 a
XX FT /*tag= b
XX FT /note="JK5 region."
XX PN W08900999-A.
XX PD 09-FEB-1989.
XX PF 25-JUL-1988; 88WO-US02514.
XX PR 24-JUL-1987; 87US-0077528.
XX PA (ITGE-) INT GENETIC ENG INC.
XX PI Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;
XX PR WPI; 1989-061144/08.
XX DR P-PSDB; AAP94778.
XX PT Polynucleotide(s) encoding Immunoglobulin molecules -
PT used for efficient prodn. of chimeric human or non-human or
PT class switched antibodies.
XX PS Disclosure; ; 7pp; English.
XX CC Sequence, derived from M13 subclones of gene fragments, carries the
CC variable region of chimeric immunoglobulin sequence. The antibodies are
CC useful in passive immunisation avoiding negative reactions. They are
CC also useful in assaying and in vitro imaging.
XX SQ Sequence 403 BP; 100 A; 112 C; 93 G; 98 T; 0 other;

Query Match 39.3%; Score 125; DB 10; Length 403;
Best Local Similarity 100.0%; Pred. No. 7.5e-52;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 149 CATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGACCTCTT 208
Db 234 CATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGACCTCTT 293
Qy 209 ACTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT 268
Db 294 ACTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT 353
Qy 269 GGAGT 273
Db 354 GGAGT 358

RESULT 15

AAV82358

ID AAV82358 standard; DNA; 404 BP.

XX AC AAV82358;

XX DT 30-MAR-1999 (first entry)

XX DE Mouse antibody 2H7 light chain variable region encoding sequence.

XX KW pelB pectate lyase; secretion signal; chimeric antibody;
KW light chain; B-cell antigen; antibody 2H7; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 21..404
XX FT /*tag= a
XX FT /note= "partial CDS"
XX PN US5846818-A.
XX PD 08-DEC-1998.
XX PF 06-JUN-1995; 95US-0472696.
XX PR 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0987555.
XX PR 22-FEB-1993; 93US-0020671.
XX PR 09-DEC-1994; 94US-0357234.
XX PR 06-JUN-1995; 95US-0472696.
XX PA (XOMA) XOMA CORP.
XX PI Better M, Horowitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX DR WPI; 1999-059072/05.
XX DR P-PSDB; AAW89541.
XX PT pelB pectate lyase signal sequence - and vector for expression of
PT secreted proteins in Gram-negative bacteria
XX PS Example 4; Fig 22; 98pp; English.
XX CC The present sequence encodes the mouse antibody 2H7 light chain
CC variable region. Antibody 2H7 is specific for human B-cell antigen. The
CC antibody sequence was used to construct a chimeric human-mouse antibody,
CC in the course of the invention. The chimeric antibody is expressed in a
CC secretion vector comprising a pelB pectate lyase secretion signal
CC peptide. The pelB pectate lyase secretion sequence is useful for
CC producing a protein such as a chimeric antibody in a bacterial host.
XX SQ Sequence 404 BP; 100 A; 113 C; 93 G; 98 T; 0 other;

Query Match 39.3%; Score 125; DB 20; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.5e-52;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 149 CATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGACCTCTT 208
Db 235 CATCCAACCTGGCTTCTCGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGACCTCTT 294
Qy 209 ACTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT 268
Db 295 ACTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT 354
Qy 269 GGAGT 273
Db 355 GGAGT 359

Search completed: November 27, 2002, 05:37:46

Job time : 177.303 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 05:31:20 ; Search time 1316.44 Seconds
(without alignments)
3912.201 Million cell updates/sec

Title: US-09-893-615-88
Perfect score: 318
Sequence: 1 CAATATGTTCTCTCCAGTC.....GGACCATGCTGGAATAAGA 318

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_estc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_est3:*
- 12: gb_est4:*
- 13: gb_est5:*
- 14: gb_estfun:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_Other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	28.9	639	13	BC968615 602836416
2	89	28.0	991	13	BC968852 602836142
3	81	25.5	413	10	BE624609 uu24c05.y
4	81	25.5	532	13	BI104783 602891329
5	81	25.5	569	13	BC964957 602829274
6	81	25.5	639	12	BF583310 602101781

7	71	22.3	396	9	AA691311	AA691311 vs14f01.r
8	71	22.3	960	12	BF581607	BF581607 602099949
9	70	22.0	918	14	BQ946795	BQ946795 AGENCOURT
10	68	21.4	959	14	BQ939046	BQ939046 AGENCOURT
11	67	21.1	798	13	BG968518	BG968518 602835104
12	64	20.1	755	13	BI150509	BI150509 602915167
13	63	19.8	950	12	BF138873	BF138873 601781783
14	60	18.9	280	12	BG149077	BG149077 uu88f09.y
15	59	18.6	918	14	BQ931133	BQ931133 AGENCOURT
16	53	16.7	728	13	BF015569	BF015569 uy23c09.y
17	53	16.7	865	13	BG962985	BG962985 602827980
18	53	16.7	865	13	BG969179	BG969179 602830945
19	53	16.7	878	12	BF137585	BF137585 601783111
20	53	16.7	934	14	BQ934947	BQ934947 AGENCOURT
21	52	16.4	711	12	BF142976	BF142976 601791755
22	52	16.4	862	13	BG962582	BG962582 602822965
23	52	16.4	865	13	BG964349	BG964349 602831966
24	52	16.4	953	12	BF583869	BF583869 602096867
25	51	16.0	857	14	BQ926839	BQ926839 AGENCOURT
26	50	15.7	472	10	BE289692	BE289692 601088922
27	49	15.4	257	12	BG148606	BG148606 uu84f12.y
28	49	15.4	312	12	BG090240	BG090240 ut58e10.y
29	49	15.4	766	13	BG967034	BG967034 602834270
30	49	15.4	1000	14	BQ937284	BQ937284 AGENCOURT
31	48	15.1	688	17	AZ399191	AZ399191 1M0164K24
32	48	15.1	793	13	BG965736	BG965736 602830592
33	48	15.1	807	17	BH035104	BH035104 RPCI-24-2
34	47	14.8	722	12	BF140170	BF140170 601786735
35	46	14.5	1058	13	BG964881	BG964881 602831773
36	45	14.2	721	17	AZ834202	AZ834202 2M0116K13
37	41	12.9	620	10	BE368918	BE368918 601221562
38	41	12.9	743	13	BI106381	BI106381 602892928
39	41	12.9	793	13	BI105963	BI105963 602890917
40	41	12.9	871	12	BF165585	BF165585 60177486
41	40	12.6	408	12	BF016419	BF016419 uy41a08.y
42	40	12.6	876	12	BF141750	BF141750 601787615
43	40	12.6	918	12	BF142385	BF142385 601786637
44	40	12.6	948	12	BF139176	BF139176 601783324
45	39	12.3	871	14	BQ956722	BQ956722 AGENCOURT

ALIGNMENTS

RESULT 1	BC968615	602836416F1	NCI_CGAP_Co24	Mus musculus	cDNA clone	linear	EST 12-JUN-2001
LOCUS	BC968615	602836416F1	NCI_CGAP_Co24	Mus musculus	cDNA clone	linear	EST 12-JUN-2001
DEFINITION	BC968615	602836416F1	NCI_CGAP_Co24	Mus musculus	cDNA clone	linear	EST 12-JUN-2001
ACCESSION	BC968615	602836416F1	NCI_CGAP_Co24	Mus musculus	cDNA clone	linear	EST 12-JUN-2001
VERSION	BC968615.1	GI:14356252					
KEYWORDS	EST.						
SOURCE	house mouse						
ORGANISM	Mus musculus						
REFERENCE	1 (bases 1 to 639)						
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)						
JOURNAL	Unpublished (1999)						
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11007 row: o column: 04 High quality sequence stop: 639. Location/Qualifiers 1. 639						

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4991067"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      172 a      173 c      151 g      143 t
ORIGIN
Query Match      28.9%; Score 92; DB 13; Length 639;
Best Local Similarity 99.0%; Pred. No. 7.3e-36;
Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  90  TTACATGCACGTGTACCAGCAGAGCCAGGATCCTCCCCAAACCCCTGGATTCTGCCAC 149
Db  164  TTACATGCACGTGTACCAGCAGAGCCAGGATCCTCCCCAAACCCCTGGATTCTGCCAC 223
QY  150  ATCCAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209
Db  224  ATCCAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 283
QY  210  CTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGTGCCACTTATTACTGCCAGCAGTG 269
Db  284  CTCTCTCACAACTCAGCAGAGTGGAGGCTGAAGATGTGCCACTTATTACTGCCAGCAGTG 343
QY  270  GAGTAGTAACCCAC 283
Db  344  GAGTAGTAACCCAC 357

RESULT 2
BG968852
LOCUS      991 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION      602836142F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4990427 5',
mRNA sequence.
ACCESSION      BG968852
VERSION
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 991)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1006 row: d column: 12
High quality sequence stop: 620.
FEATURES
      source
      1..991
      Location/Qualifiers
          /organism="Mus musculus"
          /strain="FVB/N"
          /db_xref="taxon:10090"
          /clone_lib="IMAGE:4990427"
          /clone_lib="NCI_CGAP_Co24"
          /lab_host="DH10B (T1 phage-resistant)"
          /notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4991067"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      106 a      113 c      94 g      100 t
ORIGIN
Query Match      25.5%; Score 81; DB 10; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  147  CACATCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTC 206
Db  243  CACATCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTC 302
QY  207  TTACTCTCTCACAAATCAGCAG 227
Db  303  TTACTCTCTCACAAATCAGCAG 323

```

```

RESULT 4
B1104783
LOCUS      602891329F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036622 5',
DEFINITION mRNA sequence.
ACCESSION B1104783
VERSION   B1104783.1 GI:14555676
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 532)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Gilbert Smith, Ph.D.
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1AM1101 row: 1 column: 07
           High quality sequence stop: 532.
           Location/Qualifiers
             1..532
               /organism="Mus musculus"
               /strain="CZECH II"
               /db_xref="taxon:10090"
               /clone="IMAGE:5036622"
               /clone_lib="NCI_CGAP_Lu29"
               /tissue_type="spontaneous tumor, metastatic to mammary.
               Stem cell origin."
               /lab_host="DHL08"
               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
               Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
               Library constructed by Life Technologies. Investigator
               providing samples: Gilbert Smith, NIH"
BASE COUNT 139 a 148 c 113 g 132 t
ORIGIN
Query Match      25.5%; Score 81; DB 13; Length 532;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 147 CACATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTC 206
|||||
Db 248 CACATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTC 307
|||||

Oy 207 TTACTCTCTCAATCAGCAG 227
|||||
Db 308 TTACTCTCTCAATCAGCAG 328
|||||

RESULT 5
BG964957
LOCUS      602829274F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983883 5',
DEFINITION mRNA sequence.
ACCESSION BG964957
VERSION   BG964957.1 GI:14352594
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 569)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Jeffrey E. Green, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1AM9815 row: b column: 21
           High quality sequence stop: 636.
           Location/Qualifiers
             1..639
               /organism="Mus musculus"
               /strain="FVB/N"
               /db_xref="taxon:10090"
               /clone="IMAGE:4983883"
               /clone_lib="NCI_CGAP_Co24"
               /lab_host="DHL08 (T1 phage-resistant)"
               /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
               Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
               Average insert size 1.6 kb. Constructed by Life
               Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 144 a 155 c 132 g 138 t
ORIGIN
Query Match      25.5%; Score 81; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 147 CACATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTC 206
|||||
Db 211 CACATCCAACTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTC 270
|||||

Oy 207 TTACTCTCTCAATCAGCAG 227
|||||
Db 271 TTACTCTCTCAATCAGCAG 291
|||||

RESULT 6
BF583310
LOCUS      602101781F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224692 5',
DEFINITION mRNA sequence.
ACCESSION BF583310
VERSION   BF583310.1 GI:11657028
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 639)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Jeffrey E. Green, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L1AM9815 row: b column: 21
           High quality sequence stop: 636.
           Location/Qualifiers
             1..639
               /organism="Mus musculus"
               /strain="FVB/N"
               /db_xref="taxon:10090"

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/clone="IMAGE:4224692"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      169 a 174 c 149 g 147 t
ORIGIN
Query Match      25.5%; Score 81; DB 12; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.9e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 CACATCAACCTGGCTTCCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTC 206
|||||
Db 222 CACATCAACCTGGCTTCCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTC 281
|||||

QY 207 TTACTCTCTCACAAATCAGCAG 227
|||||
Db 282 TTACTCTCTCACAAATCAGCAG 302
|||||

RESULT 7
AA691311
LOCUS
DEFINITION
AA691311.1 396 bp mRNA linear EST 16-DEC-1997
clone IMAGE:1138201 5' similar to gb:X67211 M.musculus rearranged
immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thelasing, B., Wylie, F., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:619473
Seq primer: -28ml3 rev2 ET from Amerham.
FEATURES
Location/Qualifiers
1..396
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1138201"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/seq_stage="8 weeks"
/lab_host="DH10B"
/Note="Vector: pTT73D-Pac-(Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
[5'TGTTACGATCTGAAGTGGAGCGGCCCTTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors [AATTCGATCCTTGT], digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTT73
vector. Library constructed by Bob Barstead. "
BASE COUNT      104 a 107 c 91 g 94 t
ORIGIN
Query Match      22.3%; Score 71; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.2e-25;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 CTGGCTTCCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTC 216
|||||
Db 248 CTGGCTTCCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTC 307
|||||

QY 217 ACAATCAGCAG 227
|||||
Db 308 ACAATCAGCAG 318
|||||

RESULT 8
BF581607
LOCUS
DEFINITION
602099949F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219669 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9802 row: a column: 14
High quality sequence start: 3
High quality sequence stop: 631.
FEATURES
Location/Qualifiers
1..960
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219669"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      282 a 259 c 221 g 198 t
ORIGIN
Query Match      22.3%; Score 71; DB 12; Length 960;
Best Local Similarity 100.0%; Pred. No. 3.9e-25;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 CTGGCTTCCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTC 216
|||||
Db 258 CTGGCTTCCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTC 317
|||||

QY 217 ACAATCAGCAG 227
|||||
Db 318 ACAATCAGCAG 328
|||||

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RESULT 9
B0946795          918 bp      mRNA      linear      EST 21-AUG-2002
LOCUS              AGENCOURT_8949642 NCI_CGAP_Co24 Mus musculus cDNA clone
DEFINITION          IMAGE:6474845 5', mRNA sequence.
ACCESSION           B0946795
VERSION             B0946795.1 GI:22362273
KEYWORDS            EST.
SOURCE              house mouse.
ORGANISM            Mus musculus
                    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE           1 (bases 1 to 918)
                    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE              NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL             National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT            Unpublished (1999)
                    Contact: Robert Strausberg, Ph.D.
                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Agencourt Bioscience Corporation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14012 row: k column: 06
High quality sequence stop: 714.
BASE COUNT          246 a 257 c 193 g 212 t 10 others
ORIGIN
1. .918
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6474845"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
Query Match          22.0%; Score 70; DB 14; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 TGGCTTCGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCA 217
|||||
Db 239 TGGCTTCGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCA 298
|||||

Qy 218 CAATCAGCAG 227
|||||
Db 299 CAATCAGCAG 308
|||||

RESULT 10
B0939046          959 bp      mRNA      linear      EST 21-AUG-2002
LOCUS              AGENCOURT_8946838 NCI_CGAP_Co24 Mus musculus cDNA clone
DEFINITION          IMAGE:6395050 5', mRNA sequence.
ACCESSION           B0939046
VERSION             B0939046.1 GI:22354524
KEYWORDS            EST.
SOURCE              house mouse.
ORGANISM            Mus musculus
                    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE           1 (bases 1 to 959)
                    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE              NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL             National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT            Unpublished (1999)
                    Contact: Robert Strausberg, Ph.D.
                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Agencourt Bioscience Corporation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11004 row: g column: 01
High quality sequence stop: 797.
BASE COUNT          267 a 256 c 214 g 222 t
ORIGIN
1. .959
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6395050"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
Query Match          21.4%; Score 68; DB 14; Length 959;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 CTGGCTTCGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTC 216
|||||
Db 226 CTGGCTTCGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTC 285
|||||

Qy 217 ACAATCAG 224
|||||
Db 286 ACAATCAG 293
|||||

RESULT 11
B0968518          798 bp      mRNA      linear      EST 12-JUN-2001
LOCUS              AGENCOURT_8949642 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4989720 5',
DEFINITION          mRNA sequence.
ACCESSION           B0968518
VERSION             B0968518.1 GI:14356142
KEYWORDS            EST.
SOURCE              house mouse.
ORGANISM            Mus musculus
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE           1 (bases 1 to 798)
                    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE              NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL             National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT            Unpublished (1999)
                    Contact: Robert Strausberg, Ph.D.
                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11004 row: g column: 01
High quality sequence stop: 797.
BASE COUNT          267 a 256 c 214 g 222 t
ORIGIN
1. .798
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4989720"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
```

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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      225 a  222 c  179 g  172 t
ORIGIN

Query Match      21.1%; Score 67; DB 13; Length 798;
Best Local Similarity 100.0%; Pred. No. 4e-23;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CTTCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACA 220
      |||||||
DB 244 CTTCTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACA 303
      |||||||
QY 221 TCAGCAG 227
      |||||||
DB 304 TCAGCAG 310

RESULT 12
LOCUS      BI150509
DEFINITION 602915167f1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5065720 5',
      mRNA sequence.
ACCESSION  BI150509
VERSION     BI150509.1 GI:14610510
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 755)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Inyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1177 row: e column: 17
            High quality sequence stop: 738.

FEATURES             Location/Qualifiers
     source           1..755
                     /organism="Mus musculus"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5065720"
                     /clone_lib="NCI_CGAP_Lu29"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"

BASE COUNT      218 a  204 c  168 g  165 t
ORIGIN

Query Match      20.1%; Score 64; DB 13; Length 755;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 CTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCA 223
      |||||||
DB 247 CTGGAGTCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCA 306
      |||||||
QY 224 GCAG 227
      |||||

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DB 307 GCAG 310

RESULT 13
LOCUS      BF138873
DEFINITION 601781783f1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009725 5',
      mRNA sequence.
ACCESSION  BF138873
VERSION     BF138873.1 GI:10977913
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 950)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Inyte Genomics, Inc.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9246 row: e column: 22
            High quality sequence stop: 650.

FEATURES             Location/Qualifiers
     source           1..950
                     /organism="Mus musculus"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4009725"
                     /clone_lib="NCI_CGAP_Lu30"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
                     dt. Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT      245 a  277 c  213 g  215 t
ORIGIN

Query Match      19.8%; Score 63; DB 12; Length 950;
Best Local Similarity 100.0%; Pred. No. 4.5e-21;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 CACATCCAACTGGCTTCCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTC 206
      |||||||
DB 216 CACATCCAACTGGCTTCCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGACCTC 275
      |||||||
QY 207 TTA 209
      |||
DB 276 TTA 278

RESULT 14
LOCUS      BG149077
DEFINITION uu88f09.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone
      IMAGE:3383585 5', similar to SW:KVGF_MOUSE P04940 IG KAPPA CHAIN
      V-VI REGION NQ2-17.4.1.; mRNA sequence.
ACCESSION  BG149077
VERSION     BG149077.1 GI:12652504
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```


REFERENCE

1 (bases 1 to 280)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1088581

FEATURES

source

Seq primer: -40RP from Glibco.

Location/Qualifiers

1..280

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:3383585"

/clone_lib="Soares_mouse_NMGB_bcell"

/lab_host="DH10B (phage-resistant)"

/note="Organ: germinal B-cell; Vector: pT73D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

TGTTACCAACTGAGTGGAGCGCGCTGGTTTTTTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized; constructed by Bento Soares and

M.Fatima Bonaldo."

62 a 79 c 70 g 69 t

BASE COUNT

ORIGIN

Query Match 18.9%; Score 60; DB 12; Length 280;

Best Local Similarity 100.0%; Pred. No. 1.2e-19;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 150 ATCCAACTGGCTTCTGGAGTCCCGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 209

|||||

Db 127 ATCCAACTGGCTTCTGGAGTCCCGCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTA 186

RESULT 15

B0931133

LOCUS

B0931133 918 bp mRNA linear EST 20-AUG-2002

AGENCOURT_8920980 NCI_CGAP.Co24 Mus musculus cDNA clone

IMAGE:6395584 5', mRNA sequence.

ACCESSION

B0931133.1 GI:22346164

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 918)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13890 row: h column: 17

High quality sequence stop: 719.

FEATURES

source

1..918

Location/Qualifiers

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:6395584"

/clone_lib="NCI_CGAP.Co24"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

230 a 263 c 197 g 216 t

BASE COUNT

ORIGIN

Query Match 18.6%; Score 59; DB 14; Length 918;

Best Local Similarity 100.0%; Pred. No. 4.9e-19;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 158 TGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTC 216

|||||

Db 246 TGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCTC 304

Search completed: November 27, 2002, 07:13:38

Job time : 1333.94 secs

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GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:55:59 ; Search time 35.6419 Seconds
(without alignments)
2736.194 Million cell updates/sec

Title: US-09-893-615-88
Perfect score: 318
Sequence: 1 CAATATGTTCTCTCCAGTC.....GGACCATGCTGGAATAAGA 318

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	54.1	318	3	US-08-783-853A-104
2	172	54.1	318	4	US-09-344-050-104
3	172	54.1	321	3	US-08-783-853A-6
4	172	54.1	321	4	US-09-344-050-6
5	172	54.1	335	3	US-08-783-853A-102
6	172	54.1	335	4	US-09-344-050-102
7	120	37.7	387	2	US-08-449-287-1
8	120	37.7	705	4	US-09-423-439-17
9	120	37.7	732	2	US-08-860-882A-26
10	120	37.7	732	4	US-09-423-439-57
11	120	37.7	732	4	US-09-011-769A-22
12	120	37.7	3217	4	US-09-423-439-52
13	90	28.3	222	2	US-08-308-494A-12
14	90	28.3	232	4	US-09-280-028-3
15	90	28.3	315	1	US-08-459-310-3
16	71	22.3	300	2	US-08-308-494A-20
17	71	22.3	309	1	US-08-467-393-3
18	71	22.3	331	3	US-08-836-561-32
19	71	22.3	384	2	US-08-656-586-1
20	71	22.3	384	4	US-08-619-491-1
21	71	22.3	364	5	PCT-US95-07302-1
22	70	22.0	360	1	US-08-447-422-13
23	70	22.0	648	6	5455030-4
24	70	22.0	738	6	5455030-6
25	70	22.0	786	4	US-08-635-928-31
26	70	22.0	1848	1	US-08-447-422-15
27	68	21.4	711	6	5455030-8

28	68	21.4	741	6	5455030-10
29	67	21.1	384	1	US-08-149-099C-6
30	67	21.1	384	2	US-08-478-967A-6
31	67	21.1	384	4	US-08-475-815B-6
32	67	21.1	672	2	US-08-190-199A-62
33	67	21.1	711	2	US-08-190-199A-64
34	67	21.1	738	2	US-08-956-047-24
35	67	21.1	784	2	US-08-956-047-32
36	67	21.1	793	2	US-08-956-047-29
37	67	21.1	1256	4	US-09-553-498-7
38	67	21.1	1256	4	US-09-618-869-7
39	67	21.1	9209	1	US-08-149-099C-3
40	67	21.1	9209	2	US-08-478-967A-3
41	67	21.1	9209	4	US-08-475-815B-3
42	67	21.1	18986	2	US-08-819-866-2
43	67	21.1	18986	2	US-09-023-715-2
44	67	21.1	18986	4	US-09-343-485A-2
45	63	19.8	384	3	US-08-444-644-14

ALIGNMENTS

RESULT 1
US-08-783-853A-104
; Sequence 104, Application US/08783853A
; Patent No. 6005091
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; TITLE OF INVENTION: OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783,853A
; FILING DATE: 16-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,119
; FILING DATE: 24-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```
;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...318
; OTHER INFORMATION:
US-08-783-853A-104

Query Match          54.1%; Score 172; DB 3; Length 318;
Best Local Similarity 99.6%; Pred. No. 2.le-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
Qy 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
Db 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
Qy 172 CTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Db 172 CTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Qy 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 2
US-09-344-050-104
; Sequence 104, Application US/09344050
; Patent No. 6391299
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Gloria
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,050
; FILING DATE: 24-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/783,853
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX:
```

```
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...318
; OTHER INFORMATION:
US-09-344-050-104

Query Match          54.1%; Score 172; DB 4; Length 318;
Best Local Similarity 99.6%; Pred. No. 2.le-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
Db 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
Qy 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
Db 112 AAGCCAGGATCCTCCCCAAACCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
Qy 172 CTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Db 172 CTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Qy 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 3
US-08-783-853A-6
; Sequence 6, Application US/08783853A
; Patent No. 6005091
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Gloria
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783,853A
; FILING DATE: 16-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,119
```

FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 321 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-783-853A-6

Query Match 54.1%; Score 172; DB 3; Length 321;

Best Local Similarity 99.6%; Pred. No. 2.le-80;

Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACCTGAGGCGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAG 111
|||||
DB 52 AAGGTCACAATGACCTGAGGCGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAG 111
|||||
QY 112 AAGCCAGGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
|||||
DB 112 AAGCCAGGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
|||||
QY 172 CCGTCTCGCTTCAGTGGCAGTGGGCTCGGACCTCTTACTCTCTCACAAATCAGCAGAGTG 231
|||||
DB 172 CCGTCTCGCTTCAGTGGCAGTGGGCTCGGACCTCTTACTCTCTCACAAATCAGCAGAGTG 231
|||||
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||
DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||

RESULT 4

US-09-344-050-6

Sequence 6, Application US/09344050

Patent No. 6391299

GENERAL INFORMATION:

APPLICANT: Blackburn, Michael

APPLICANT: Church, William

APPLICANT: Gross, Mitchell

APPLICANT: Feuerstein, Giora

APPLICANT: Nichols, Andrew

APPLICANT: Padlan, Eduardo

APPLICANT: Patel, Arunbhai

APPLICANT: Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

TITLE OF INVENTION: OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/344,050

FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 321 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-09-344-050-6

Query Match 54.1%; Score 172; DB 4; Length 321;

Best Local Similarity 99.6%; Pred. No. 2.le-80;

Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACCTGAGGCGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAG 111
|||||
DB 52 AAGGTCACAATGACCTGAGGCGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAG 111
|||||
QY 112 AAGCCAGGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
|||||
DB 112 AAGCCAGGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTGGCTTCTGGAGTC 171
|||||
QY 172 CCGTCTCGCTTCAGTGGCAGTGGGCTCGGACCTCTTACTCTCTCACAAATCAGCAGAGTG 231
|||||
DB 172 CCGTCTCGCTTCAGTGGCAGTGGGCTCGGACCTCTTACTCTCTCACAAATCAGCAGAGTG 231
|||||
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||
DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||

RESULT 5

US-08-783-853A-102

Sequence 102, Application US/08783853A

Patent No. 6005091

GENERAL INFORMATION:

APPLICANT: Blackburn, Michael

APPLICANT: Church, William

APPLICANT: Gross, Mitchell

APPLICANT: Feuerstein, Giora

APPLICANT: Nichols, Andrew

APPLICANT: Padlan, Eduardo

APPLICANT: Patel, Arunbhai

APPLICANT: Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

TITLE OF INVENTION: OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:

NAME/KEY: Coding Sequence
LOCATION: 1...335
OTHER INFORMATION:

US-08-783-853A-102

Query Match 54.1%; Score 172; DB 3; Length 335;

Best Local Similarity 99.6%; Pred. No. 2.1e-80;

Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACCTGGTACCAGCAG 111

DB 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACCTGGTACCAGCAG 111

QY 112 AAGCCAGGATCTCCCAACCCCTGGATTTCGCCACATCCAACTGGCTTCTGGAGTC 171

DB 112 AAGCCAGGATCTCCCAACCCCTGGATTTCGCCACATCCAACTGGCTTCTGGAGTC 171

QY 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTACTCTCTCAATCAGCAGAGTG 231

DB 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTACTCTCTCAATCAGCAGAGTG 231

QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 6

US-09-344-050-102

Sequence 102, Application US/09344050

Patent No. 6391299

GENERAL INFORMATION:

APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

TITLE OF INVENTION: OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:

NAME/KEY: Coding Sequence
LOCATION: 1...335
OTHER INFORMATION:

US-09-344-050-102

Query Match

Best Local Similarity 99.6%; Pred. No. 2.1e-80;

Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACCTGGTACCAGCAG 111

DB 52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAATATACATGCACCTGGTACCAGCAG 111

QY 112 AAGCCAGGATCTCCCAACCCCTGGATTTCGCCACATCCAACTGGCTTCTGGAGTC 171

DB 112 AAGCCAGGATCTCCCAACCCCTGGATTTCGCCACATCCAACTGGCTTCTGGAGTC 171

QY 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTACTCTCTCAATCAGCAGAGTG 231

DB 172 CTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTCTTACTCTCTCAATCAGCAGAGTG 231

QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 7

US-08-449-287-1

Sequence 1, Application US/08449287

Patent No. 5877293

GENERAL INFORMATION:

APPLICANT: ADAIR, John Robert
APPLICANT: BODMER, Mark William
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and

TITLE OF INVENTION: Their Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,287
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: A5B7 light chain V1 domain
FEATURE:
NAME/KEY: CDS
LOCATION: 1..387
US-08-449-287-1

Query Match 37.7%; Score 120; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.6e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 TGCCACATCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
|||||
Db 210 TGCCACATCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGAC 269
QY 204 CTCCTACTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 263
|||||
Db 270 CTCCTACTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 329

RESULT 8
US-09-423-439-17
Sequence 17, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-423-439-17

Query Match 37.7%; Score 120; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 2.7e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 TGCCACATCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
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Db 210 TGCCACATCAACCTGGCTTCTGGAGTCCCTCGCTTCAGTGGCAGTGGGTCTGGGAC 269
QY 204 CTCCTACTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 263
|||||
Db 270 CTCCTACTCTCACAAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 329

RESULT 9
US-08-860-882A-26
Sequence 26, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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US-09-423-439-57

Query Match          37.7%; Score 120; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 2.7e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 TGGCACATCCAACCTGGCTTCTTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
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Db 225 TGGCACATCCAACCTGGCTTCTTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 284
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QY 204 CTCCTACTCTCTCACATCAGCAGAGTGAGGCTGAAGATGCTGCCCACTTATTACTGCCA 263
|||||
Db 285 CTCCTACTCTCTCACATCAGCAGAGTGAGGCTGAAGATGCTGCCCACTTATTACTGCCA 344
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RESULT 11
US-09-011-769A-22
; Sequence 22, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAW, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 732 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..720
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-011-769A-22

Query Match          37.7%; Score 120; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 2.7e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 TGGCACATCCAACCTGGCTTCTTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
|||||

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Db 225 TGCCACATCAACCTGGCTTCTGGAGTCCCTGCTGCTTTCAGTGGCAGTGGGTCTGGGAC 284
QY 204 CTCTTACTCTCTCACATCAGCAGAGTGGAGCTGAAGATGCTGCCACTTATTACTGCCA 263
Db 285 CTCTTACTCTCTCACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 344

RESULT 12

US-09-423-439-52

; Sequence 52, Application US/09423439

; Patent No. 6339070

; GENERAL INFORMATION:

; APPLICANT: EMERY, Stephen Charles

; BLAKEY, David Charles

; TITLE OF INVENTION: CHEMICAL COMPOUNDS

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Winthrop, L.L.P.

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/423,439

; FILING DATE: 09-NO. 6339070-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/01294

; FILING DATE: 05-MAY-1998

; APPLICATION NUMBER: GB 9709421.3

; FILING DATE: 10-MAY-1997

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3217 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-423-439-52

Query Match 37.7%; Score 120; DB 4; Length 3217;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 TGCCACATCAACCTGGCTTCTGGAGTCCCTGCTGCTTTCAGTGGCAGTGGGTCTGGGAC 203
Db 225 TGCCACATCAACCTGGCTTCTGGAGTCCCTGCTGCTTTCAGTGGCAGTGGGTCTGGGAC 284

QY 204 CTCTTACTCTCTCACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 263

Db 285 CTCTTACTCTCTCACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCA 344

RESULT 13

US-08-308-494A-12

; Sequence 12, Application US/08308494A

; Patent No. 5959083

; GENERAL INFORMATION:

; APPLICANT: Bosslet, Klaus

; APPLICANT: Seeman, Gerhard

; TITLE OF INVENTION: Tetravalent Bispecific Receptors, The

; TITLE OF INVENTION: Preparation and Use Thereof

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-308-494A-12

Query Match 28.3%; Score 90; DB 2; Length 292;
Best Local Similarity 99.0%; Pred. No. 1.1e-37;
Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 67 TTACATGCACTGGTACCAGCAGAGGATCCTCCCCAAACCTGGATTCTGCCAC 126

QY 150 ATCCAACTGGCTTCTGGAGTCCCTGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209

Db 127 ATCCAACTGGCTTCTGGAGTCCCTGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTA 186

QY 210 CTCTCTCAACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269

Db 187 CTCTCTCAACATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 246

QY 270 GAGTAGTAACCC 281

Db 247 GAGTAGTAACCC 258

RESULT 14

US-09-280-028-3

; Sequence 3, Application US/09280028

; Patent No. 6241961

; GENERAL INFORMATION:

; APPLICANT: BENES, IVAN FRIEDRICH

; APPLICANT: BOSSLET, KLAUS

; TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND

; TITLE OF INVENTION: METHOD FOR THEIR PREPARATION

; FILE REFERENCE: BENES

; CURRENT APPLICATION NUMBER: US/09/280,028

; CURRENT FILING DATE: 1999-03-26

; EARLIER APPLICATION NUMBER: 199 11 329.7

; EARLIER FILING DATE: 1999-03-15

; EARLIER APPLICATION NUMBER: 198 13 687.0

EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 292
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: cDNA sequence of codons for amino acids 9-105 of
OTHER INFORMATION: VL exon for k-light chain gene (VK) which codes
OTHER INFORMATION: for the MAb light chain and the amino acid
OTHER INFORMATION: sequence associated therewith
FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(292)
US-09-280-028-3

Query Match 28.3%; Score 90; DB 4; Length 292;
Best Local Similarity 99.0%; Pred. No. 1.1e-37;
Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 90 TTACATGACCTGGTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 209
Db 67 TTACATGACCTGGTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 126
Qy 150 ATCCAACTGGCTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 209
Db 127 ATCCAACTGGCTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 186
Qy 210 CTCCTCTCACATGACGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
Db 187 CTCCTCTCACATGACGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 246
Qy 270 GAGTAGTAACCC 281
Db 247 GAGTAGTAACCC 258

RESULT 15
US-08-459-310-3
Sequence 3, Application US/08459310
Patent No. 5645817
GENERAL INFORMATION:
APPLICANT: Seemann, Gerhard
APPLICANT: Bosslet, Klaus
TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
TITLE OF INVENTION: Their Preparation and Use
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,310
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,963
FILING DATE: 03-AUG-1993
APPLICATION NUMBER: DE P 422 58 53.7
FILING DATE: 05-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218

REFERENCE/DOCKET NUMBER: 02481.1317-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-459-310-3

Query Match 28.3%; Score 90; DB 1; Length 315;
Best Local Similarity 99.0%; Pred. No. 1.1e-37;
Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 90 TTACATGACCTGGTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 209
Db 90 TTACATGACCTGGTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 149
Qy 150 ATCCAACTGGCTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 209
Db 150 ATCCAACTGGCTTCCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGCTCTGGACCTCTTA 209
Qy 210 CTCCTCTCACATGACGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
Db 210 CTCCTCTCACATGACGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
Qy 270 GAGTAGTAACCC 281
Db 270 GAGTAGTAACCC 281

Search completed: November 27, 2002, 05:39:27
Job time : 39.6419 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 05:34:00 ; Search time 35.6419 Seconds
(without alignments)
3436.030 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318

Sequence: 1 CAAATTGTTCTCTCCAGTC.....GGACCATGCTGGAATAAGA 318

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 341543 seqs, 192557720 residues

Word size : 0

Total number of hits satisfying chosen parameters: 693086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	318	10	US-09-893-615-88
2	172	54.1	318	10	US-09-965-099-104
3	172	54.1	318	12	US-10-051-852-104
4	172	54.1	321	10	US-09-965-099-6
5	172	54.1	321	12	US-10-051-852-6
6	172	54.1	335	10	US-09-965-099-102
7	172	54.1	335	12	US-10-051-852-102
8	55	17.3	390	10	US-09-753-436-79
9	53	16.7	165	10	US-09-965-099-63
10	53	16.7	165	12	US-10-051-852-63
11	53	16.7	280	10	US-09-965-099-65
12	53	16.7	280	12	US-10-051-852-65
13	53	16.7	321	10	US-09-965-099-73
14	53	16.7	321	12	US-10-051-852-73
15	53	16.7	357	10	US-09-808-037-27
16	53	16.7	717	8	US-08-940-344-3
17	53	16.7	717	10	US-09-808-037-5
18	51	16.0	5691	10	US-09-897-006-11
19	48	15.1	318	10	US-09-976-787-27

20	48	15.1	318	10	US-09-865-198-26
21	48	15.1	322	9	US-09-982-107-11
22	48	15.1	324	10	US-09-976-787-16
23	48	15.1	324	10	US-09-865-198-16
24	48	15.1	357	10	US-09-910-059-8
25	48	15.1	705	10	US-09-910-059-16
26	48	15.1	714	10	US-09-976-787-31
27	48	15.1	720	10	US-09-976-787-30
28	48	15.1	2059	9	US-09-807-721-1
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32	44	13.8	412	12	US-10-051-852-98
33	41	12.9	165	10	US-09-965-099-32
34	41	12.9	165	12	US-10-051-852-32
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ALIGNMENTS

RESULT 1

US-09-893-615-88

; Sequence 88 Application US/09893615

; Patent No. US20020082395A1

; GENERAL INFORMATION:

; APPLICANT: Fischer, Gerald W.

; Schuman, Richard F.

; Wong, Hing

; Stinson, Jeffrey L.

; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND

; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR

; POSITIVE BACTERIA

; NUMBER OF SEQUENCES: 89

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

; CITY: Washington

; STREET: 1300 I Street, NW

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/893,615

; FILING DATE: 29-Jun-2001

; ATTORNEY/AGENT INFORMATION:

; NAME: Elnaudi, Carol P.

; REGISTRATION NUMBER: 32,220

; REFERENCE/DOCKET NUMBER: 04995.0041-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 88:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 318 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..318
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-893-615-88

Query Match 100.0%; Score 318; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.7e-155; Indels 0; Gaps 0;
Matches 318; Conservative 0; Mismatches 0;

QY 1 CAAATTGTTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTTCACA 60
DB 1 CAAATTGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTTCACA 60

QY 61 ATGACTTGAGGGCCAGCTCAAGTGTAAATTACATGCATCTGGTACCAAGAGCCAGGA 120
DB 61 ATGACTTGAGGGCCAGCTCAAGTGTAAATTACATGCATCTGGTACCAAGAGCCAGGA 120

QY 121 TCTCCCCCAAAACCTGGGATTTCTGCCACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
DB 121 TCTCCCCCAAAACCTGGGATTTCTGCCACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180

QY 181 TTCAGTGGCAGTGGGCTGGGACCTCTTACTCTCTCACAAATCAGCAGAGTGGAGGGCTGAA 240
DB 181 TTCAGTGGCAGTGGGCTGGGACCTCTTACTCTCTCACAAATCAGCAGAGTGGAGGGCTGAA 240

QY 241 GATGCTGCCACTATTACTGCCAGCAGTGGAGTAGTAACCCACCCAGCTTCCGAGGGGGG 300
DB 241 GATGCTGCCACTATTACTGCCAGCAGTGGAGTAGTAACCCACCCAGCTTCCGAGGGGGG 300

QY 301 ACCATGCTGGAATAAGA 318
DB 301 ACCATGCTGGAATAAGA 318

RESULT 2
US-09-965-099-104
; Sequence 104, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Giora
; Patel, Arunbhai
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
; TREATMENT OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/965,099
; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/346,487
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: <Unknown>

TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..318
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-965-099-104

Query Match 54.1%; Score 172; DB 10; Length 318;
Best Local Similarity 99.6%; Pred. No. 8.1e-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 52 AAGGTCACAATGACTTTCAGAGGCCAGCTCAAGTGTAAATTACATGCATCTGGTACCAAGCAG 111

QY 112 AAGCCAGGAGTCTCCCCCAACCCCTGGATTTCTGCCACATCCAACTGGCTTCTGGAGTC 171
DB 112 AAGCCAGGAGTCTCCCCCAACCCCTGGATTTCTGCCACATCCAACTGGCTTCTGGAGTC 171

QY 172 CCGTCTCGCTTCAGTGGCAGTGGGCTCTGGAGCTCTTACTCTCTCAATCAGCAGAGTG 231
DB 172 CCGTCTCGCTTCAGTGGCAGTGGGCTCTGGAGCTCTTACTCTCTCAATCAGCAGAGTG 231

QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
DB 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 3
US-10-051-852-104
; Sequence 104, Application US/10051852
; Patent No. US2002014641A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Church, William
; Gross, Mitchell
; Feuerstein, Giora
; Nicholls, Andrew
; Padlan, Eduardo
; Patel, Arunbhai
; Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/051,852
; FILING DATE: 17-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...318
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-051-852-104

Query Match 54.1%; Score 172; DB 12; Length 318;
Best Local Similarity 99.6%; Pred. No. 8.1e-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 AAGGTCAACATGACTTGCGAGGCCAGCTCAAGTGTAAATTACATGCCTGGTACCAGCAG 111
Db 52 AAGGTCAACATGACTTGCGAGGCCAGCTCAAGTGTAAATTACATGCCTGGTACCAGCAG 111

Qy 112 AAGCCAGAGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTCGCTTCTGGAGTC 171
Db 112 AAGCCAGAGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTCGCTTCTGGAGTC 171

Qy 172 CCTGCTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Db 172 CCTGCTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231

Qy 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 4
US-09-965-099-6
Sequence 6, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Giora
Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-965-099-6

Query Match 54.1%; Score 172; DB 10; Length 321;
Best Local Similarity 99.6%; Pred. No. 8.1e-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 AAGGTCAACATGACTTGCGAGGCCAGCTCAAGTGTAAATTACATGCCTGGTACCAGCAG 111
Db 52 AAGGTCAACATGACTTGCGAGGCCAGCTCAAGTGTAAATTACATGCCTGGTACCAGCAG 111

Qy 112 AAGCCAGAGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTCGCTTCTGGAGTC 171
Db 112 AAGCCAGAGATCCTCCCAAAACCCCTGGATTCTGCCACATCCAACTCGCTTCTGGAGTC 171

Qy 172 CCTGCTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
Db 172 CCTGCTCGCTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231

Qy 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 5
US-10-051-852-6
Sequence 6, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-051-852-6

Query Match 54.1%; Score 172; DB 12; Length 321;
Best Local Similarity 99.6%; Pred. No. 8.1e-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATACATGCACTGGTACCAGCAG 111
Db 52 AAGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATACATGCACTGGTACCAGCAG 111
QY 112 AAGCCAGGATCTCCCAAAACCCCTGGATTTCAGCACATCCAACTGCTTCTGGAGTC 171
Db 112 AAGCCAGGATCTCCCAAAACCCCTGGATTTCAGCACATCCAACTGCTTCTGGAGTC 171
QY 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTTTACTCTCTCAATCAGCAGAGTG 231
Db 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTTTACTCTCTCAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 6
US-09-965-099-102
; Sequence 102, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Giora
; Patel, Arunbhai
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
; TREATMENT OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia

STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...335
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-965-099-102

Query Match 54.1%; Score 172; DB 10; Length 335;
Best Local Similarity 99.6%; Pred. No. 8.1e-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 52 AAGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATACATGCACTGGTACCAGCAG 111
Db 52 AAGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATACATGCACTGGTACCAGCAG 111
QY 112 AAGCCAGGATCTCCCAAAACCCCTGGATTTCGCCACATCCAACTGGCTTCTGGAGTC 171
Db 112 AAGCCAGGATCTCCCAAAACCCCTGGATTTCGCCACATCCAACTGGCTTCTGGAGTC 171
QY 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTTACTCTCTCAATCAGCAGAGTG 231
Db 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGACCTTACTCTCTCAATCAGCAGAGTG 231
QY 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274

RESULT 7
US-10-051-852-102
; Sequence 102, Application US/10051852
; Patent No. US2002014641A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Church, William
; Gross, Mitchell
; Feuerstein, Giora
; Nichols, Andrew
; Padlan, Eduardo

Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...335
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-051-852-102

Query Match 54.1%; Score 172; DB 12; Length 335;
Best Local Similarity 99.6%; Pred. No. 8.le-80;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 AAGGTCACAATGACTTGCGAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
|||||
Db 52 AAGGTCACAATGACTTGCGAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
|||||
Qy 112 AAGCCAGGATCCTCCCAACCCCTGGATTTCTGCCACATCAACCTGGCTTCTGGAGTC 171
|||||
Db 112 AAGCCAGGATCCTCCCAACCCCTGGATTTATGCCACATCAACCTGGCTTCTGGAGTC 171
|||||
Qy 172 CCGTCTCGCTCAGTGGGAGTGGGCTCGGACCTCTTACTCTCTCACAAATCAGCAGAGTG 231
|||||
Db 172 CCGTCTCGCTCAGTGGGAGTGGGCTCGGACCTCTTACTCTCTCACAAATCAGCAGAGTG 231
|||||
Qy 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||
Db 232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
|||||

RESULT 8
US-09-753-436-79
Sequence 79, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753.436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-753-436-79

Query Match 17.3%; Score 55; DB 10; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.6e-19;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 CACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGTCTGGG 201
|||||
Db 219 CACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGTCTGGG 273
|||||

RESULT 9

US-09-965-099-63
; Sequence 63, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Giora
; Patel, Arunbhai
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
; TREATMENT OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/965,099
; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/346,487
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-09-965-099-63
Query Match 16.7%; Score 53; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. NO. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACCGAGGCGCAGG 119
|||||
Db 62 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACCGAGGCGCAGG 114
|||||
RESULT 10
US-10-051-852-63
; Sequence 63, Application US/10051852
; Patent No. US2002014641A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Church, William
; Gross, Mitchell
; Feuerstein, Giora
; Nichols, Andrew
; Padlan, Eduardo

Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-051-852-63
Query Match 16.7%; Score 53; DB 12; Length 165;
Best Local Similarity 100.0%; Pred. NO. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACCGAGGCGCAGG 119
|||||
Db 62 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACCGAGGCGCAGG 114
|||||
RESULT 11
US-09-965-099-65
; Sequence 65, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Giora
; Patel, Arunbhai
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
; TREATMENT OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA

;
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/965,099
; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/346,487
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...280
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-965-099-65

Query Match 16.7%; Score 53; DB 10; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACACAGAGCCAGG 119
Db 62 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACACAGAGCCAGG 114

RESULT 12
US-10-051-852-65
; Sequence 65, Application US/10051852
; Patent No. US2002014611A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Church, William
; Gross, Mitchell
; Feuerstein, Giora
; Nichols, Andrew
; Padlan, Eduardo
; Patel, Arunbhai
; Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/051,852
; FILING DATE: 17-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/344,050
; FILING DATE: 25-JUN-1999
; APPLICATION NUMBER: 08/783,853
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...280
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-051-852-65

Query Match 16.7%; Score 53; DB 12; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACACAGAGCCAGG 119
Db 62 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGCTACACAGAGCCAGG 114

RESULT 13
US-09-965-099-73
; Sequence 73, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Giora
; Patel, Arunbhai
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
; TREATMENT OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/965,099

; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/346,487
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...321
; OTHER INFORMATION: F9HZLC 2-0
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-965-099-73

Query Match 16.7%; Score 53; DB 10; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAGAGCCAGG 119
|||||
Db 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAGAGCCAGG 119

RESULT 14
US-10-051-852-73
; Sequence 73, Application US/10051852
; Patent No. US20020146411A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Church, William
; Gross, Mitchell
; Feuerstein, Giora
; Nichols, Andrew
; Padlan, Eduardo
; Patel, Arunbhai
; Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/051,852
; FILING DATE: 17-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/344,050
; FILING DATE: 25-JUN-1999
; APPLICATION NUMBER: 08/783,853
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...321
; OTHER INFORMATION: F9HZLC 2-0
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-10-051-852-73

Query Match 16.7%; Score 53; DB 12; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAGAGCCAGG 119
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Db 67 TGCAGGCCAGCTCAAGTGTAAATTACATGCTGGTACCAGCAGAGCCAGG 119

RESULT 15
US-09-808-037-27
; Sequence 27, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 357
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(357)
US-09-808-037-27

Query Match 16.7%; Score 53; DB 10; Length 357;
Best Local Similarity 100.0%; Pred. No. 3.9e-18;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 157 CTGGCTTCTCGAGTCCCTCGCTTCAGTGGCAGTGGGTCTCGGACCTCTTA 209

Db 196 CTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGTCTCTGGGACCTCTTA 248
|||||

Search completed: November 27, 2002, 07:14:52
Job time : 36.6419 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:19:05 ; Search time 37.5525 Seconds
(without alignments)
375.129 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 106

Sequence: 1 QIVLSQSPAILASPGKVT.....CQWSSNPPTFGGTMLEIR 106

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	44.3	106	AAW24532	Anti-Factor IX MAB
2	47	44.3	106	AAU81002	Mouse-human light
3	47	44.3	107	AAW24520	Mouse anti-human F
4	47	44.3	107	AAU80976	Murine BC2 light c
5	47	44.3	112	AAW24531	Anti-Factor IX MAB
6	47	44.3	112	AAU81001	Murine BC2 light c
7	46	43.4	105	AAW19914	Kappa light chain
8	43	40.6	633	AA194965	Amino acid sequenc
9	42	39.6	106	AAU72834	Anti-NKG2D hybrido
10	42	39.6	108	AAU79883	Anti-EGFR antibody

11	42	39.6	412	22	AA330694	A fusion of anti-C
12	42	39.6	423	22	AA330695	A fusion of anti-C
13	41	38.7	128	8	AAU70628	Sequence encoded b
14	41	38.7	128	10	AAU94781	2 H7 VL gene. Syn
15	41	38.7	128	18	AAW10589	2H7 antibody light
16	41	38.7	128	18	AAW16344	2H7 light chain va
17	41	38.7	128	18	AAW10243	Light chain variab
18	41	38.7	128	18	AAW47521	Mouse 2H7 antibody
19	41	38.7	128	19	AAW41071	Mouse 2H7 antibody
20	41	38.7	128	19	AAW47514	Mouse 2H7 antibody
21	41	38.7	128	20	AAW89541	Mouse antibody 2H7
22	41	38.7	128	22	AAW89093	2H7 light chain va
23	40	37.7	129	13	AAW20789	Unprocessed variab
24	40	37.7	129	13	AAW30430	ASB7 antibody ligh
25	40	37.7	235	17	AAW06178	Murine ASB7 Light
26	40	37.7	235	20	AAW82740	Plasmid pNG3/ASB7
27	40	37.7	235	20	AAW82746	Plasmid pEE14/ASB7
28	35	33.0	145	12	AAW15323	IL-2 chimeric anti
29	35	33.0	145	14	AAW32127	Anti-IL2R-alpha an
30	32	30.2	32	20	AAW94743	Anti-Staph (HAV) 9
31	31	29.2	128	15	AAW55214	Murine variable re
32	31	29.2	235	21	AAW808025	A dimeric anti-CD2
33	27	25.5	105	17	AAW03182	Guy's 13 anti-Stre
34	27	25.5	106	13	AAW24105	Anti-Tac light cha
35	27	25.5	106	19	AAW58511	Protein SEQ ID NO:
36	27	25.5	106	22	AAE13144	Humanised antibody
37	27	25.5	106	22	AAE13144	Murine anti-Tac an
38	27	25.5	106	22	AAW69651	Murine anti-Tac an
39	27	25.5	106	23	AAU74418	Antigen-binding pr
40	27	25.5	107	14	AAW34263	Mab32 V-gene heavy
41	27	25.5	107	22	AAW83159	Mouse ganglioside
42	27	25.5	107	22	AAW83167	Ganglioside GM2 an
43	27	25.5	108	13	AAW21294	Murine VL kappa gr
44	27	25.5	108	16	AAW79884	Anti-EGFR antibody
45	27	25.5	108	18	AAW41388	Anti-CEA antibody

ALIGNMENTS

RESULT 1
AAW24532
ID AAW24532 standard; Protein; 106 AA.
XX
AC AAW24532;
XX
DT 27-DEC-1997 (first entry)
XX
DE Anti-Factor IX MAB chimeric light chain.
XX
KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
XX Chimeric antibody; antibody engineering; light chain.
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
XX Chimeric synthetic.
PN WO9726010-A1.
XX
PD 24-JUL-1997.
XX
PF 17-JAN-1997; 97WO-US000759.
XX
PR 24-OCT-1996; 96US-0029119.
PR 17-JAN-1996; 96US-0010108.
PA (SMIX) SMITHKLINE BEECHAM CORP.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
PI Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
XX
DR WPI; 1997-385117/35.

CC This sequence comprises the light chain variable region of mouse
 CC anti-human Factor IX monoclonal antibody BC2. Claimed humanised
 CC antibodies (see AAW24510-18) contain CDRs (see AAW24504-09) of BC2
 CC heavy and light chain variable regions inserted into framework
 CC regions of selected human antibody sequences. They have self-
 CC limiting neutralising activity, and are useful as anticoagulant
 CC agents in treatment of thrombosis associated with myocardial
 CC infarction, unstable angina, atrial fibrillation, stroke, renal
 CC damage, pulmonary embolism, deep vein thrombosis, percutaneous
 CC transluminal coronary angioplasty, disseminated intravascular
 CC coagulation, sepsis, or artificial organs, shunts or prostheses
 CC (claimed). Also claimed are chimeric antibodies (see AAW24532), and
 CC Fab and Fab'2 fragments. The claimed antibodies do not cause
 CC uncontrolled bleeding (contrast heparin and warfarin) since they
 CC provide only partial inhibition of coagulation.

XX Sequence 107 AA;
 SQ

Query Match 44.3%; Score 47; DB 18; Length 107;
 Best Local Similarity 100.0%; Pred. No. 7.4e-35;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIVLSOSPAILSPGKVTMTCRASSVNYMHYQOKPGSSPKPWI 47
 |||||
 Db 1 QIVLSOSPAILSPGKVTMTCRASSVNYMHYQOKPGSSPKPWI 47
 |||||

RESULT 4
 AAU80976
 ID AAU80976 standard; Protein: 107 AA.
 AC AAU80976;
 XX
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Murine BC2 light chain variable region.
 XX
 KW Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
 KW thrombolytic agent; anti-factor IX antibody; plasminogen activator;
 KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
 KW vasotropic; cardiant; anti-respiratory syncytial virus;
 KW heavy chain variable region; light chain variable region.
 XX
 OS Mus sp.
 XX
 XX WO200187339-A1.
 XX
 XX 22-NOV-2001.
 PD
 PF 05-OCT-2000; 2000WO-US27438.
 XX
 PR 15-MAY-2000; 2000US-0571434.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
 XX
 XX WPI: 2002-082944/11.
 DR N-PSDB; ABK23937.
 XX
 XX Treating post-thromboembolic induced ischaemia in an animal by
 PT administering anti-factor IX antibody in combination with a plasminogen
 PT activator
 XX
 XX Example 5; Page 97; 163pp; English.
 XX
 XX The invention relates to a method for treating an animal
 CC post-thromboembolic induced ischaemia or reducing a required dose of a
 CC thrombolytic agent in treatment of an animal post-thromboembolic induced
 CC ischaemia, comprising administering an anti-factor IX antibody or its
 CC fragment, optionally in combination with a plasminogen activator or
 CC thrombolytic agent. The method is useful for treating
 CC post-thromboembolic-induced ischaemia, for preventing thromboembolic

CC stroke in an animal, and for reducing a required dose of a thrombolytic
 CC agent. Sequences AAU80972-AAU81004 represent antibodies and vector
 CC polypeptides used in the method of the invention.

XX Sequence 107 AA;
 SQ

Query Match 44.3%; Score 47; DB 23; Length 107;
 Best Local Similarity 100.0%; Pred. No. 7.4e-35;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIVLSOSPAILSPGKVTMTCRASSVNYMHYQOKPGSSPKPWI 47
 |||||
 Db 1 QIVLSOSPAILSPGKVTMTCRASSVNYMHYQOKPGSSPKPWI 47
 |||||

RESULT 5
 AAW24531
 ID AAW24531 standard; Protein: 112 AA.
 XX
 XX AAW24531;
 XX
 DT 27-DEC-1997 (first entry)
 XX
 DE Anti-Factor IX Mab BC2 modified light chain.
 XX
 KW Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
 KW chimeric antibody; antibody engineering; light chain.
 XX
 OS Chimeric Mus musculus.
 OS Chimeric synthetic.
 XX
 XX WO9726010-A1.
 XX
 XX 24-JUL-1997.
 PD
 PF 17-JAN-1997; 97WO-US00759.
 XX
 PR 24-OCT-1996; 96US-0029119.
 PR 17-JAN-1996; 96US-0010108.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX
 XX Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
 PI Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
 XX
 XX WPI: 1997-385117/35.
 DR N-PSDB; AAT79899.
 XX
 XX Inhibiting thrombosis with self-limiting antibody to coagulation
 PT factor - avoids uncontrolled bleeding by providing only partial
 PT inhibition
 XX
 XX Example 7; Page 126; 150pp; English.
 XX
 XX This polypeptide sequence comprises a modified light chain variable
 CC region (see also AAW24520) of mouse anti-human factor IX monoclonal
 CC antibody BC2. It is encoded by a DNA fragment (see AAT79899)
 CC produced by PCR amplification of BC2 cDNA. The modified BC2 VL
 CC region is incorporated into novel mouse-human chimeric light chain
 CC F9CHLC (see AAW24532). Claimed anti-Factor IX chimeric antibodies
 CC are useful in the treatment of thrombosis.

XX Sequence 112 AA;
 SQ

Query Match 44.3%; Score 47; DB 18; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.7e-35;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIVLSOSPAILSPGKVTMTCRASSVNYMHYQOKPGSSPKPWI 47
 |||||
 Db 1 QIVLSOSPAILSPGKVTMTCRASSVNYMHYQOKPGSSPKPWI 47
 |||||

RESULT 6
AAU81001
ID AAU81001 standard; Protein: 112 AA.
XX AC AAU81001;
XX DT
XX 09-APR-2002 (first entry)
XX DE Murine BC2 light chain modified variable region.
XX Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
KW thrombolytic agent; anti-factor IX antibody; plasminogen activator;
KW thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
KW vasotropic; cardiant; anti-respiratory syncytial virus;
XX heavy chain variable region; light chain variable region.
OS Mus sp.
OS Synthetic.
XX WO200187339-A1.
XX PD 22-NOV-2001.
XX PF 05-OCT-2000; 2000WO-US27438.
XX PR 15-MAY-2000; 2000US-0571434.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Barone FC, Blackburn MN, Feuerstein GZ, Toomey JR;
XX WPI: 2002-082944/11.
XX DR N-PSDB; ABK24004.
XX PT Treating post-thromboembolic induced ischaemia in an animal by
PT administering anti-factor IX antibody in combination with a plasminogen
PT activator -
XX Example 7; Page 153-154; 163pp; English.
XX The invention relates to a method for treating an animal
CC post-thromboembolic induced ischaemia or reducing a required dose of a
CC thrombolytic agent in treatment of an animal post-thromboembolic induced
CC ischaemia, comprising administering an anti-factor IX antibody or its
CC fragment, optionally in combination with a plasminogen activator or
CC thrombolytic agent. The method is useful for treating
CC post-thromboembolic-induced ischaemia, for preventing thromboembolic
CC stroke in an animal, and for reducing a required dose of a thrombolytic
CC agent. Sequences AAU80972-AAU81004 represent antibodies and vector
CC polypeptides used in the method of the invention.
XX SQ Sequence 112 AA;
Query Match 44.3%; Score 47; DB 23; Length 112;
Best Local Similarity 100.0%; Pred. No. 7.7e-35;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QIVLSQSPAILASPGKVTWTCRASSSVNMYQKPGSSPKPWI 47
DB 1 QIVLSQSPAILASPGKVTWTCRASSSVNMYQKPGSSPKPWI 47
RESULT 7
AAU19914
ID AAU19914 standard; Protein: 105 AA.
XX AC AAU19914;
XX DT
XX 24-FEB-1998 (first entry)
XX DE Kappa light chain of MAB 5C3.
XX

TrkA receptor; monoclonal antibody; docking site; human p140 TrkA; NGF;
KW hormone-receptor interactive site mapping; artificial receptor agonist;
KW receptor-domain functional correlation; NGF docking site; therapy;
KW nerve growth factor; tumour growth inhibitor; neurological disease.
KW neuroma; neoplastic tumour.
XX Homo sapiens.
OS
XX FH Key Location/Qualifiers
XX Region 24..33
FT /note= "complementarity determining region 1"
FT Region 49..55
FT /note= "complementarity determining region 2"
FT Region 88..96
FT /note= "complementarity determining region 3"
XX
PN WO9721732-A1.
XX 19-JUN-1997.
XX PD
XX PF 06-DEC-1996; 96WO-CA00815.
XX PR 08-DEC-1995; 95GB-0025180.
XX (UYMC-) UNIV MCGILL.
XX Lesauter L, Saragovi HU;
XX WPI: 1997-332727/30.
XX Anti-human TrkA antibody recognising nerve growth factor docking
PT site - useful e.g. for treatment of neurological diseases,
PT neuroma(s) or neoplastic tumours
XX Example 3; Page 31; 61pp; English.
XX AAU19914 and AAU19915 represent the kappa light chain and the heavy chain
CC of the monoclonal antibody (MAB) 5C3. MAB 5C3 is an example of an MAB of
CC the invention. The MAB of the invention, optionally having
CC complementarity determining region (CDR)-like domains of hormones, binds
CC the TrkA receptor under physiological conditions. MAB 5C3, directed
CC against human p140 TrkA, is a structural and functional mimic of NGF and
CC an artificial receptor agonist. It binds in the NGF docking site and
CC promotes TrkA internalisation, TrkA and phosphotyrosine kinase
CC tyrosine phosphorylation and increases transformation of TrkA-expressing
CC fibroblasts. The Ab or a TrkA docking site, are used to screen for
CC agents that inhibit or mimic nerve growth factor (NGF) biological
CC activity. The agents and Ab inhibit tumour growth in situ for treatment
CC or prevention of neurological diseases, neuromas and neoplastic tumours
CC expressing TrkA receptor by preventing binding of NGF to TrkA receptor or
CC down-regulating the receptor. The Ab is also used for mapping
CC hormone-receptor interactive sites and receptor-domain functional
CC correlation. The Ab can also induce NGF-like responses, especially
CC differentiation/neuritogenesis or trophic functions, by cells expressing
CC TrkA. The prognosis and diagnosis of human tumours can be performed using
CC the Ab in biopsies and immunocytochemistry or by labelling the Ab and
CC nuclear imaging. Treatment of these tumours involves coupling the Ab to a
CC cytotoxic agent and administering the complex to the patient.
XX SQ Sequence 105 AA;
Query Match 43.4%; Score 46; DB 18; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.8e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 ATSNLASGVPARFSGSGSGTSLTISRVEAEDAATYYCQWSSNP 94
DB 49 ATSNLASGVPARFSGSGSGTSLTISRVEAEDAATYYCQWSSNP 94
RESULT 8
AAU84965
ID AAU84965 standard; Protein: 633 AA.


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Db 49 ATSNLASGVPAFSGSGTSTSYSLTISRVEADAATYYCQW 90
RESULT 10
AAR79883
ID AAR79883 standard; Protein; 108 AA.
XX
AC AAR79883;
XX
DT 02-JUL-1996 (first entry)
XX
DE Anti-EGFR antibody light chain variable region (Clone L2 1C).
XX
KW Single chain antibody; antibody; epidermal growth factor receptor;
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
KW assessment; phage antibody library.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /label= Framework region 1.
FT Region 24..33
FT /label= CDR1.
FT Region 34..48
FT /label= Framework region 2.
FT Region 49..55
FT /label= CDR2.
FT Region 56..87
FT /label= Framework region 3.
FT Region 88..96
FT /label= CDR3.
FT Region 97..108
FT /label= Framework region 4.
XX
PN WO9525167-A1.
XX
PD 21-SEP-1995.
XX
PE 16-MAR-1995; 95WO-EP00978.
XX
PR 02-DEC-1994; 94EP-0118970.
PR 17-MAR-1994; 94EP-0104160.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;
PI Kettleborough AC, Mitjans F, Pluats J, Rosell E;
XX
WPI; 1995-336972/43.
XX
PT Anti-EGFR antibodies and single chain Fv antibody fragments -
PT obtained from phage-antibody libraries, useful for diagnosis and
PT therapy of tumours
XX
PS Disclosure; Figure 1A; 93pp; English.
XX
CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
CC and antibodies constructed from anti-EGFR antibody fragments can be
CC used for diagnosis of tumours and assessment of tumour growth in
CC vitro and in vivo. They may also be used in a pharmaceutical
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
CC The antibodies and fragments are derived from mice but are humanised
CC so as to cause minimum reaction against them. They are produced
CC using the phage antibody library.
XX
SQ Sequence 108 AA;
Query Match 39.6%; Score 42; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5e-30;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 ATSNLASGVPAFSGSGTSTSYSLTISRVEADAATYYCQW 90
Db 49 ATSNLASGVPAFSGSGTSTSYSLTISRVEADAATYYCQW 90
RESULT 11
AAB30694
ID AAB30694 standard; Protein; 412 AA.
XX
AC AAB30694;
XX
DT 02-APR-2001 (first entry)
XX
DE A fusion of anti-CD20 single chain antibody/streptavidin.
XX
KW Streptavidin; tumour cell; cancer; adenocarcinoma;
KW hematological malignancy; B9E9.
XX
OS Synthetic.
OS Streptomyces avidinii.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..108
FT /note= "VL chain"
FT Peptide 109..126
FT /note= "linker"
FT Protein 127..248
FT /note= "VH chain"
FT Peptide 249..253
FT /note= "linker"
FT Protein 254..412
FT /note= "streptavidin"
XX
PN WO200075333-A1.
XX
PD 14-DEC-2000.
XX
PE 05-JUN-2000; 2000WO-US15595.
XX
PR 07-JUN-1999; 99US-0137900.
PR 03-DEC-1999; 99US-0168976.
XX
PA (NEOR-) NEORX CORP.
XX
PI Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX
WPI; 2001-091213/10.
DR N-PSDB; AAC86563.
XX
PT New vector constructs for expressing genomic streptavidin fusion
PT proteins which are useful for targeting tumour cells associated with
PT cancer, e.g. adenocarcinomas -
XX
PS Example 2; Fig 11B; 100pp; English.
XX
CC The present sequence represents a fusion of an anti-CD20 single chain
CC antibody (B9E9) streptavidin. The fusion protein is expressed using
CC vectors of the invention. The specification describes vector constructs
CC for expressing streptavidin fusion proteins. The vector comprises a
CC nucleic acid encoding streptavidin or its functional variant operatively
CC linked to a promoter, and a cloning site for insertion of a second
CC nucleic acid sequence encoding a polypeptide to be fused with
CC streptavidin, interposed between the promoter and the first nucleic
CC acid sequence. Alternatively, the vector construct comprises a nucleic
CC acid, operatively linked to a promoter, encoding a polypeptide to be
CC fused with streptavidin, and a cloning site for insertion of a second
CC nucleic acid encoding at least 129 amino acids of streptavidin or its
CC functional variant. The fusion proteins are useful for targeting tumour
CC cells, particularly tumour cells associated with cancer,
CC e.g. adenocarcinomas or hematological malignancies. The vector construct
CC is useful for expressing of streptavidin fusion proteins. In particular,
CC these are useful as tools for medical diagnostics and therapeutic
CC purposes, e.g. for detecting the presence or absence of, or treating, a
```

CC target site within a mammalian host.

XX Sequence 412 AA;

Query Match 39.6%; Score 42; DB 22; Length 412;

Best Local Similarity 100.0%; Pred. No. 7.8e-30;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 ATSNLASGVPARFSGSGTSLTISRVEAEDAATYYCQOW 90

Db 49 ATSNLASGVPARFSGSGTSLTISRVEAEDAATYYCQOW 90

RESULT 12

AAB30695

ID AAB30695 standard; Protein; 423 AA;

XX

AC AAB30695;

XX 02-APR-2001 (first entry)

XX A fusion of anti-CD20 single chain antibody/streptavidin.

DE Streptavidin; tumour cell; cancer; adenocarcinoma;

XX Streptomyces avidinii.

OS Synthetic.

OS Streptomyces avidinii.

XX Homo sapiens.

XX Key

Location/Qualifiers

1..126

Protein

/note="VH chain"

127..150

Peptide

/note="linker"

151..259

Protein

/note="VL chain"

260..264

Peptide

/note="linker"

265..423

Protein

/note="streptavidin"

XX

WO200075333-A1.

XX

14-DEC-2000.

XX

05-JUN-2000; 2000WO-US15595.

XX

07-JUN-1999; 99US-0137900.

XX

03-DEC-1999; 99US-0168976.

XX

(NEOR-) NEORX CORP.

XX

Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;

XX

WPI; 2001-091213/10.

XX

N-PSDB; AAC86564.

XX

New vector constructs for expressing genomic streptavidin fusion

XX

proteins which are useful for targeting tumour cells associated with

XX

cancer, e.g. adenocarcinomas -

XX

Example 2; Fig 11C; 100pp; English.

XX

The present sequence represents a fusion of an anti-CD20 single chain

XX

antibody (B9E9) streptavidin. The fusion protein is expressed using

CC

vectors of the invention. The specification describes vector constructs

CC acid, operatively linked to a promoter, encoding a polypeptide to be

CC fused with streptavidin, and a cloning site for insertion of a second

CC nucleic acid encoding at least 129 amino acids of streptavidin or its

CC functional variant. The fusion proteins are useful for targeting tumour

CC cells, particularly tumour cells associated with cancer,

CC e.g. adenocarcinomas or hematological malignancies. The vector construct

CC is useful for expressing of streptavidin fusion proteins. In particular,

CC these are useful as tools for medical diagnostics and therapeutic

CC purposes, e.g. for detecting the presence or absence of, or treating, a

CC target site within a mammalian host.

XX

SQ Sequence 423 AA;

Query Match 39.6%; Score 42; DB 22; Length 423;

Best Local Similarity 100.0%; Pred. No. 8e-30;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 ATSNLASGVPARFSGSGTSLTISRVEAEDAATYYCQOW 90

Db 200 ATSNLASGVPARFSGSGTSLTISRVEAEDAATYYCQOW 241

RESULT 13

AAP70628

ID AAP70628 standard; protein; 128 AA.

XX

AC AAP70628;

XX 03-OCT-2002 (updated)

DT 09-APR-1991 (first entry)

XX

Sequence encoded by the 2H7 VL sequence in which the Vk gene

XX contains JK5 sequences.

DE Chimeric antibody; Anti-cancer antibody.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

XX

Key

Location/Qualifiers

1..23

Region

/tag= a

/label=leader peptide

24..47

Region

/tag= b

/label=FR1

48..56

Region

/tag= c

/label=CDR1

57..71

Region

/tag= d

/label=FR2

72..78

Region

/tag= e

/label=CDR2

79..110

Region

/tag= f

/label=FR3

111..119

Region

/tag= g

/label=CDR3

118..128

Region

/tag= h

/label=JK5

120..128

Region

/tag= i

/label=FR4

XX

WO8702671-A.

XX

07-MAY-1987.

XX

27-OCT-1986;

86WO-US02269.

XX

```
XX 01-NOV-1985; 85US-0793980.
XX (ITGE-) INT GENETIC ENG INC.
XX (ROBI/) ROBINSON R R.
XX Robinson RR, Liu AY, Horwitz AH, Wall R;
XX WPI; 1987-136004/19.
XX DR N-PSDB; AAN70972.
XX
XX Prodn. of immunoglobulin chains and molecules - is by recombinant
XX DNA procedures, with chimeric antibodies etc. related to cancer
XX specific antigens.
XX
XX Example; Fig 22; 126pp; English.
XX
XX The patentors claim a chimeric antibody molecule comprising 2 light
XX chains and 2 heavy chains, each comprising a constant human region
XX and a variable non-human region. Coding sequences for the Ig chains
XX are also claimed. The invention provides consensus sequences of
XX light and heavy chain J regions useful in the design of
XX oligonucleotides (UIGs) for use as primers or probes for cloning
XX immunoglobulinlight or heavy chain mRNAs or genes. Depending on the
XX nature of design of a particular UIG, it may be capable of
XX hybridizing to all Ig mRNAs or genes containing a single specific J
XX sequence. UIG denotes universal immunoglobulin gene.
XX (Updated on 03-OCR-2002 to add missing OS field.)
XX
XX Query Match 38.7%; Score 41; DB 8; Length 128;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-29;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 51 SNLASGVPARFSGSGTSLTISRVEADAATYYCQOWS 91
Db 73 SNLASGVPARFSGSGTSLTISRVEADAATYYCQOWS 113
|||||
RESULT 14
AAP94781
ID AAP94781 standard; protein; 128 AA.
XX
XX AAP94781;
XX
XX 06-JUL-1990 (first entry)
XX
XX 2 H7 VL gene.
XX
XX Antibodies; passive immunisation; pH3-12a; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX Domain /label=leader peptide.
XX Domain 23..46
XX Domain /label=FR1.
XX Domain 50..55
XX Domain /label=CDR1
XX Domain 56..70
XX Domain /label=FR2
XX Domain 71..77
XX Domain /label=CDR2.
XX Domain 78..109
XX Domain /label=FR3.
XX Domain 110..118
XX Domain /label=CDR3.
XX Domain 119..128
XX Domain /label=FR4.
XX
XX WO8900999-A.
```

```
XX 09-FEB-1989.
XX
XX 25-JUL-1988; 88WO-US02514.
XX
XX 24-JUL-1987; 87US-0077528.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX
XX Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;
XX
XX WPI; 1989-061144/08.
XX DR N-PSDB; AAN91147.
XX
XX Polynucleotide(s) encoding immunoglobulin molecules -
XX used for efficient prodn. of chimeric human or non-human or
XX class switched antibodies.
XX
XX Disclosure; 7pp; English.
XX
XX Sequence carries the variable region of the chimeric immunoglobulin
XX sequence. The antibodies are useful in passive immunisation avoiding
XX negative immune reactions. They are also useful in assaying and in vitro
XX imaging.
XX
XX Sequence 128 AA;
XX
XX Query Match 38.7%; Score 41; DB 10; Length 128;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-29;
XX Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 51 SNLASGVPARFSGSGTSLTISRVEADAATYYCQOWS 91
Db 73 SNLASGVPARFSGSGTSLTISRVEADAATYYCQOWS 113
|||||
RESULT 15
AAW10589
ID AAW10589 standard; Protein; 128 AA.
XX
XX AAW10589;
XX
XX 21-OCT-1997 (first entry)
XX
XX 2H7 antibody light chain variable region.
XX
XX Immunoglobulin G; IgG; light chain; recombinant production;
XX antibody; passive immunisation; serum sickness; anaphylactic shock;
XX immunoassay; imaging; reagent; complement mediated lysis;
XX therapy; variable; region; complementarity determining; CDR;
XX framework.
XX
XX Mus spp.
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX Peptide /label= sig_peptide
XX Region 23..128
XX Region /label= mat_peptide
XX Region 23..46
XX Region /label= framework_1
XX Region 47..55
XX Region /label= CDR_1
XX Region 56..70
XX Region /label= framework_2
XX Region 71..77
XX Region /label= CDR_2
XX Region 78..109
XX Region /label= framework_3
XX Region 110..118
XX Region /label= CDR_3
XX Region 119..128
XX Region /label= framework_4
XX
```

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XX US5595898-A.
PN
XX
PD 21-JAN-1997.
XX
XX PF 01-NOV-1985; 85US-0793980.
XX
XX PR 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02269.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0987555.
XX PR 18-AUG-1994; 94US-0299085.
XX
XX PA (XOMA ) XOMA CORP.
XX
XX PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
XX PI Wall R, Wilcox GL;
XX
XX DR WPI; 1997-107579/10.
XX DR N-PSDB; AAT36317.
XX
XX PT Nucleic acid encoding immunoglobulin fragment - comprising
XX PT di:cistronic transcription unit with pectate lyase signal sequences
XX
XX PS Example; Fig 22; 95pp; English.
XX
XX CC The present sequence is the light chain variable region of
XX CC the 2H7 antibody. The 2H7 cDNA was used in the preparation of
XX CC a novel polynucleotide molecule encoding an Ig fragment. The DNA
XX CC molecule comprises 2 DNA sequences encoding 2 pectate lyase
XX CC secretion signal sequences respectively linked to a DNA sequence
XX CC encoding an Ig Fd molecule or Ig light chain, operably linked to a
XX CC single prokaryotic promoter so as to form a dicistronic
XX CC transcription unit, provided that the Ig fragment can bind an
XX CC antigen and is produced and secreted by an E. coli host cell when
XX CC the nucleic acid molecule is expressed in the host cell.
XX CC The polynucleotide molecule is used for the production of
XX CC recombinant antibodies, which can be used for passive immunisation
XX CC without negative immune reactions (e.g. serum sickness and
XX CC anaphylactic shock), in labelled forms as immunoassay or imaging
XX CC reagents, in complement mediated lysis and for therapeutic
XX CC purposes when coupled to a toxin or other therapeutic agent.
XX
XX SQ Sequence 128 AA;

Query Match 38.7%; Score 41; DB 18; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e-29;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 SNLASGVPARFSGSGTYSLTISRVEAEDAATYYCQWS 91
DB 73 SNLASGVPARFSGSGTYSLTISRVEAEDAATYYCQWS 113

Search completed: November 27, 2002, 07:28:00
Job time : 38.6525 secs
```

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2002, 07:25:20 ; Search time 15.9614 Seconds
(without alignments)
638.431 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 106

Sequence: 1 QIVLSQSPAILASPGKVT.....CQWSSNPPTFGGTMLEIR 106

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	37.7	106	2	Ig kappa chain V r
2	38	35.8	107	2	Ig kappa chain V r
3	29	27.4	107	2	Ig kappa chain V r
4	27	25.5	91	2	Ig kappa chain V r
5	27	25.5	93	2	Ig kappa chain V r
6	27	25.5	99	2	Ig kappa chain V r
7	26	24.5	86	2	Ig heavy chain V r
8	26	24.5	86	2	Ig heavy chain V r
9	26	24.5	90	2	Ig kappa chain V r
10	26	24.5	93	2	Ig kappa chain V r
11	26	24.5	93	2	Ig kappa chain V r
12	26	24.5	93	2	Ig kappa chain V r
13	26	24.5	94	2	Ig light chain V r
14	26	24.5	96	2	Ig kappa chain V r
15	26	24.5	97	2	Ig light chain V r
16	26	24.5	98	2	Ig light chain V r
17	26	24.5	99	2	Ig light chain V r
18	26	24.5	99	2	Ig light chain V r
19	26	24.5	105	2	Ig kappa chain V r
20	26	24.5	108	2	Ig kappa chain V r
21	26	24.5	108	2	Ig kappa chain V r
22	26	24.5	108	2	Ig kappa chain V r
23	26	24.5	129	1	Ig kappa chain pre
24	26	24.5	130	2	Ig kappa chain pre
25	26	24.5	130	2	Ig kappa chain pre
26	25	23.6	93	2	Ig kappa chain V r
27	25	23.6	93	2	Ig kappa chain V r
28	25	23.6	93	2	Ig kappa chain V r
29	25	23.6	93	2	Ig kappa chain V r

30 25 23.6 93 2 S17634 Ig kappa chain V r
31 25 23.6 93 2 S17635 Ig kappa chain V r
32 25 23.6 93 2 S17636 Ig kappa chain V r
33 25 23.6 101 2 S13696 Ig heavy chain V r
34 25 23.6 102 2 S13697 Ig heavy chain V r
35 25 23.6 102 2 S29582 Ig kappa chain V r
36 25 23.6 102 2 S29588 Ig kappa chain V r
37 25 23.6 103 2 S13695 Ig kappa chain - m
38 25 23.6 103 2 S13698 Ig heavy chain V r
39 25 23.6 106 2 S29583 Ig kappa chain V r
40 25 23.6 108 2 PS0069 Ig kappa chain V r
41 25 23.6 109 2 S13699 Ig kappa chain V r
42 25 23.6 109 2 PT0405 Ig light chain V r
43 25 23.6 120 2 S66536 Ig light chain V r
44 25 23.6 123 2 S05269 Ig kappa chain pre
45 25 23.6 124 2 S05267 Ig kappa chain pre

ALIGNMENTS

RESULT 1

PL0082

Ig kappa chain V region (2D3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000

C:Accession: PL0082

R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slouli, M.; Urbain, J.;

J. Exp. Med. 169, 519-533, 1989

A:Title: Structural characterization of antidiotytic antibodies; evidence that Ab2s

A:Reference number: PL0080; MUID:89094248; PMID:2492056

A:Accession: PL0082

A:Molecule type: mRNA

A:Residues: 1-106 <MEM>

A:Experimental source: strain BALB/c

A:Note: the sequence shown here is from the V kappa region of an antidiotytic monoclonal

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 37.7%; Score 40; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 7.3e-33;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 48 SATSNLASGVPARFSGSGTSTSLTISRVEADAATTC 87

Db 48 SATSNLASGVPARFSGSGTSTSLTISRVEADAATTC 87

RESULT 2

PC4405

Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 21-Jan-2000

C:Accession: PC4405

R:Deng, J.B.; Han, H.; Su, C.-Z.; Chen, C.O.

Chinese Biochem. J. 12, 648-653, 1996

A:Title: Generation of a phage display library of the immunoglobulin repertoire from

A:Reference number: PC4405

A:Accession: PC4405

A:Molecule type: mRNA

A:Residues: 1-107 <DEN>

A:Experimental source: spleen cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 38; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 7.6e-31;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 53 LASGVPARFSGSGTSTSLTISRVEADAATTCQW 90

Db 53 LASGVPARFSGSGTSTSLTISRVEADAATTCQW 90

A:Reference number: S20639

A:Accession: S20651

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <LOS>

A:Cross-references: EMBL:X65007; NID:q52647; PID:CAA4140.1; PID:q52648; EMBL:X65010; N

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 24.5%; Score 26; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 7.7e-19; Indels 0;

Matches 26; Conservative 0; Mismatches 0; Gaps 0;

Qy 50 TSNLASGVPARFSGSGTSLTIS 75

|||||

Db 52 TSNLASGVPARFSGSGTSLTIS 77

RESULT 9

S26339

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26339

R:Clarkson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-90 <STA>

A:Cross-references: EMBL:X5195; NID:q52325; PID:CAA41905.1; PID:g1334068

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:3-76/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 90;

Best Local Similarity 100.0%; Pred. No. 8e-19;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 TSNLASGVPARFSGSGTSLTIS 75

|||||

Db 37 TSNLASGVPARFSGSGTSLTIS 62

RESULT 10

S17623

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17623

R:Clarkson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17623

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 8.2e-19;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 TSNLASGVPARFSGSGTSLTIS 75

|||||

Db 44 TSNLASGVPARFSGSGTSLTIS 69

RESULT 11

S17640

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17640

R:Clarkson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17640

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 8.2e-19;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 TSNLASGVPARFSGSGTSLTIS 75

|||||

Db 44 TSNLASGVPARFSGSGTSLTIS 69

RESULT 12

S17642

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17642

R:Clarkson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17642

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 8.2e-19;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 TSNLASGVPARFSGSGTSLTIS 75

|||||

Db 44 TSNLASGVPARFSGSGTSLTIS 69

RESULT 13

S26340

Ig light chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000

C:Accession: S26340

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26340

A:Molecule type: mRNA

A:Residues: 1-94 <STA>

A:Cross-references: EMBL:X59205; NID:q52333; PID:CAA41915.1; PID:g1334072

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-80/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 94;

Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASGVPARFSGSGTGYSLTIS 75
|||||
Db 41 TSNLASGVPARFSGSGTGYSLTIS 66

RESULT 14

C33730
Ig kappa chain V region (4.68) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C:Accession: C33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlinked
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: C33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
A:Cross-references: GB:M25999; NID:gl97117; PIDN:AAA38915.1; PID:gl97118
A:Note: the authors translated the codon TIG for residue 34 as Phe
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASGVPARFSGSGTGYSLTIS 75
|||||
Db 52 TSNLASGVPARFSGSGTGYSLTIS 77

RESULT 15

PHI085
Ig light chain V region (clone 163.42) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PHI085
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PHI085
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-97 <TIL>
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 24.5%; Score 26; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 8.5e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASGVPARFSGSGTGYSLTIS 75
|||||
Db 50 TSNLASGVPARFSGSGTGYSLTIS 75

Search completed: November 27, 2002, 07:31:21
Job time : 15.9614 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:23:05 ; Search time 10.2317 Seconds
(without alignments)
429.695 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 106

Sequence: 1 QIVLSQSPAILASPGKVT.....CQWSSNPPTFGGTMLEIR 106

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	24.5	129	1 KV4A_MOUSE	P01680 mus musculus
2	23	21.7	107	1 KV6A_MOUSE	P01675 mus musculus
3	23	21.7	107	1 KV6B_MOUSE	P01676 mus musculus
4	23	21.7	107	1 KV6C_MOUSE	P01677 mus musculus
5	23	21.7	107	1 KV6D_MOUSE	P01678 mus musculus
6	22	20.8	107	1 KV6E_MOUSE	P01679 mus musculus
7	16	15.1	107	1 KV6F_MOUSE	P04940 mus musculus
8	16	15.1	107	1 KV6G_MOUSE	P04941 mus musculus
9	16	15.1	107	1 KV6H_MOUSE	P04942 mus musculus
10	16	15.1	107	1 KV6I_MOUSE	P04943 mus musculus
11	16	15.1	107	1 KV6J_MOUSE	P04944 mus musculus
12	14	13.2	108	1 KV3V_MOUSE	P01674 mus musculus
13	14	13.2	108	1 KV6K_MOUSE	P04945 mus musculus
14	14	13.2	111	1 KV3A_MOUSE	P01654 mus musculus
15	14	13.2	111	1 KV3C_MOUSE	P01656 mus musculus
16	14	13.2	111	1 KV3D_MOUSE	P03977 mus musculus
17	14	13.2	111	1 KV3E_MOUSE	P01657 mus musculus
18	14	13.2	111	1 KV3R_MOUSE	P01670 mus musculus
19	14	13.2	111	1 KV3S_MOUSE	P01671 mus musculus
20	14	13.2	111	1 KV3T_MOUSE	P01672 mus musculus
21	14	13.2	111	1 KV3U_MOUSE	P01673 mus musculus
22	14	13.2	112	1 KV3B_MOUSE	P01655 mus musculus
23	12	11.3	111	1 KV3J_MOUSE	P01662 mus musculus
24	12	11.3	111	1 KV3K_MOUSE	P01663 mus musculus
25	12	11.3	131	1 KV3I_MOUSE	P01661 mus musculus
26	11	10.4	109	1 KV3F_HUMAN	P01624 homo sapien
27	11	10.4	110	1 KV3P_MOUSE	P01668 mus musculus
28	11	10.4	111	1 KV3L_MOUSE	P01664 mus musculus
29	11	10.4	111	1 KV3M_MOUSE	P01665 mus musculus
30	11	10.4	111	1 KV3N_MOUSE	P01666 mus musculus
31	11	10.4	111	1 KV3O_MOUSE	P01667 mus musculus
32	11	10.4	111	1 KV3Q_MOUSE	P01669 mus musculus
33	11	10.4	115	1 KV3I_HUMAN	P04433 homo sapien

34 11 10.4 116 1 KV3J_HUMAN P04434 homo sapien
35 11 10.4 129 1 KV3H_HUMAN P04207 homo sapien
36 9 8.5 107 1 KV1D_HUMAN P01596 homo sapien
37 9 8.5 108 1 KV1E_HUMAN P01597 homo sapien
38 9 8.5 108 1 KV1H_HUMAN P01600 homo sapien
39 9 8.5 108 1 KV1L_HUMAN P01604 homo sapien
40 9 8.5 108 1 KV1M_HUMAN P01605 homo sapien
41 9 8.5 108 1 KV1N_HUMAN P01606 homo sapien
42 9 8.5 108 1 KV1O_HUMAN P01607 homo sapien
43 9 8.5 108 1 KV1R_HUMAN P01609 homo sapien
44 9 8.5 108 1 KV1S_HUMAN P01610 homo sapien
45 9 8.5 108 1 KV1S_HUMAN P01611 homo sapien

ALIGNMENTS

RESULT 1
KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00577; AAA38780.1; -;
CC EMBL; V00780; CAA24157.1; -;
CC PIR; A01943; KVM57B.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 22
CC CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
CC DOMAIN 23 45 FRAMEWORK-1.
CC DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 58 72 FRAMEWORK-2.
CC DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 80 111 FRAMEWORK-3.
CC DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 119 128 FRAMEWORK-4.
CC DISULFID 45 111 BY SIMILARITY.
CC NON_TER 129 129
CC SEQUENCE 129 AA; 13833 MW; E4BB73072DCF6BE4 CRC64;

Query Match 24.5%; Score 26; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 50 TSNLASGVPARFSGSGTYSYLSITIS 75
      |||||
Db 74 TSNLASGVPARFSGSGTYSYLSITIS 99

RESULT 2
KV6A_MOUSE
ID KV6A_MOUSE STANDARD; PRT; 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
      BIND GALACTAN.
CC PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;

Query Match 21.7%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LASGVPARFSGSGTYSYLSITIS 75
      |||||
Db 53 LASGVPARFSGSGTYSYLSITIS 75

RESULT 3
KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).

```

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CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
      BIND GALACTAN.
CC PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11584 MW; 36E6D022A5EC34D7 CRC64;

Query Match 21.7%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LASGVPARFSGSGTYSYLSITIS 75
      |||||
Db 53 LASGVPARFSGSGTYSYLSITIS 75

RESULT 4
KV6C_MOUSE
ID KV6C_MOUSE STANDARD; PRT; 107 AA.
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 601).
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins.";
RL Biochemistry 17:5555-5559(1978).
RN [2]
RP SEQUENCE (TEPC 191).
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "kappa Chain Joining segments and structural diversity of antibody
combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
      THAT BIND GALACTAN.
CC PIR; A01941; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87

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FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match 21.7%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 LASGVPARFSGSGTSLTIS 75
Db 53 LASGVPARFSGSGTSLTIS 75

RESULT 5
ID KV6D_MOUSE STANDARD; PRT; 107 AA.
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region SAPC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
PIR: A01941; KVMX4.
HSP: P01679; 2FBJ.
InterPro: IPR003006; Ig_MHC.
Pfam: PF00047; Ig; 1.
SMART: SM00406; Ig; 1.
Immunoglobulin V region.
DOMAIN 1 23
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
DOMAIN 24 33
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
DOMAIN 34 48
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
DOMAIN 49 55
FRAMEWORK-4.
COMPLEMENTARITY-DETERMINING-4.
DOMAIN 56 87
DISULFID 23 87
NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 21.7%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 LASGVPARFSGSGTSLTIS 75
Db 53 LASGVPARFSGSGTSLTIS 75

RESULT 6
ID KV6E_MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
PIR: A01941; KVMX4.
HSP: P01679; 2FBJ.
InterPro: IPR003006; Ig_MHC.
Pfam: PF00047; Ig; 1.
SMART: SM00406; Ig; 1.
Immunoglobulin V region.
DOMAIN 1 23
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
DOMAIN 24 33
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
DOMAIN 34 48
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
DOMAIN 49 55
FRAMEWORK-4.
COMPLEMENTARITY-DETERMINING-4.
DOMAIN 56 87
DISULFID 23 87
NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 21.7%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 LASGVPARFSGSGTSLTIS 75
Db 53 LASGVPARFSGSGTSLTIS 75

RESULT 7
ID KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DE 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
PIR: A01942; KVMXJ5.
PDB: 2FBJ; 15-OCT-90.
InterPro: IPR003006; Ig_MHC.
Pfam: PF00047; Ig; 1.
SMART: SM00406; Ig; 1.
Immunoglobulin V region; 3D-structure.
DOMAIN 1 23
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
DOMAIN 24 33
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
DOMAIN 34 48
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
DOMAIN 49 55
FRAMEWORK-4.
COMPLEMENTARITY-DETERMINING-4.
DOMAIN 56 87
DISULFID 23 87
NON_TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;

Query Match 20.8%; Score 22; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 LASGVPARFSGSGTSLTI 74
Db 53 LASGVPARFSGSGTSLTI 74

RESULT 7
ID KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DE 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
combining sites."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
PIR: A01942; KVMXJ5.
PDB: 2FBJ; 15-OCT-90.
InterPro: IPR003006; Ig_MHC.
Pfam: PF00047; Ig; 1.
SMART: SM00406; Ig; 1.
Immunoglobulin V region; 3D-structure.
DOMAIN 1 23
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
DOMAIN 24 33
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
DOMAIN 34 48
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
DOMAIN 49 55
FRAMEWORK-4.
COMPLEMENTARITY-DETERMINING-4.
DOMAIN 56 87
DISULFID 23 87
NON_TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;

Query Match 20.8%; Score 22; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 LASGVPARFSGSGTSLTI 74
Db 53 LASGVPARFSGSGTSLTI 74
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SQ SEQUENCE 107 AA; 11505 MW; CA6C4284ECFCB550 CRC64;
Query Match 15.1%; Score 16; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AEDAATYYCQWSSNP 94
KV6J_MOUSE
|||||
DB 79 AEDAATYYCQWSSNP 94

RESULT 10
KV6J_MOUSE
ID KV6J_MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC -----
DR EMBL; K00740; AAA38685.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region; Hybridoma.
KW DOMAIN 1 23
FT DOMAIN 24 33 FRAMEWORK-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 FRAMEWORK-3.
FT DOMAIN 56 87 FRAMEWORK-4.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECFC08E6 CRC64;

Query Match 15.1%; Score 16; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AEDAATYYCQWSSNP 94
KV6J_MOUSE
|||||
DB 79 AEDAATYYCQWSSNP 94

RESULT 11
KV6J_MOUSE
ID KV6J_MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)

```

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00744; AAA38689.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region; Hybridoma.
KW DOMAIN 1 23
FT DOMAIN 24 33 FRAMEWORK-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11611 MW; A38290781F3C30D3 CRC64;

Query Match 15.1%; Score 16; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AEDAATYYCQWSSNP 94
KV6J_MOUSE
|||||
DB 79 AEDAATYYCQWSSNP 94

RESULT 12
KV3V_MOUSE
ID KV3V_MOUSE STANDARD; PRT; 108 AA.
AC P01674;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 2154.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01940; KVM554.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

```

DR Pfam: PF00047; Ig: 1.
KW SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 108
FT DISULFID 23 92
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11699 MW; D40921D18DAC4B9E CRC64;

Query Match 13.2%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 SGVPARFSGSGGT 68
DB 60 SGVPARFSGSGGT 73

RESULT 13

ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."
RL Nature 304:320-324(1983).

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DR EMBL; R00746; AAA38691.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 98
FT DOMAIN 99 108
FT DISULFID 23 87
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match 13.2%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AEDAATYYCQWSS 92
DB 79 AEDAATYYCQWSS 92

RESULT 14

ID KV3A_MOUSE STANDARD; PRT; 111 AA.
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin diversity."
RL Nature 276:785-790(1978).
CC -I- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
DR PIR; A01930; KVM580.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 13.2%; Score 14; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 SGVPARFSGSGGT 68
DB 60 SGVPARFSGSGGT 73

RESULT 15

ID KV3C_MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.E.;
RT "Mechanism of antibody synthesis: size differences between mouse kappa chains."
RL Science 155:465-467(1967).
CC -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01930; KVM580.

DR HSP; P01679; 2EBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;
Query Match 13.2%; Score 14; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 55 SGVPARFSGSGST 68
Db 60 SGVPARFSGSGST 73

Search completed: November 27, 2002, 07:28:47
Job time : 10.2317 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: November 27, 2002, 07:24:25 : Search time: 29.8764 Seconds
(without alignments)
731.044 Million cell updates/sec

Title: US-09-893-615-89
Perfect score: 106
Sequence: 1 QIVLSQSPAILASPGKVT.....CQWSSNPPTFGGTMLEIR 106

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 671580 seqs, 206047115 residues

Word size : 0
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	41.5	97	Q9JL76	Q9JL76 mus musculus
2	23	21.7	134	Q8VDD0	Q8VDD0 mus musculus
3	17	16.0	106	Q9U410	Q9U410 schistosoma
4	16	15.1	235	Q91W12	Q91W12 mus musculus
5	15	14.2	101	Q9JL78	Q9JL78 mus musculus
6	14	13.2	103	Q9JL80	Q9JL80 mus musculus
7	14	13.2	111	Q920E9	Q920E9 mus musculus
8	11	10.4	108	Q9UL83	Q9UL83 homo sapien
9	11	10.4	109	Q9UL85	Q9UL85 homo sapien
10	9	8.5	104	Q9JL82	Q9JL82 mus musculus
11	9	8.5	107	Q9UL81	Q9UL81 homo sapien
12	9	8.5	107	Q96SA9	Q96SA9 homo sapien
13	9	8.5	108	Q9UL79	Q9UL79 homo sapien
14	9	8.5	108	Q9UL77	Q9UL77 homo sapien
15	9	8.5	108	Q9UL70	Q9UL70 homo sapien
16	9	8.5	109	Q9UL78	Q9UL78 homo sapien

17	9	8.5	109	6	Q9NOW5	Q9NOW5 oryctolagus
18	9	8.5	109	11	Q9ET13	Q9ET13 mus musculus
19	9	8.5	109	11	Q920E6	Q920E6 mus musculus
20	9	8.5	114	4	Q9UL80	Q9UL80 homo sapien
21	9	8.5	129	11	Q8VDE2	Q8VDE2 mus musculus
22	9	8.5	233	11	Q91WS9	Q91WS9 mus musculus
23	9	8.5	234	11	Q91WF8	Q91WF8 mus musculus
24	9	8.5	234	11	Q8R062	Q8R062 mus musculus
25	9	8.5	238	11	Q9M37	Q9M37 mus musculus
26	9	8.5	238	11	Q8VC16	Q8VC16 mus musculus
27	9	8.5	239	4	Q8TCD0	Q8TCD0 homo sapien
28	9	8.5	239	11	Q8VC55	Q8VC55 mus musculus
29	9	8.5	298	11	Q9QYF0	Q9QYF0 mus musculus
30	8	7.5	107	11	Q9JL84	Q9JL84 mus musculus
31	8	7.5	214	11	Q9JL85	Q9JL85 mus musculus
32	8	7.5	241	11	Q921A6	Q921A6 mus musculus
33	8	7.5	338	5	Q8T8J5	Q8T8J5 drosophila
34	8	7.5	385	5	Q9NHV3	Q9NHV3 drosophila
35	8	7.5	385	5	Q9NHV2	Q9NHV2 drosophila
36	8	7.5	385	5	Q9NHV1	Q9NHV1 drosophila
37	8	7.5	385	5	Q9NHV0	Q9NHV0 drosophila
38	8	7.5	385	5	Q9NHU9	Q9NHU9 drosophila
39	8	7.5	385	5	Q9NHU8	Q9NHU8 drosophila
40	8	7.5	385	5	Q9NHU7	Q9NHU7 drosophila
41	8	7.5	385	5	Q9NHU6	Q9NHU6 drosophila
42	8	7.5	385	5	Q9NHU5	Q9NHU5 drosophila
43	8	7.5	385	5	Q9N666	Q9N666 drosophila
44	8	7.5	385	5	Q8T8L2	Q8T8L2 drosophila
45	8	7.5	385	5	Q8T8L0	Q8T8L0 drosophila

ALIGNMENTS

RESULT. 1

Q9JL76 PRELIMINARY: PRT: 97 AA.
ID Q9JL76;
AC Q9JL76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region (Fragment).
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.:
RT "T-cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin".
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206030; AAF69328.1;
DR HSSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFELF49DA1C CHK64;

Query Match 41.5%; Score 44; DB 11; Length 97;

Best Local Similarity 100.0%; Pred. No. 1.5e-37;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 ATSNLASGVPARTSGSGSGTYSLTISRVEADAATYTCOWSS 92

Db 39 ATSNLASGVPARTSGSGSGTYSLTISRVEADAATYTCOWSS 82

```

RESULT 2
Q8VDD0      PRELIMINARY;      PRT;      134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Anti-MOG 212 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Sembl P.;
RT "targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;

Query Match      21.7%; Score 23; DB 11; Length 134;
Best Local Similarity 100.0%; Pred. No. 9.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LASGVPARFSGSGTSYSLTIS 75
   |||||
DB 75 LASGVPARFSGSGTSYSLTIS 97

RESULT 3
Q9U410      PRELIMINARY;      PRT;      106 AA.
AC Q9U410;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T.; Feng Z.Q.; Qiu Z.N.; Li Y.Q.; Huang H.L.; Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR NON_TER 1 1
FT NON_TER 106 106

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SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match      16.0%; Score 17; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFGSGSGTSYSLTISR 76
   |||||
DB 60 RFGSGSGTSYSLTISR 76

RESULT 4
Q9IW12      PRELIMINARY;      PRT;      235 AA.
AC Q9IW12;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match      15.1%; Score 16; DB 11; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFGSGSGTSYSLTIS 75
   |||||
DB 82 RFGSGSGTSYSLTIS 97

RESULT 5
Q9JL78      PRELIMINARY;      PRT;      101 AA.
AC Q9JL78;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S.; Liao L.; Cunningham M.W.; Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206028; AAF69326.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR NON_TER 1 1
FT NON_TER 101 101

```


RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 10.4%; Score 11; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 PARFSGSGSGT 68
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 DB 59 PARFSGSGSGT 69

RESULT 10

O9JL82 PRELIMINARY; PRT; 104 AA.
 ID O9JL82
 AC O9JL82
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=20448942; PubMed=1092488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206024; AAF69322.1; -.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AAIAE CRC64;

Query Match 8.5%; Score 9; DB 11; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 RFGSGSGT 68
 |||||
 DB 58 RFGSGSGT 66

RESULT 11

O9JL81 PRELIMINARY; PRT; 107 AA.
 ID O9JL81
 AC O9JL81
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035033; AAD56269.1; -.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 8.5%; Score 9; DB 4; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 RFGSGSGT 68
 |||||
 DB 61 RFGSGSGT 69

RESULT 12

O96SA9 PRELIMINARY; PRT; 107 AA.
 ID O96SA9
 AC O96SA9
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal antibodies from
 rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 antibody V region genes.";
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL; U96396; AAB68785.1; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 8.5%; Score 9; DB 4; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 RFGSGSGT 68
 |||||
 DB 61 RFGSGSGT 69

RESULT 13

O9UL79 PRELIMINARY; PRT; 108 AA.
 ID O9UL79
 AC O9UL79
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 8.5%; Score 9; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFSGSGSGT 68
DB 61 RFSGSGSGT 69

RESULT 14
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 8.5%; Score 9; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFSGSGSGT 68
DB 61 RFSGSGSGT 69
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RESULT 15
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 8.5%; Score 9; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFSGSGSGT 68
DB 61 RFSGSGSGT 69

Search completed: November 27, 2002, 07:30:27
Job time : 31.1264 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:26:06 ; Search time 14.7336 Seconds
(without alignments)
211.682 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 106

Sequence: 1 QIVLSQSPAILASPGKVT.....COQSSNPPTFGGCTMLEIR 106

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	44.3	106	3	US-08-783-853A-105
2	47	44.3	106	4	US-09-344-050-105
3	47	44.3	107	3	US-08-783-853A-11
4	47	44.3	107	4	US-09-344-050-11
5	47	44.3	112	3	US-08-783-853A-103
6	47	44.3	112	4	US-09-344-050-103
7	40	37.7	129	2	US-08-449-287-2
8	40	37.7	235	4	US-09-423-439-18
9	40	37.7	235	4	US-09-423-439-58
10	40	37.7	235	4	US-09-011-769A-23
11	31	29.2	128	1	US-08-476-275-4
12	31	29.2	128	4	US-08-475-815B-7
13	27	25.5	105	3	US-08-434-000A-12
14	27	25.5	105	4	US-09-312-157-12
15	27	25.5	106	1	US-07-634-278-1
16	27	25.5	106	1	US-07-634-278-16
17	27	25.5	106	1	US-08-477-728-1
18	27	25.5	106	1	US-08-477-728-16
19	27	25.5	106	1	US-08-474-040-1
20	27	25.5	106	1	US-08-474-040-16
21	27	25.5	106	1	US-08-487-200-1
22	27	25.5	106	1	US-08-487-200-16
23	27	25.5	106	1	US-08-488-113B-163
24	27	25.5	106	1	US-08-477-484B-163
25	27	25.5	106	1	US-08-107-669D-49
26	27	25.5	106	1	US-08-472-788A-83
27	27	25.5	106	2	US-08-477-531B-49

28	27	25.5	106	2	US-08-646-360-163
29	27	25.5	106	2	US-08-082-842A-83
30	27	25.5	106	4	US-08-839-765-163
31	27	25.5	106	4	US-09-136-389-163
32	27	25.5	106	4	US-08-484-537-1
33	27	25.5	106	4	US-08-484-537-16
34	27	25.5	106	4	US-09-610-838-163
35	27	25.5	107	1	US-08-211-202-3
36	27	25.5	108	4	US-09-171-945-9
37	27	25.5	129	2	US-08-116-778E-2
38	27	25.5	129	2	US-08-438-562-2
39	27	25.5	129	2	US-08-483-528B-92
40	27	25.5	130	4	US-09-393-385B-113
41	27	25.5	230	4	US-09-485-737B-102
42	27	25.5	233	4	US-09-485-737B-69
43	27	25.5	235	4	US-09-171-945-17
44	27	25.5	235	4	US-09-485-737B-93
45	27	25.5	239	3	US-08-279-772A-8

ALIGNMENTS

RESULT 1

US-08-783-853A-105
; Sequence 105, Application US/08783853A
; Patent No. 6005091
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/783,853A
; APPLICATION NUMBER: 16-JAN-1997
; FILING DATE: 16-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,119
; FILING DATE: 24-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
US-08-783-853A-105

Query Match 44.3%; Score 47; DB 3; Length 106;

Best Local Similarity 100.0%; Pred. No. 1.8e-34;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSOSPAILSPGCKVTMTCRASSVNMHWYQKPGSSPKPWI 47
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DB 1 QIVLSOSPAILSPGCKVTMTCRASSVNMHWYQKPGSSPKPWI 47
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RESULT 2

US-09-344-050-105
; Sequence 105, Application US/09344050
; Patent No. 6391299
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,050
; FILING DATE: 24-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/783,853
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-09-344-050-105

Query Match 44.3%; Score 47; DB 4; Length 106;

Best Local Similarity 100.0%; Pred. No. 1.8e-34;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QIVLSOSPAILSPGCKVTMTCRASSVNMHWYQKPGSSPKPWI 47
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DB 1 QIVLSOSPAILSPGCKVTMTCRASSVNMHWYQKPGSSPKPWI 47
|||||

RESULT 3

US-08-783-853A-11
; Sequence 11, Application US/08783853A
; Patent No. 6005091
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783,853A
; FILING DATE: 16-JAN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,119
; FILING DATE: 24-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-783-853A-11

Query Match 44.3%; Score 47; DB 3; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
DB 1 QIVLSOSPAILSPGCKVTMTCRASSVNMHWYQKPGSSPKPWI 47
|||||

RESULT 4

US-09-344-050-11
; Sequence 11, Application US/09344050
; Patent No. 6391299

GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael
; APPLICANT: Church, William
; APPLICANT: Gross, Mitchell
; APPLICANT: Feuerstein, Giora
; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel

; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

; TITLE OF INVENTION: OF THROMBOSIS

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/344,050

; FILING DATE: 24-JUN-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/783,853

; FILING DATE: 16-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Kirk

; REGISTRATION NUMBER: 33,833

; REFERENCE/DOCKET NUMBER: P50438

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5096

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

US-09-344-050-11

Query Match 44.3%; Score 47; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.9e-34;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QIVLSQSPAILSPGSEKVTMTCRASSSYNMYHWYQKPGSSPKPWI 47

RESULT 5

US-08-783-853A-103

; Sequence 103, Application US/08783853A

; Patent No. 6005091

; GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael

; APPLICANT: Church, William

; APPLICANT: Gross, Mitchell

; APPLICANT: Feuerstein, Giora

; APPLICANT: Nichols, Andrew
; APPLICANT: Padlan, Eduardo
; APPLICANT: Patel, Arunbhai
; APPLICANT: Sylvester, Daniel
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; TITLE OF INVENTION: OF THROMBOSIS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/783,853A

; FILING DATE: 16-JAN-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/029,119

; FILING DATE: 24-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Kirk

; REGISTRATION NUMBER: 33,833

; REFERENCE/DOCKET NUMBER: P50438

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5096

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 103:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

US-08-783-853A-103

Query Match 44.3%; Score 47; DB 3; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.9e-34;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSQSPAILSPGSEKVTMTCRASSSYNMYHWYQKPGSSPKPWI 47

Db 1 QIVLSQSPAILSPGSEKVTMTCRASSSYNMYHWYQKPGSSPKPWI 47

RESULT 6

US-09-344-050-103

; Sequence 103, Application US/09344050

; Patent No. 6391299

; GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael

; APPLICANT: Church, William

; APPLICANT: Gross, Mitchell

; APPLICANT: Feuerstein, Giora

; APPLICANT: Nichols, Andrew

; APPLICANT: Padlan, Eduardo

; APPLICANT: Patel, Arunbhai

; APPLICANT: Sylvester, Daniel

; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT

; TITLE OF INVENTION: OF THROMBOSIS

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-344-050-103

Query Match 44.3%; Score 47; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 QIVLSQSPAILASPGKVTMTCRASSVNMHWYQKPGSSPKPW 47
|||||
Db 1 QIVLSQSPAILASPGKVTMTCRASSVNMHWYQKPGSSPKPW 47

RESULT 7
US-08-449-287-2
Sequence 2, Application US/08449287
Patent No. 5877293
GENERAL INFORMATION:
APPLICANT: ADAIR, John Robert
APPLICANT: BOWMER, Mark William
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
TITLE OF INVENTION: Their Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,287

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-287-2

Query Match 37.7%; Score 40; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 49 ATSNLASGVPARFSGSGTSTSLTISRVEADAATYYCQ 88
|||||
Db 71 ATSNLASGVPARFSGSGTSTSLTISRVEADAATYYCQ 110

RESULT 8
US-09-423-439-18
Sequence 18, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match 37.7% Score 40; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 5.3e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 ATSNLASGVPARFSGSGTSLTISRVEADAATYYCQ 88
Db 71 ATSNLASGVPARFSGSGTSLTISRVEADAATYYCQ 110

RESULT 9

US-09-423-439-58
Sequence 58, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

FILING DATE: 09-NOV-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-423-439-58

Query Match 37.7% Score 40; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 5.3e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 ATSNLASGVPARFSGSGTSLTISRVEADAATYYCQ 88
Db 71 ATSNLASGVPARFSGSGTSLTISRVEADAATYYCQ 110

RESULT 10

US-09-011-769A-23
Sequence 23, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKE, David C.

DAVIES, David H.

HENNAW, John F.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.
DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011.769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-011-769A-23

Query Match 37.7% Score 40; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 5.3e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 ATSNLASGVPARFSGSGTSLTISRVEADAATYYCQ 88
Db 71 ATSNLASGVPARFSGSGTSLTISRVEADAATYYCQ 110

RESULT 11

US-08-476-275-4
Sequence 4, Application US/08476275
Patent No. 5776456
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

APPLICANT: Hanna, Nabil

APPLICANT: Leonard, John E.

APPLICANT: Newman, Roland A.

APPLICANT: Reff, Mitchell E.

APPLICANT: Rastetter, William H.

TITLE OF INVENTION: Therapeutic Application of Chimeric and

TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted

TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell

TITLE OF INVENTION: Lymphoma

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-275-4

Query Match 29.2%; Score 31; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFGSGSGTSYSLTISRVEADAATYYCQW 90
|||||
DB 82 RFGSGSGTSYSLTISRVEADAATYYCQW 112

RESULT 12

US-08-475-815B-7
Sequence 7, Application US/08475815B
Patent No. 6399061
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: REFF, MITCHELL E.
APPLICANT: RASTETER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New York Avenue, N.W., Ninth FL.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891

FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-815B-7

Query Match 29.2%; Score 31; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RFGSGSGTSYSLTISRVEADAATYYCQW 90
|||||
DB 82 RFGSGSGTSYSLTISRVEADAATYYCQW 112

RESULT 13

US-08-434-000A-12
Sequence 12, Application US/08434000A
Patent No. 6046037
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 1
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

TOPOLOGY: DESCRIPTION: Guy's 13 Kappa
US-08-434-000A-12

Query Match 25.5%; Score 27; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 7.5e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASSVPAFSGSGTYSLTISR 76
|||||

DB 50 TSNLASSVPAFSGSGTYSLTISR 76
|||||

RESULT 14

US-09-312-157-12
Sequence 12, Application US/09312157

Patent No. 6303341

GENERAL INFORMATION:

APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER

TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/312,157

FILING DATE: 14-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/434,000

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-351

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 12

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: Guy's 13 Kappa

US-09-312-157-12

Query Match 25.5%; Score 27; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 7.5e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASSVPAFSGSGTYSLTISR 76
|||||

DB 50 TSNLASSVPAFSGSGTYSLTISR 76
|||||

RESULT 15

US-07-634-278-1

Sequence 1, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..106
OTHER INFORMATION: /note= "Variable region of the mouse
anti-tac antibody light chain."
US-07-634-278-1

Query Match 25.5%; Score 27; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.5e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASSVPAFSGSGTYSLTISR 76
|||||

DB 50 TSNLASSVPAFSGSGTYSLTISR 76
|||||

Search completed: November 27, 2002, 07:32:11
Job time : 15.7336 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:28:06 ; Search time 9.82239 Seconds
(without alignments)
171.849 Million cell updates/sec

Title: US-09-893-615-89
Perfect score: 106
Sequence: 1 QIVLSQSPAILASPGKVT.....CQWSSNPPTFGGTMLEIR 106

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 102317 seqs, 15924203 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	106	10	US-09-893-615-89
2	47	44.3	106	10	US-09-965-099-105
3	47	44.3	106	12	US-10-051-852-105
4	47	44.3	107	10	US-09-965-099-11
5	47	44.3	107	12	US-10-051-852-11
6	47	44.3	112	10	US-09-965-099-103
7	47	44.3	112	12	US-10-051-852-103
8	27	25.5	105	9	US-09-982-107-12
9	27	25.5	106	10	US-09-976-787-24
10	27	25.5	106	10	US-09-865-198-23
11	27	25.5	107	9	US-09-144-886-88
12	27	25.5	108	10	US-09-976-787-8
13	27	25.5	108	10	US-09-865-198-8
14	27	25.5	108	10	US-09-910-059-9
15	27	25.5	112	9	US-09-144-886-89
16	27	25.5	235	10	US-09-910-059-17
17	27	25.5	238	10	US-09-976-787-29
18	27	25.5	238	10	US-09-865-198-28
19	27	25.5	240	10	US-09-976-787-28

Sequence 27, Appl
Sequence 2, Appl
Sequence 76, Appl
Sequence 92, Appl
Sequence 98, Appl
Sequence 82, Appl
Sequence 83, Appl
Sequence 28, Appl
Sequence 6, Appl
Sequence 57, Appl
Sequence 62, Appl
Sequence 57, Appl
Sequence 62, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 74, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 99, Appl
Sequence 99, Appl
Sequence 6, Appl
Sequence 91, Appl
Sequence 80, Appl

20 27 25.5 240 10 US-09-865-198-27
21 26 24.5 669 9 US-09-807-721-2
22 26 24.5 107 9 US-09-144-886-76
23 25 23.6 109 9 US-09-144-886-92
24 25 23.6 109 9 US-09-144-886-98
25 23 21.7 107 9 US-09-144-886-82
26 23 21.7 107 9 US-09-144-886-83
27 23 21.7 119 10 US-09-808-037-28
28 23 21.7 239 10 US-09-808-037-6
29 20 18.9 107 10 US-09-965-099-57
30 20 18.9 107 10 US-09-965-099-62
31 20 18.9 107 12 US-10-051-852-57
32 20 18.9 107 12 US-10-051-852-62
33 20 18.9 125 10 US-09-965-099-78
34 20 18.9 125 12 US-10-051-852-78
35 19 17.9 93 10 US-09-965-099-66
36 19 17.9 93 12 US-10-051-852-66
37 19 17.9 107 10 US-09-965-099-74
38 19 17.9 107 12 US-10-051-852-74
39 19 17.9 109 10 US-09-965-099-95
40 19 17.9 109 12 US-10-051-852-95
41 19 17.9 129 10 US-09-965-099-99
42 19 17.9 129 12 US-10-051-852-99
43 19 17.9 131 10 US-09-881-823-6
44 18 17.0 109 9 US-09-144-886-91
45 18 17.0 127 10 US-09-753-436-80

ALIGNMENTS

RESULT 1
US-09-893-615-89
; Sequence 89, Application US/09893615
; Patent No. US20020082395A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
; Schuman, Richard F.
; Wong, Hing
; Stinson, Jeffrey L.
; TITLE OF INVENTION: CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
; POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 04995.0041-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-893-615-89

Query Match 100.0%; Score 106; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSQSPAILSPGKVTMTCRASSVNYMHYQKPGSSPKPWISATSNLASGVPAR 60
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DB 1 QIVLSQSPAILSPGKVTMTCRASSVNYMHYQKPGSSPKPWISATSNLASGVPAR 60
|||||

QY 61 FSGSGSGTSYLSIRVEADAATYYCQWSSNPPTFGGTMLEIR 106
|||||
DB 61 FSGSGSGTSYLSIRVEADAATYYCQWSSNPPTFGGTMLEIR 106
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RESULT 2

US-09-965-099-105
; Sequence 105, Application US/09965099
; Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Feuerstein, Giora
Patel, Arunbhai

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-965-099-105

Query Match 44.3%; Score 47; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSQSPAILSPGKVTMTCRASSVNYMHYQKPGSSPKPW 47

DB 1 QIVLSQSPAILSPGKVTMTCRASSVNYMHYQKPGSSPKPW 47
|||||

RESULT 3

US-10-051-852-105
; Sequence 105, Application US/10051852
; Patent No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-051-852-105

Query Match 44.3%; Score 47; DB 12; Length 106;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSQSPAILSPGKVTMTCRASSVNYMHYQKPGSSPKPW 47
|||||
DB 1 QIVLSQSPAILSPGKVTMTCRASSVNYMHYQKPGSSPKPW 47
|||||

RESULT 4

US-09-965-099-11
; Sequence 11, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Michael
; Feuerstein, Giora
; Patel, Arunbhai

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/965,099

FILING DATE: 26-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/346,487

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-965-099-11

Query Match 44.3%; Score 47; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. le-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIVLSQSPAILSPGKVTMTCRASSVYNNMHWTQKPGSSPKPWI 47

Db 1 QIVLSQSPAILSPGKVTMTCRASSVYNNMHWTQKPGSSPKPWI 47

RESULT 5

US-10-051-852-11

; Sequence 11, Application US/10051852

; Patent No. US20020146411A1

; GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael

; Church, William

; Gross, Mitchell

; Feuerstein, Giora

; Nichols, Andrew

; Padlan, Eduardo

; Patel, Arunbhai

; Sylvester, Daniel

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,852

FILING DATE: 17-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/344,050

FILING DATE: 25-JUN-1999

APPLICATION NUMBER: 08/783,853

FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-051-852-11

Query Match 44.3%; Score 47; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. le-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIVLSQSPAILSPGKVTMTCRASSVYNNMHWTQKPGSSPKPWI 47

Db 1 QIVLSQSPAILSPGKVTMTCRASSVYNNMHWTQKPGSSPKPWI 47

RESULT 6

US-09-099-103

; Sequence 103, Application US/09965099

; Patent No. US20020136725A1

; GENERAL INFORMATION:

; APPLICANT: Blackburn, Michael

; Feuerstein, Giora

; Patel, Arunbhai

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN

TREATMENT OF THROMBOSIS

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-965-099-103

Query Match 44.3%; Score 47; DB 10; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.le-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSQPAILSPGKVTMTCRASSVNMHWYQKPGSSPKPW 47
DB 1 QIVLSQPAILSPGKVTMTCRASSVNMHWYQKPGSSPKPW 47

RESULT 7
US-10-051-852-103
Sequence 103, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Gloria
Nichols, Andrew
Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852

FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-051-852-103

Query Match 44.3%; Score 47; DB 12; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.le-34;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIVLSQPAILSPGKVTMTCRASSVNMHWYQKPGSSPKPW 47
DB 1 QIVLSQPAILSPGKVTMTCRASSVNMHWYQKPGSSPKPW 47

RESULT 8
US-09-982-107-12
Sequence 12, Application US/09982107
Patent No. US2002015958A1
GENERAL INFORMATION:
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING PROTECTION PROTEINS IN PLANTS AND THEIR USE
FILE REFERENCE: EPI3002E
CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 105
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12

Query Match 25.5%; Score 27; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASGVPARFSGSGTYSLTISR 76
DB 50 TSNLASGVPARFSGSGTYSLTISR 76

RESULT 9
US-09-976-787-24
Sequence 24, Application US/09976787
Patent No. US20020064528A1

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Query Match      25.5%; Score 27; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 27: Conservative 0; Mismatches 0; Indels
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Job time : 9.82239 secs

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Db 50 TSNLASGVPARFSGSGGTYSYSLTISR 76

RESULT 14
US-09-910-059-9
; Sequence 9, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-9

Query Match 25.5%; Score 27; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASGVPARFSGSGGTYSYSLTISR 76
|||||
Db 50 TSNLASGVPARFSGSGGTYSYSLTISR 76

RESULT 15
US-09-144-886-89
; Sequence 89, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 3C3 region VL epitope 2
US-09-144-886-89

Query Match 25.5%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSNLASGVPARFSGSGGTYSYSLTISR 76
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 05:38:32 ; Search time 8.28185 Seconds
(without alignments)
241.342 Million cell updates/sec

Title: US-09-893-615-1

Perfect score: 91

Sequence: 1 WRMYFSRRAHLRSP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	15	AAW94701	Lipoteichoic acid
2	91	100.0	19	AAW94733	Sequence 15mer 2nd
3	91	100.0	19	AAW94714	Sequence 15mer2-12
4	91	100.0	19	AAW94715	Sequence 15mer2-13
5	91	100.0	19	AAW94717	Sequence 15mer2-10
6	91	100.0	19	AAW94718	Sequence 15mer2-16
7	91	100.0	19	AAW94719	Sequence 15mer2-17
8	66	72.5	19	AAW94716	Sequence 15mer2-14
9	47	51.6	757	20 AAY34472	Porphorymonas ging
10	47	51.6	763	20 AAY34348	Porphorymonas ging

11	45	49.5	117	22	AAO10712	Human polypeptide
12	45	49.5	684	22	ABG2691	Drosophila melanog
13	45	49.5	684	23	AAU74625	Oestrogen-regulate
14	43	47.3	82	22	AAU52691	Propionibacterium
15	43	47.3	88	22	AAU41763	Propionibacterium
16	43	47.3	95	19	AAU21419	Human high mobil
17	43	47.3	860	22	AAU88351	Human membrane or
18	43	47.3	1358	19	AAW57837	Aldehyde oxidase p
19	43	47.3	1358	19	AAW57838	Aldehyde oxidase p
20	42	46.2	147	23	AAU48365	Insulin-like growt
21	42	46.2	252	23	ABB49295	Listeria monocytog
22	42	46.2	486	22	ABB59435	Drosophila melanog
23	42	46.2	2785	21	AAU57148	Human down-regulat
24	41.5	45.6	248	22	ABB53062	Escherichia coli p
25	41	45.1	127	22	AAU60591	Human brain expres
26	41	45.1	127	22	AAU73259	Human bone marrow
27	41	45.1	127	22	AAU33460	Peptide #7497 enco
28	41	45.1	127	23	ABG43106	Human peptide enco
29	41	45.1	191	23	AAU69540	Human G protein-co
30	41	45.1	196	22	ABG26403	Novel human diago
31	41	45.1	221	22	ABG05725	Novel human diago
32	41	45.1	230	22	AAU93340	Human polypeptide,
33	41	45.1	344	22	AAU65923	Propionibacterium
34	41	45.1	428	22	AAU64689	Propionibacterium
35	41	45.1	434	22	AAU96758	Putative P. abyssi
36	41	45.1	452	22	AAU94445	Human protein sequ
37	41	45.1	519	22	ABG09372	Novel human diago
38	41	45.1	651	21	AAU29652	Human membrane-ass
39	41	45.1	680	23	AAU19421	Human furin mutant
40	41	45.1	809	22	ABG09902	Novel human diago
41	41	45.1	1014	22	AAU40124	Human polypeptide
42	41	45.1	1063	23	ABU90934	Herbicidally activ
43	41	45.1	1066	22	AAU41910	Human polypeptide
44	41	45.1	1069	21	AAU42717	Human ORFX ORF2481
45	41	45.1	1069	22	ABG09904	Novel human diago

ALIGNMENTS

RESULT 1

AAW94701

ID AAW94701 standard; peptide; 15 AA.

XX AAW94701;

XX 22-APR-1999 (first entry)

XX Lipoteichoic acid epitope peptide mimic for Mab 96-110.

XX Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;

XX Immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

XX Mab 96-110.

XX Staphylococcus sp.

XX WO9857994-A2.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-US12402.

XX 16-JUN-1997; 97US-0049871.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Fischer GW, Schuman RF, Stinson JL, Wong H;

XX WPI; 1999-095329/08.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria

XX PS Claim 16; Page 120; 150pp; English.

XX CC The invention relates to a monoclonal antibody (Mab) to lipoteichoic acid

CC of gram positive bacteria, where the Mab is a chimeric immunoglobulin

CC comprising at least part of a human immunoglobulin constant region and

CC at least part of a non-human immunoglobulin variable region having

CC specificity to lipoteichoic acid of gram positive bacteria. The

CC antibodies bind to whole bacteria and enhance phagocytosis and killing of

CC the bacteria and enhance protection from lethal infection. The antibodies

CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic

CC acid antibody or characterised by amino acids corresponding to one or

CC more of the complementarity determining regions (CDRs) of the variable

CC region of the antibody) can be used for treating or preventing infections

CC caused by gram positive bacteria. They can also be used for the diagnosis

CC of gram positive bacterial infections. The present sequence represents a

CC specifically claimed lipoteichoic acid epitope peptide mimic that can be

CC bound by the antibody of the invention (Mab 96-110).

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 91; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLRSP 15
 ID AAW94733 standard; Protein; 19 AA.
 XX AC AAW94733;
 XX DT 22-APR-1999 (first entry)
 XX DE Sequence 15mer 2nd.12 resulting from library panning experiments.
 XX KW Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW Mab 96-110; panning.
 XX OS Staphylococcus sp.
 XX PN WO9857994-A2.
 XX PD 23-DEC-1998.
 XX PF 16-JUN-1998; 98WO-US12402.
 XX PR 16-JUN-1997; 97US-0049871.
 XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX PI Fischer GW, Schuman RE, Stinson JL, Wong H;
 XX DR WPI: 1999-095329/08.
 DR N-PSDB; AAX05359.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used

PT to develop products for the diagnosis, prevention and treatment of

PT infections caused by gram positive bacteria

XX Example 5; Fig 8; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic

CC acid of gram positive bacteria, where the Mab is a chimeric

CC immunoglobulin comprising at least part of a human immunoglobulin

CC constant region and at least part of a non-human immunoglobulin variable

CC region having specificity to lipoteichoic acid of gram positive bacteria.

CC The antibodies bind to whole bacteria and enhance phagocytosis and

CC killing of the bacteria and enhance protection from lethal infection. The

CC antibodies or peptides (encoded by a DNA of the variable region of

CC anti-lipoteichoic acid antibody or characterised by amino acids

CC corresponding to one or more of the complementarity determining regions

CC (CDRs) of the variable region of the antibody) can be used for treating

CC or preventing infections caused by gram positive bacteria. They can also

CC be used for the diagnosis of gram positive bacterial infections.

CC Sequences AAW94726-34 represent common peptide sequences resulting from

CC all library panning experiments. Three series of panning experiments were

CC conducted to identify peptide sequences to which antibody of the

CC invention (Mab 96-110) bound strongly. The translated sequences provide

CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 91; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.4e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLRSP 15
 ID AAW94714 standard; Protein; 19 AA.
 XX AC AAW94714;
 XX DT 22-APR-1999 (first entry)
 XX DE Sequence 15mer2-12/0 resulting from 15mer library panning experiment.
 XX KW Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW Mab 96-110; panning.
 XX OS Staphylococcus sp.
 XX PN WO9857994-A2.
 XX PD 23-DEC-1998.
 XX PF 16-JUN-1998; 98WO-US12402.
 XX PR 16-JUN-1997; 97US-0049871.
 XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX PI Fischer GW, Schuman RE, Stinson JL, Wong H;
 XX DR WPI: 1999-095329/08.
 DR N-PSDB; AAX05540.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used

PT to develop products for the diagnosis, prevention and treatment of

PT infections caused by gram positive bacteria

XX Example 5; Fig 6A-B; 150pp; English.

XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic

CC acid of gram positive bacteria, where the Mab is a chimeric

CC immunoglobulin comprising at least part of a human immunoglobulin

CC constant region and at least part of a non-human immunoglobulin variable

CC region having specificity to lipoteichoic acid of gram positive bacteria.

CC The antibodies bind to whole bacteria and enhance phagocytosis and

CC killing of the bacteria and enhance protection from lethal infection. The

CC antibodies or peptides (encoded by a DNA of the variable region of

CC anti-lipoteichoic acid antibody or characterised by amino acids

CC corresponding to one or more of the complementarity determining regions

CC (CDRs) of the variable region of the antibody) can be used for treating

CC or preventing infections caused by gram positive bacteria. They can also

CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAW94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 XX

SO Sequence 19 AA;

Query Match 100.0%; Score 91; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.4e-09; Mismatches 0; Gaps 0;
 Matches 15; Conservative 0; Indels 0;

Qy 1 WRMYFSHRHAHLRSP 15

Db 3 WRMYFSHRHAHLRSP 17

RESULT 4

AAW94715
 ID AAW94715 standard; Protein: 19 AA.

AC AAW94715;

DT 22-APR-1999 (first entry)

Sequence 15mer2-13/0 resulting from 15mer library panning experiment.

Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 Mab 96-110; panning.

OS Staphylococcus sp.

WO9857994-A2.

23-DEC-1998.

16-JUN-1998; 98WO-US12402.

16-JUN-1997; 97US-0049871.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Fischer GW, Schuman RF, Stinson JL, Wong H;

WPI; 1999-095329/08.

N-PSDB; AAX05541.

New antibodies to lipoteichoic acid of gram positive bacteria - used
 to develop products for the diagnosis, prevention and treatment of
 infections caused by gram positive bacteria

Example 5; Fig 6A-B; 150pp; English.

The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 acid of gram positive bacteria, where the Mab is a chimeric
 immunoglobulin comprising at least part of a human immunoglobulin
 constant region and at least part of a non-human immunoglobulin
 region having specificity to lipoteichoic acid of gram positive bacteria.
 The antibodies bind to whole bacteria and enhance phagocytosis and
 killing of the bacteria and enhance protection from lethal infection. The
 antibodies or peptides (encoded by a DNA of the variable region of
 anti-lipoteichoic acid antibody or characterised by amino acids
 corresponding to one or more of the complementarity determining regions
 (CDRs) of the variable region of the antibody) can be used for treating
 or preventing infections caused by gram positive bacteria. They can also
 be used for the diagnosis of gram positive bacterial infections.

Sequences AAW94705-22 represent sequences resulting from a 15mer library
 panning second experiment. Three series of panning experiments were
 conducted to identify peptide sequences to which antibody of the
 invention (Mab 96-110) bound strongly. The translated sequences provide
 lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

XX Sequence 19 AA;

Query Match 100.0%; Score 91; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.4e-09; Mismatches 0; Gaps 0;
 Matches 15; Conservative 0; Indels 0;

Qy 1 WRMYFSHRHAHLRSP 15

Db 3 WRMYFSHRHAHLRSP 17

RESULT 5

AAW94717
 ID AAW94717 standard; Protein: 19 AA.

AC AAW94717;

DT 22-APR-1999 (first entry)

Sequence 15mer2-10/0 resulting from 15mer library panning experiment.

Monoclonal antibody; Mab; lipoteichoic acid; gram positive; bacteria;
 immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 Mab 96-110; panning.

OS Staphylococcus sp.

WO9857994-A2.

23-DEC-1998.

16-JUN-1998; 98WO-US12402.

16-JUN-1997; 97US-0049871.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Fischer GW, Schuman RF, Stinson JL, Wong H;

WPI; 1999-095329/08.

N-PSDB; AAX05543.

New antibodies to lipoteichoic acid of gram positive bacteria - used
 to develop products for the diagnosis, prevention and treatment of
 infections caused by gram positive bacteria

Example 5; Fig 6A-B; 150pp; English.

The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 acid of gram positive bacteria, where the Mab is a chimeric
 immunoglobulin comprising at least part of a human immunoglobulin
 constant region and at least part of a non-human immunoglobulin
 region having specificity to lipoteichoic acid of gram positive bacteria.
 The antibodies bind to whole bacteria and enhance phagocytosis and
 killing of the bacteria and enhance protection from lethal infection. The
 antibodies or peptides (encoded by a DNA of the variable region of
 anti-lipoteichoic acid antibody or characterised by amino acids
 corresponding to one or more of the complementarity determining regions
 (CDRs) of the variable region of the antibody) can be used for treating
 or preventing infections caused by gram positive bacteria. They can also
 be used for the diagnosis of gram positive bacterial infections.

Sequences AAW94705-22 represent sequences resulting from a 15mer library
 panning second experiment. Three series of panning experiments were
 conducted to identify peptide sequences to which antibody of the
 invention (Mab 96-110) bound strongly. The translated sequences provide
 lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.

Sequence 19 AA;

Query Match 100.0%; Score 91; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.4e-09; Mismatches 0; Gaps 0;
 Matches 15; Conservative 0; Indels 0;

XX
XX
NOT RECOMMENDED

DT 22-APR-1999 (first entry)
 DE Sequence 15mer2-14/0 resulting from 15mer library panning experiment.
 XX Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW Mab 96-110; panning.
 XX Staphylococcus sp.
 OS
 XX WO9857994-A2.
 PN
 XX 23-DEC-1998.
 PD
 XX 16-JUN-1998; 98WO-US12402.
 PF
 XX 16-JUN-1997; 97US-0049871.
 PR
 XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 PA
 XX Fischer GW, Schuman RF, Stinson JL, Wong H;
 PI WPI; 1999-095329/08.
 DR N-PSDB; AAX05542.
 DR
 XX New antibodies to lipoteichoic acid of gram positive bacteria - used
 PT to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 XX
 XX Example 5; Fig 6A-B; 150pp; English.
 PS
 XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAM94705-22 represent sequences resulting from a 15mer library
 CC panning second experiment. Three series of panning experiments were
 CC conducted to identify peptide sequences to which antibody of the
 CC invention (Mab 96-110) bound strongly. The translated sequences provide
 CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
 XX
 SQ Sequence 19 AA;
 Query Match 72.5%; Score 66; DB 20; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.00015;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 WRMYFSHRHAHLRSP 15
 II III: IIII II
 Db 3 WRKYFSYHHAHLCSF 17
 RESULT 9
 AAY34472
 ID AAY34472 standard; Protein; 757 AA.
 XX
 AC AAY34472;
 XX
 DT 25-AUG-1999 (first entry)
 XX Porphorymonas gingivalis protein PG13.
 DE
 XX Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
 KW vaccine; antigenic.
 KW

XX Porphorymonas gingivalis.
 OS
 XX WO9929870-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX 10-DEC-1998; 98WO-AU01023.
 PF
 XX 04-AUG-1998; 98AU-0005028.
 PR 10-DEC-1997; 97AU-0000839.
 PR 31-DEC-1997; 97AU-0001182.
 PR 30-JAN-1998; 98AU-0001546.
 PR 10-MAR-1998; 98AU-0002264.
 PR 09-APR-1998; 98AU-0002911.
 PR 23-APR-1998; 98AU-0003128.
 PR 05-MAY-1998; 98AU-0003338.
 PR 22-MAY-1998; 98AU-0003654.
 PR 29-JUL-1998; 98AU-0004917.
 XX
 XX (CSLC-) CSL LTD.
 PA
 XX Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
 PI Ross BC, Rothel LJ, Webb EA;
 PI
 XX WPI; 1999-385613/32.
 DR N-PSDB; AAX91690.
 DR
 XX Antigenic Porphorymonas gingivalis peptides for preventing
 PT gingivitis
 PT
 XX Claim 1; Page 450-451; 588pp; English.
 PS
 XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
 CC AAX91583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphorymonas gingivalis. Probes can
 CC be used to detect Porphorymonas gingivalis in standard hybridisation
 CC assays. Porphorymonas gingivalis is involved in periodontal disease
 CC especially gingivitis.
 XX
 SQ Sequence 757 AA;
 Query Match 51.6%; Score 47; DB 20; Length 757;
 Best Local Similarity 61.5%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 WRMYFSHRHAHLR 13
 II: IIII II
 Db 700 WRLATSHRFAHR 712
 RESULT 10
 AAY34348
 ID AAY34348 standard; Protein; 763 AA.
 XX
 AC AAY34348;
 XX
 DT 25-AUG-1999 (first entry)
 XX Porphorymonas gingivalis protein PG13.
 DE
 XX Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
 KW vaccine; antigenic.
 KW
 XX Porphorymonas gingivalis.
 OS
 XX WO9929870-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX

PF 10-DEC-1998; 98WO-AU01023.
 XX
 PR 04-AUG-1998; 98AU-0005028.
 PR 10-DEC-1997; 97AU-0000839.
 PR 31-DEC-1997; 97AU-0001182.
 PR 30-JAN-1998; 98AU-0001546.
 PR 10-MAR-1998; 98AU-0002264.
 PR 09-APR-1998; 98AU-0002911.
 PR 23-APR-1998; 98AU-0003128.
 PR 05-MAY-1998; 98AU-0003338.
 PR 22-MAY-1998; 98AU-0003654.
 PR 29-JUL-1998; 98AU-0004917.
 XX
 PA (CSLC-) CSL LTD.
 XX Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
 PI Ross BC, Rothel LJ, Webb EA;
 XX
 DR WPI; 1999-385613/32.
 DR N-PSDB; AAX91566.
 XX
 PT Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 XX
 PS Claim 1; Page 308-309; 588pp; English.
 XX
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to
 CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis.
 XX
 SQ Sequence 763 AA;
 Query Match 51.6%; Score 47; DB 20; Length 763;
 Best Local Similarity 61.5%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WRMYFSHRHAHLR 13
 II: III III I
 DB 706 WRLATSHRFAHR 718
 XX
 RESULT 11
 AAO10712
 ID AAO10712 standard; Protein; 117 AA.
 XX
 AC AAO10712;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 24604.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX

PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI90843.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 24604; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 117 AA;
 Query Match 49.5%; Score 45; DB 22; Length 117;
 Best Local Similarity 66.7%; Pred. No. 4.5;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 YFSHRHAHLRSP 15
 I I I I I I I I
 DB 71 YRSHTHAHTSP 82
 XX
 RESULT 12
 ABB62691
 ID ABB62691 standard; Protein; 684 AA.
 XX
 AC ABB62691;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 14865.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL06794.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 82 AA;

Query Match 47.3%; Score 43; DB 22; Length 82;

Best Local Similarity 70.0%; Pred. No. 6.6;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRMYFSRHA 10

Db 35 WRWRWSRHA 44

RESULT 15

AAU41763

ID AAU41763 standard; Protein; 88 AA.

XX

AC AAU41763;

XX

DT 13-FEB-2002 (first entry)

XX

DE Propionibacterium acnes immunogenic protein #2659.

XX

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

FN WO200181581-A2.

XX

PD 01-NOV-2001.

XX

PF 20-APR-2001; 2001WO-US12865.

XX

PR 21-APR-2000; 2000US-199047P.

XX

PR 02-JUN-2000; 2000US-208841P.

XX

PR 07-JUL-2000; 2000US-216747P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhátia A;

XX

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX

DR WPI: 2001-616774/71.

XX

DR N-PSDB; AAS59515.

XX

PS Example 1; SEQ ID No 2958; 1069pp; English.

XX

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 88 AA;

Query Match 47.3%; Score 43; DB 22; Length 88;

Best Local Similarity 72.7%; Pred. No. 7.1;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YFSHRRAHLRS 14

Db 7 YVHRRRLRS 17

Search completed: November 27, 2002, 07:17:47

Job time : 19.2819 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:15:05 ; Search time 4.11197 Seconds
(without alignments)
350.688 Million cell updates/sec

Title: US-09-893-615-1

Perfect score: 91

Sequence: 1 WRMYFSHRHAHLRSP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73.*

1: pirl.*

2: pirl2.*

3: pirl3.*

4: pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	49.5	215	2	probable membrane
2	45	49.5	215	2	hypothetical prote
3	44	48.4	307	2	hypothetical prote
4	44	48.4	703	2	hypothetical prote
5	44	48.4	743	2	hypothetical prote
6	43	47.3	424	2	omega 6 desaturase
7	43	47.3	1358	2	aldehyde oxidase (
8	42	46.2	134	2	hypothetical prote
9	42	46.2	252	2	hypothetical prote
10	42	46.2	252	2	hypothetical prote
11	42	46.2	929	2	hypothetical prote
12	41.5	45.6	248	2	trax protein - Esc
13	41	45.1	208	2	hypothetical prote
14	41	45.1	241	2	transcription regu
15	41	45.1	257	1	formate dehydrogen
16	41	45.1	286	2	hypothetical prote
17	41	45.1	346	2	hypothetical prote
18	41	45.1	370	2	transcription regu
19	41	45.1	434	2	asparagine-tRNA li
20	41	45.1	470	2	hypothetical prote
21	41	45.1	822	2	hypothetical prote
22	41	45.1	838	2	DNA helicase/prima
23	41	45.1	1063	2	endo-1,4-beta-xyla
24	40	44.0	167	2	hypothetical prote
25	40	44.0	321	2	hypothetical prote
26	40	44.0	349	2	hypothetical prote
27	40	44.0	351	1	transcription fact
28	40	44.0	431	2	LPS biosynthesis p
29	40	44.0	433	2	probable hemolysin

30	40	44.0	555	2	cytochrome c oxida
31	40	44.0	710	2	hypothetical prote
32	40	44.0	838	2	ring-infected eryt
33	40	44.0	899	2	hypothetical prote
34	40	44.0	1349	2	aldehyde oxidase (
35	40	44.0	1495	2	transcription co-r
36	39.5	43.4	1167	2	hypothetical prote
37	39	42.9	95	2	hypothetical prote
38	39	42.9	296	2	phenylalanine 4-mo
39	39	42.9	303	2	probable ABC trans
40	39	42.9	323	2	probable ABC trans
41	39	42.9	349	2	phosphatidylcholin
42	39	42.9	351	2	phosphatidylcholin
43	39	42.9	508	2	galactose-1-phosph
44	39	42.9	548	2	probable asparagin
45	39	42.9	562	2	hydrogenase regula

ALIGNMENTS

RESULT 1

AI0355

probable membrane protein YP02924 [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AI0355

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, G.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AI0355

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-215 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92172.1; PID:g15980886; GSPDB:GN00175

C:Genetics:

A:Gene: YP02924

Query Match 49.5%; Score 45; DB 2; Length 215;

Best Local Similarity 61.5%; Pred. No. 4.7;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WRMYFSHRHAHLR 13

Db 72 WAMTGRREAHRLR 84

RESULT 2

T48357

hypothetical protein F12B4.90 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T48357

R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke,

submitted to the Protein Sequence Database, March 2000

A:Reference number: 224492

A:Accession: T48357

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-684 <BEV>

A:Cross-references: EMBL:AL162751

A:Experimental source: cultivar Columbia; BAC clone F12E4

C:Genetics:

A:Map position: 5

A>Note: F12B4.90

Query Match 49.5%; Score 45; DB 2; Length 684;

Best Local Similarity 70.0%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YFSHRHAHLR 13
 :|||: |||
 Db 412 HFSKHHLR 421
 RESULT 3
 hypothetical protein yobF - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: F69898
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tojgoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: F69898
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-307 <KUN>
 A:Cross-references: GB:Z99114; GB:AL009126; NID:G2634230; PIDN:CAB13781.1; PID:G2634282
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yobF
 C:Superfamily: Bacillus subtilis hypothetical protein yobF
 Query Match 48.4%; Score 44; DB 2; Length 307;
 Best Local Similarity 58.3%; Pred. No. 10;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WRMYFSHRHAHL 12
 : ||| : ||| : |||
 Db 247 YAMYFKDRHSL 258
 RESULT 4
 hypothetical protein T4F9.20 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 C:Accession: T04191
 R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15260
 A:Accession: T04191
 A:Molecule type: DNA
 A:Residues: 1-703 <BEV>
 A:Cross-references: EMBL:AL049523
 A:Experimental source: cultivar Columbia; BAC clone T4F9
 C:Genetics:
 A:Map position: 4
 A:Note: T4F9.20
 Query Match 48.4%; Score 44; DB 2; Length 703;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 YFSHRHAHLR 13
 :|||: |||
 Db 412 HFSKHHLR 421

RESULT 5
 T02147
 hypothetical protein F8K4.22 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 22-Oct-1999
 C:Accession: T02147
 R:Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.;
 rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel
 submitted to the EMBL Data Library, August 1998
 A:Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.
 A:Reference number: Z14574
 A:Accession: T02147
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-743 <VYS>
 A:Cross-references: EMBL:AC004392; NID:G3282170; PID:G3367535; GSPDB:CN00059; ATSP:F8
 C:Genetics:
 A:Gene: ATSP:F8K4.22
 A:Map position: 1
 Query Match 48.4%; Score 44; DB 2; Length 743;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 YFSHRHAHLR 13
 :|||: |||
 Db 418 HFSKHHLR 427
 RESULT 6
 JCS891
 omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 20-Jun-2000
 C:Accession: JCS891
 R:Sato, N.; Fujiwara, S.; Kawaguchi, A.; Tsuzuki, M.
 J. Biochem. 122, 1224-1232, 1997
 A:Title: Cloning of a gene for chloroplast omega 6 desaturase of a green alga, Chlamy
 A:Reference number: JCS891; MUID:98158334; PMID:9498569
 A:Accession: JCS891
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-424 <SAT>
 A:Cross-references: DBDJ:AB007640; NID:G2696716; PIDN:BAA23881.1; PID:G2696717
 C:Comment: This enzyme catalyzes the desaturation of monoenoic to dienoic acids.
 C:Genetics:
 A:Gene: des6
 C:Superfamily: omega-3 fatty acid desaturase
 C:Keywords: chloroplast; oxidoreductase
 F:1-40/Domain: transit peptide (chloroplast) #status predicted <TPS>
 Query Match 47.3%; Score 43; DB 2; Length 424;
 Best Local Similarity 54.5%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WRMYFSHRHAHL 11
 : ||| : |||
 Db 178 WRKHNHHHAHL 188
 RESULT 7
 T01698
 aldehyde oxidase (EC 1.2.3.1) - maize
 C:Species: Zea mays (maize)
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 28-Jul-2000
 C:Accession: T01698
 R:Sekimoto, H.; Seo, M.; Dohmae, N.; Takio, K.; Kamiya, Y.; Koshiba, T.
 J. Biol. Chem. 272, 15280-15285, 1997
 A:Title: Cloning and molecular characterization of plant aldehyde oxidase.
 A:Reference number: Z14401; MUID:97326103; PMID:9182554
 A:Accession: T01698
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA

A:Residues: 1-1358 <SEK>
A:Cross-references: EMBL:D88451; NID:g2589161; PIDN:BAA23226.1; PID:g2589162
C:Genetics:
A:Gene: AO-1
C:Function:
A:Description: catalyzes oxidation of aldehydes into respective acids
C:Superfamily: xanthine dehydrogenase; ferredoxin (2Fe-2S) homology
C:Keywords: 2Fe-2S; metalloprotein; oxidoreductase
F:33-81/Domain: ferredoxin (2Fe-2S) homology <PDX>
F:50,55,58,80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 47.3%; Score 43; DB 2; Length 1358;
Best Local Similarity 58.7%; Pred. No. 75;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 MYFSHRHAHLRSP 14
: : : : :
Db 619 IYSTHPAHVRSP 630

RESULT 8

C69849
hypothetical protein yjdh - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: C69849

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choc, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallet, lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M. A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PID:9384377

A:Accession: C69849
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-134 <KUN>
A:Cross-references: GB:299110; GB:AL009126; NID:g2633472; PIDN:CAB13062.1; PID:g2633559
A:Experimental source: strain 168
C:Genetics:
A:Gene: yjdh
C:Superfamily: Bacillus subtilis hypothetical protein yjdh

Query Match 46.2%; Score 42; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 YFSHRHAHLRSP 15
: : : : :
Db 21 YFSHTNPQRSP 32

RESULT 9

AC1181

hypothetical protein lmo0851 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1181

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1181
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC98929.1; PID:g16410254; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0851

Query Match 46.2%; Score 42; DB 2; Length 252;
Best Local Similarity 53.8%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 MYFSHRHAHLRSP 15
: : : : :
Db 103 LYLAHTGRHLRSP 115

RESULT 10

AD1538

hypothetical protein lin0844 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1538

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloek, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1538
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96076.1; PID:g16413295; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0844

Query Match 46.2%; Score 42; DB 2; Length 252;
Best Local Similarity 53.8%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 MYFSHRHAHLRSP 15
: : : : :
Db 103 LYLAHTGRHLRSP 115

RESULT 11

T29162

hypothetical protein C01B7.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29162

R:Woessner, J.; Bradshaw, H.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid C01B7.
A:Reference number: 220581
A:Accession: T29162

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-929 <WOB>

A:Cross-references: EMBL:U53147; PIDN:AAA96114.1; GSPDB:GN00023; CESP:C01B7.1
A:Experimental source: strain Bristol N2; clone C01B7
C:Genetics:
A:Gene: CESP:C01B7.1
A:Map position: 5
A:Introns: 288/1; 447/3; 478/3; 514/3; 541/1; 567/3; 883/2

Query Match 46.2%; Score 42; DB 2; Length 929;
 Best Local Similarity 46.2%; Pred. No. 72;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 MYFSHRHAHLRSP 15
 :: :||| | |
 Db 453 LFVAHRGRHASP 465

RESULT 12
 JQ1340
 trax protein - Escherichia coli plasmids
 C:Species: Escherichia coli
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Oct-1999
 C:Accession: JQ1340; S10661
 R:Cran, D.S.; Loh, S.M.; Cheah, K.C.; Skurray, R.A.
 Gene 104, 85-90, 1991
 A:Title: Sequence and conservation of genes at the distal end of the transfer region on
 A:Reference number: JQ1338; MUID:92009201; PMID:1916281
 A:Accession: JQ1340
 A:Molecule type: DNA
 A:Residues: 1-248 <CRA>
 A:Cross-references: GB:M38048; NID:g151835; PIDN:AAA98314.1; PID:g151836
 A:Experimental source: plasmid R6-5
 R:Yoshioka, Y.; Fujita, Y.; Ohtsubo, E.
 J. Mol. Biol. 214, 39-53, 1990
 A:Title: Nucleotide sequence of the promoter-distal region of the tra operon of plasmid
 A:Reference number: S10658; MUID:90317835; PMID:2164585
 A:Accession: S10661
 A:Molecule type: DNA
 A:Residues: 1-248 <YOS>
 A:Cross-references: EMBL:X55815; NID:g42620; PIDN:CAA39339.1; PID:g42625
 A:Experimental source: plasmid R100
 C:Genetics:
 A:Gene: trax
 A:Genome: plasmid
 C:Keywords: transmembrane protein
 F:39-55/Domain: transmembrane #status predicted <TM1>
 F:180-196/Domain: transmembrane #status predicted <TM2>
 F:200-216/Domain: transmembrane #status predicted <TM3>
 F:232-248/Domain: transmembrane #status predicted <TM4>

Query Match 45.6%; Score 41.5; DB 2; Length 248;
 Best Local Similarity 53.3%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 WRMYFSHRHAHLRSP 15
 | : | ||| | |
 Db 75 WGLNLS-RHAHTRP 88

RESULT 13
 AE2378
 hypothetical protein all4581 [Imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AE2378
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2378
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-208 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BAB76280.1; PID:g17133717; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all4581

Query Match 45.1%; Score 41; DB 2; Length 208;

Best Local Similarity 52.9%; Pred. No. 21;
 Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 WRMYFSH--RHAHLRSP 15
 ||| | : | ||| |
 Db 81 WRMRSSNPIRRHIRP 97

RESULT 14
 G69899
 transcription regulator AraC/XylS family homolog yobQ - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
 C:Accession: G69899
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 C.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrarri,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hollsappel, S.; Hosono, S.; Hullo, S.;
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Teynoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtili
 A:Title: The complete genome sequence of the Gram-positive bacterium
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: G69899
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-241 <KUN>
 A:Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13797.1; PID:ell1853
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yobQ

Query Match 45.1%; Score 41; DB 2; Length 241;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RMVFSHRHAH 11
 | : | ||| |
 Db 18 RLYHSHKHAY 27

RESULT 15
 B64042
 formate dehydrogenase (EC 1.2.1.2) O gamma chain - Haemophilus influenzae (strain Rd
 C:Species: Haemophilus influenzae
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: B64042
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
 Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glöck, A.; Kelley, J.M.; Weidman
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: B64042
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-257 <TIG>
 A:Cross-references: GB:L42023; TIGR:HI0008
 C:Superfamily: formate dehydrogenase gamma chain
 C:Keywords: NAD; oxidoreductase

Query Match 45.1%; Score 41; DB 1; Length 257;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WRMYFESH 7
 |||
Db 159 WRQYFESH 165

Search completed: November 27, 2002, 07:24:07
Job time : 12.112 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 05:39:34 ; Search time 2.14286 Seconds
(without alignments)
290.334 Million cell updates/sec

Title: US-09-893-615-1

Perfect score: 91

Sequence: 1 WRMYFSRHAHLRSP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	45	49.5	724	1	CCT1_MOUSE	O9qvv9 mus musculus
2	42	46.2	272	1	TNFS_CHICK	Q918d8 gallus gall
3	41.5	45.6	248	1	TRX2_ECOLI	P22710 escherichia
4	41	45.1	238	1	FDX1_HABIN	P44451 haemophilus
5	41	45.1	434	1	SYN_PYRAB	Q9v251 pyrococcus
6	40	44.0	260	1	AG22_SHEEP	O28929 ovis aries
7	40	44.0	351	1	SGF3_BOMMO	Q17237 bombyx mori
8	40	44.0	540	1	RIK2_HUMAN	O43353 h receptor
9	40	44.0	2517	1	NCR2_HUMAN	Q9v618 h nuclear r
10	39	42.9	85	1	HEPC_MORCS	P82951 morone chry
11	39	42.9	351	1	DESA_SYNV3	P20388 synechocyst
12	39	42.9	508	1	GALT_BACHD	O8kdv2 bacillus ha
13	39	42.9	539	1	RIK2_MOUSE	P58801 mus musculus
14	39	42.9	566	1	MASY_CUCMA	P24571 cucurbita m
15	39	42.9	568	1	MASY_CUCSA	P08216 cucumis sat
16	39	42.9	1004	1	CARE_HUMAN	Q9bxl6 homo sapien
17	39	42.9	1021	1	Y2R2_DROME	P16425 drosophila
18	39	42.9	1312	1	DPOL_PYRSD	Q51334 pyrococcus
19	38	41.8	64	1	RL35_ECOLI	P07085 escherichia
20	38	41.8	274	1	MEPA_ECOLI	P14007 escherichia
21	38	41.8	358	1	RECF_PASMU	Q9clq6 pasteurella
22	38	41.8	420	1	KC2A_THEPA	P28547 theileria p
23	38	41.8	427	1	CG23_YEAST	P24870 saccharomyc
24	38	41.8	434	1	SYN_PYRFU	Q8u4d3 pyrococcus
25	38	41.8	434	1	SYN_PYRHO	Q57980 pyrococcus
26	38	41.8	459	1	RSP6_CHLRE	Q01657 chlamydomon
27	38	41.8	488	1	SUOX_HUMAN	P51687 homo sapien
28	38	41.8	881	1	HELI_HSVEB	P28934 equine herp
29	38	41.8	881	1	HELI_VZVD	P09303 varicella-z
30	38	41.8	943	1	ODOL_AZOVI	P20707 azotobacter
31	38	41.8	2054	1	YCF2_PINTH	P41653 pinus thunb
32	38	41.8	3430	1	POLG_WNV	P06935 w genome po
33	38	41.8	3433	1	POLG_KUNJM	P14335 k genome po

RESULT 1

ID	CCT1_MOUSE	STANDARD	PRT	724 AA
AC	Q9QWV9; Q9ZOU7;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Cyclin T1 (Cyclin T) (CyclT).			
GN	CCNT1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALE/C;			
RX	MEDLINE=99059742; PubMed=9843510;			
RA	Bieniasz P.D., Grdina T.A., Bogerd H.P., Cullen B.R.;			
RT	"Recruitment of a protein complex containing Tat and cyclin T1 to TAR			
RT	governs the species specificity of HIV-1 Tat.,"			
RL	EMBO J. 17:7056-7065(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CS7BL/6; TISSUE=Brain;			
RX	MEDLINE=99051315; PubMed=9832504;			
RA	Garber M.E., Wei P., Kewairamani V.N., Mayall T.P., Herrmann C.H.,			
RA	Rice A.P., Littman D.R., Jones K.A.;			
RT	"The interaction between HIV-1 Tat and human cyclin T1 requires zinc			
RT	and a critical cysteine residue that is not conserved in the murine			
RT	CyclT protein.,"			
RL	Genes Dev. 12:3512-3527(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.			
RC	TISSUE=Spleen;			
RX	MEDLINE=99263519; PubMed=10329126;			
RA	Kwak Y.T., Ivanov D., Guo J., Nee E., Gaynor R.B.;			
RT	"Role of the human and murine cyclin T proteins in regulating HIV-1			
RT	Tat-activation.,"			
RL	J. Mol. Biol. 288:57-69(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.			
RC	TISSUE=Fibroblast;			
RX	MEDLINE=99145542; PubMed=9990016;			
RA	Fujinaga K., Taube R., Wimmer J., Cujec T.P., Peterlin B.M.;			
RT	"Interactions between human cyclin T, Tat, and the transactivation			
RT	response element (TAR) are disrupted by a cysteine to tyrosine			
RT	substitution found in mouse cyclin T.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:1285-1290(1999).			
RN	[5]			
RP	FUNCTION: REGULATORY SUBUNIT OF THE CYCLIN-DEPENDENT KINASE PAIR			
RC	(CDK9/CYCLIN T) COMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION			
CC	ELONGATION FACTOR B (P-TEFb), WHICH IS PROPOSED TO FACILITATE THE			
CC	TRANSITION FROM ABORTIVE TO PRODUCTION ELONGATION BY			
CC	PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE			
CC	SUBUNIT OF RNA POLYMERASE II (RNAP II). DOES NOT BIND EFFICIENTLY			
CC	TO THE TRANSCRIPTIONAL DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL			
CC	ACTIVATOR, TAT.			

ALIGNMENTS

34	37	40.7	102	1	YACL_MAIZE	P08771 zea mays (m
35	37	40.7	112	1	YE14_YEAST	P39973 saccharomyc
36	37	40.7	207	1	NU6M_PROMI	Q37626 prototheca
37	37	40.7	273	1	TC1A_CABEL	P03934 caenorhabdi
38	37	40.7	365	1	CMLE_NEUCR	P38677 neurospora
39	37	40.7	395	1	SYT8_MOUSE	Q9r0n6 mus musculu
40	37	40.7	411	1	LAG1_YEAST	P38703 saccharomyc
41	37	40.7	426	1	PYRC_THBAQ	P36081 thermus aqu
42	37	40.7	498	1	GSHB_SCHPO	P35669 schizosacch
43	37	40.7	529	1	YB98_HUMAN	Q9ulm2 homo sapien
44	37	40.7	632	1	YO22_CABEL	P34672 caenorhabdi
45	37	40.7	653	1	PPE1_HUMAN	O14829 homo sapien

CC -1- SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFB. CYCLIN T1 IS THE
 CC PREDOMINANT CYCLIN ASSOCIATED WITH CDK9.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONG TO CYCLIN C
 CC SUBFAMILY.
 CC
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 CC
 DR EMBL: AF095640; AAD13656.1; -
 DR EMBL: AF109179; AAD19654.1; -
 DR EMBL: AF087662; AAD17798.1; -
 DR EMBL: AF113951; AAD17205.1; -
 DR MGD: MGI:1328363; Ccnt1.
 DR InterPro: IPR004366; Ccnt1.
 DR Pfam: PF00134; cyclin; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; FALSE_NEG.
 KW Cyclin; Cell cycle; Cell division; Coiled coil;
 KW Transcription regulation; Nuclear protein.
 FT DOMAIN 253 270
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT TAT-TAR RECOGNITION MOTIF (TRM).
 FT POLY-SER. 254 272
 FT COILED COIL (POTENTIAL).
 FT DOMAIN 319 322
 FT POLY-SER. 384 425
 FT DOMAIN 516 525
 FT POLY-HIS.
 FT DOMAIN 565 569
 FT POLY-SER.
 FT DOMAIN 715 723
 FT POLY-PRO.
 FT CONFLICT 48 48
 FT V -> M (IN REF. 3).
 FT SEQUENCE 724 AA; 80565 MW; 7396E428F5A8B91B CRC64;
 SQ
 Query Match 49.5%; Score 45; DB 1; Length 724;
 Best Local Similarity 58.3%; Pred. No. 6.9;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 YFSRRAHLRSP 15
 Db 522 HHSHRHSLQLP 533
 RESULT 2
 ID TNF5_CHICK STANDARD; PRT; 272 AA.
 AC Q918D8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CDA0-
 DE L) (CD154 protein).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-White leghorn; TISSUE=Spleen;
 RA Tregaskes C.A., Young J.R., Burnside J.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell
 CC proliferation in the absence of co-stimulus as well as IgE
 CC production in the presence of IL-4. Involved in immunoglobulin
 CC class switching (By similarity).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC
 DR EMBL: AJ243435; CAB95748.1; -
 DR HSSP: P29965; ITALY.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS00049; TNF_2; 1.
 DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 KW TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY.
 FT CHAIN 1 272
 FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY.
 FT MEMBER 5, MEMBRANE FORM.
 FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT SITE 110 111
 FT CLEAVAGE (BY SIMILARITY).
 FT DISULFID 190 229
 FT POTENTIAL.
 FT CARBOHYD 124 124
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 146 146
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 251 251
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 272 AA; 30862 MW; 5409F24A8E53CCD7 CRC64;
 Query Match 46.2%; Score 42; DB 1; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.5;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WRMYFSRRAHLRS 14
 Db 109 FEMHRSHEPHLKS 122
 RESULT 3
 ID TRX2_ECOLI STANDARD; PRT; 248 AA.
 AC P22710;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Trax protein.
 DE Trax protein.
 GN Trax.
 OS Escherichia coli.
 OG Plasmid IncFII R100, and Plasmid R6-5.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID-INC FII R100;
 RX MEDLINE=90317835; PubMed=2164585;
 RA Yoshioka Y., Fujita Y., Ohtsubo E.;
 RT "Nucleotide sequence of the promoter-distal region of the tra operon
 RT of plasmid R100, including traI (DNA helicase I) and traD genes.";
 RL J. Mol. Biol. 214:39-53(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID-R6-5;
 RX MEDLINE=92009201; PubMed=1916281;
 RA Cram D.S., Loh S.M., Cheah K.C., Skurray R.A.;

DR PRINTS; PRO1042; TRNASYNTHASP.
 DR TIGRFAMS; TIGR00457; asns; 1.
 DR PROSITE; PS50862; AA.TRNA.LIGASE.II; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 434 AA; 50242 MW; 9A08BCE2458A6A3 CRC64;
 Query Match 45.1%; Score 41; DB 1; Length 434;
 Best Local Similarity 46.2%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 MYFSHRHAHLRSP 15
 : :||| :|||
 Db 117 LLLDYRHHLRSP 129
 RESULT 6
 AG22_SHEEP STANDARD; PRT; 260 AA.
 ID AG22_SHEEP
 AC Q28929;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Type-2 angiotensin II receptor (AT2) (Fragment).
 GN AGTR2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96159644; PubMed=8618791;
 RA Robillard J.E., Page W.V., Mathews M.S., Schutte B.C., Nuyt A.M.,
 Segar J.L.;
 RT "Differential gene expression and regulation of renal angiotensin II
 receptor subtypes (AT1 and AT2) during fetal life in sheep.";
 RL Pediatr. Res. 38:896-904(1995).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
 MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 DR EMBL; S81979; AAB36404.1; -
 DR HSSP; P34996; 1DDO.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 NON_TER 1
 FT TRANSMEM <1 24 1 (POTENTIAL).
 FT DOMAIN 25 33 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 34 55 2 (POTENTIAL).
 FT DOMAIN 56 72 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 73 93 3 (POTENTIAL).
 FT DOMAIN 94 113 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 114 132 4 (POTENTIAL).
 FT DOMAIN 133 161 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 162 187 5 (POTENTIAL).
 FT DOMAIN 188 209 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 210 231 6 (POTENTIAL).
 FT TRANSMEM 232 238 7 (POTENTIAL).
 FT TRANSMEM 239 >260

FT NON_TER 260 260
 SQ SEQUENCE 260 AA; 29549 MW; BB5B48FF029A0B42 CRC64;
 Query Match 44.0%; Score 40; DB 1; Length 260;
 Best Local Similarity 40.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 WRMYFSHRHAHLRSP 15
 : :||| :|||
 Db 53 WATYYSRHWIRGP 67
 RESULT 7
 SGF3_BOMMO STANDARD; PRT; 351 AA.
 ID SGF3_BOMMO
 AC Q17237;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Silk gland factor 3 (SGF-3) (POU domain protein M1).
 GN SGF3 OR POU-M1
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Bombycoidea; Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kinshu X Showa; TISSUE=silk gland;
 RX MEDLINE=93374935; PubMed=7690034;
 RA Fukuta M., Matsuno K., Hui C.-C., Nagata T., Takiya S., Xu P.-X.,
 Ueno K., Suzuki Y.;
 RT "Molecular cloning of a POU domain-containing factor involved in the
 regulation of the Bombyx sericin-1 gene.";
 RL J. Biol. Chem. 268:19471-19475(1993).
 CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF SERICIN-1
 GENE.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO THE MIDDLE SILK GLAND.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DIFFERENTIALLY REGULATED IN THE
 POSTERIOR AND MIDDLE SILK GLANDS DURING THE FOURTH MOLT/FIFTH
 INTERMOLT.
 CC -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
 CC CLASS-3 SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
 CC
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 CC
 DR EMBL; M64781; AAA27841.1; -
 DR HSSP; P14859; 1OCT.
 DR TRANSFAC; T00746; -
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000327; POU_domain.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00157; pou; 1.
 DR PRINTS; PR00028; POUDOMAIN.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000583; POU_domain; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00352; POU; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00035; POU_1; 1.
 DR PROSITE; PS00465; POU_2; 1.
 KW Homeobox; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Neurogenesis.
 FT DOMAIN 152 223 POU.

FT DNA_BIND 241 300 HOMEBOX.
SQ SEQUENCE 351 AA; 38591 MW; A6DFA4A59E9322B6 CRC64;

Query Match 44.0%; Score 40; DB 1; Length 351;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WRMYFSHRAH 11
| : | | |
DB 64 WAMHQHAAH 74

RESULT 8

ID RIK2_HUMAN STANDARD; PRT; 540 AA.
AC Q4353;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE RECEPTOR-INTERACTING SERINE/THREONINE PROTEIN KINASE 2 (EC 2.7.1.-)
DE (RIP-2) (CARD-CONTAINING INTERLEUKIN-1 BETA CONVERTING ENZYME
DE ASSOCIATED KINASE) (CARD-CONTAINING IL-1 BETA ICE-KINASE).
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX MEDLINE-98241596; PubMed-9575181;
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RT "RICK, a novel protein kinase containing a caspase recruitment domain,
interacts with CLARP and regulates CD95-mediated apoptosis.";
RL J. Biol. Chem. 273:12296-12300(1998).
[2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RC TISSUE-Endothelial cells;
RX MEDLINE-98307936; PubMed-9642260;
RA McCarthy J.V., Ni J., Dixit V.M.;
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing
kinase.";
RT Identification of CARDIAK, a RIP-like kinase that associates with
caspase-1.";
RL Curr. Biol. 8:885-888(1998).
[3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
RX MEDLINE-98381580; PubMed-9705938;
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
RA Matmann C., Tschopp J.;
RT "Identification of CARDIAK, a RIP-like kinase that associates with
caspase-1.";
RL Curr. Biol. 8:885-888(1998).
[4]
RP SEQUENCE FROM N.A.
RA Ozersky P., Holmes A., Broy M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA Platzner M., Varon R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC TISSUE-Skin;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB.
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,

CC pancreas and lymph node.
CC -!- PTM: Autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC
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CC
CC EMBL; AF027706; AAC34970.1; -
DR EMBL; AF078530; AAC27722.1; -
DR EMBL; AF064824; AAC25668.1; -
DR EMBL; AC004003; AAC24561.1; -
DR EMBL; AF117829; AAD04634.1; -
DR EMBL; BC004553; AAH04553.1; -
DR Genbank; HGNC:10020; RIPK2.
DR MIM: 603455; -
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00221; STYKc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transphosphatase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN KINASE.
FT DOMAIN 432 524 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP.
FT ACT_SITE 146 146
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;
Query Match 44.0%; Score 40; DB 1; Length 540;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 WRMYFSHRAH 15
| : | | |
DB 40 WRVQVAVKHLHTP 54
RESULT 9
NCR2_HUMAN
ID NCR2_HUMAN STANDARD; PRT; 2517 AA.
AC Q9Y618; Q9Y5U0; Q13354; O00613; O15416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nuclear receptor co-repressor 2 (N-COR2) (Silencing mediator of
DE retinoid acid and thyroid hormone receptor) (SMRT) (Thyroid-,
DE retinoid-acid-receptor-associated co-repressor) (TRAC) (CTG26).
DE associating factor) (TRAC) (CTG26).
GN NCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM SMRT).
RC TISSUE-Pituitary;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OX Moronidae; Morone.
RN NCBI_TaxID=45352;
RP SEQUENCE FROM N.A., SEQUENCE OF 65-85, TISSUE SPECIFICITY, AND
RP ANTI-BIOTIC ACTIVITY.
RC TISSUE=GI, and SKIN;
RX MEDLINE=21982021; PubMed=11985602;
RA Shike H., Lauth X., Westerman M.E., Ostland V.E., Carlberg J.M.,
RA Van Oost J.C., Shimizu C., Bulet P., Burns J.C.;
RT "Bass hepcidin is a novel antimicrobial peptide induced by bacterial
RT challenge.";
RL Eur. J. Biochem. 269:2232-2237(2002).
CC -!- FUNCTION: Seems to act as a signaling molecule involved in the
CC maintenance of iron homeostasis. Seems to be required in
CC conjunction with HFE to regulate both intestinal iron absorption
CC and iron storage in macrophages (By similarity).
CC -!- FUNCTION: Antimicrobial activity against Gram-negative bacteria
CC such as E.coli.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in liver.
CC -!- MASS SPECTROMETRY: MW=2255.97; METHOD=MALDI; RANGE=65-85.
CC -!- INDUCTION: By bacterial challenge.
CC -!- SIMILARITY: BELONGS TO THE HEPcidIN FAMILY.
CC
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CC
DR EMBL; AF394246; AAM28440.1; -
KW Antibiotic; Hormone; Signal.
FT SIGNAL 1 24
FT PROPEP 25 64
FT CHAIN 65 85
FT DISULFID 66 72
FT DISULFID 69 82
FT DISULFID 70 83
FT DISULFID 73 79
SQ SEQUENCE 85 AA; 9484 MW; 0FEA55CF0A522C84 CRC64;
Query Match 42.9%; Score 39; DB 1; Length 85;
Best Local Similarity 40.0%; Pred. No. 6.6;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 WRMYFSHRHAHLRSP 15
Db 49 WRMPYNNRHKRHSSP 63
RESULT 11
ID DESA_SYNY3 STANDARD; PRT; 351 AA.
AC P20388;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid desaturase (EC 1.14.99.-) (Delta 12 desaturase).
GN DESA OR SLR1350.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370121; PubMed=2118597;
RA Wada H., Gombos Z., Murata N.;
RT "Enhancement of chilling tolerance of a cyanobacterium by genetic
RT manipulation of fatty acid desaturation.";
RL Nature 347:200-203(1990).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANE GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC
DR EMBL; X53508; CAA37584.1; -
DR EMBL; D90912; BAA18169.1; -
PIR; S11519; S11519.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 1.
DR PROSITE; PS00574; FATTY-ACID-DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Membrane; Complete proteome.
FT DOMAIN 90 94
FT DOMAIN 126 130
FT DOMAIN 287 291
FT HISTIDINE BOX-1.
FT HISTIDINE BOX-2.
FT HISTIDINE BOX-3.
SQ SEQUENCE 351 AA; 40495 MW; 85DBEE341F73F77 CRC64;
Query Match 42.9%; Score 39; DB 1; Length 351;
Best Local Similarity 45.5%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 WRMYFSHRHAH 11
Db 122 WRLLDHHHLH 132
RESULT 12
ID GALT_BACHD STANDARD; PRT; 508 AA.
AC Q9KDV2; Q9RC74;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10) (Gal-1-P
DE uridylyltransferase).
GN GALT OR BHL109.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki K., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
RN [2]
RN SEQUENCE OF 1-450 FROM N.A.

```
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE-994111980; PubMed=10484179;
RA Takami H., Takaki Y., Nakasone K., Sakiyama T., Maeno G., Sasaki R.,
RA Hirama C., Fuji F., Masui N.;
RT Genetic analysis of the chromosome of alkaliphilic Bacillus
RT halodurans C-125.;
RL Extremophiles 3:227-233(1999).
CC -|- CATALYTIC ACTIVITY: UTP + alpha-D-galactose 1-phosphate =
CC diphosphate + UDP-galactose.
CC -|- PATHWAY: Galactose metabolism; second step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -|- SIMILARITY: BELONGS TO THE GALACTOSE-1-PHOSPHATE
CC URIDYLTRANSFERASE FAMILY 2.
CC
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CC -----
CC EMBL: AP001510; BAB04828.1; -.
CC EMBL: AB024554; BAA83925.1; -.
CC InterPro: IPR000880; GalP_UDP_transf.
CC Pfam: PF01087; GalP_UDP_transf_II.
CC Pfam: PF02744; GalP_UDP_tr.C; 1.
CC TIGRfams: TIGR01239; galT_2; 1.
CC PROSITE: PS01163; GAL_P_UDP_TRANSF_II; 1.
CC Transferrase; Nucleotidyltransferase; Galactose metabolism;
CC Complete proteome.
CC SEQUENCE 508 AA; 57989 MW; 16AF6F607FCEAE2E CRC64;
CC
CC Query Match 42.9%; Score 39; DB 1; Length 508;
CC Best Local Similarity 50.0%; Pred. No. 45;
CC Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 WRMYFSHRHAHL 12
CC I : : : : :
CC DB 451 WALAIKRAHL 462
CC
CC RESULT 13
CC RIK2_MOUSE STANDARD; PRT; 539 AA.
CC AC P58801;
CC DT 15-JUN-2002 (Rel. 41, Created)
CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-).
CC GN RIK2.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-C57BL/6;
CC MEDLINE-21891093; PubMed=11894097;
CC Chin A.I., Dempsey P.W., Bruhn K.J., Miller J.F., Xu Y., Cheng G.;
CC "Involvement of receptor-interacting protein 2 in innate and adaptive
CC immune responses.";
CC Nature 416:190-194(2002).
CC -|- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).
CC -|- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -|- PTM: Autophosphorylated (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC -|- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
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CC -----
CC EMBL: AF461040; AAL96436.1; -.
CC PROSITE: PS50209; CARD; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation; Apoptosis.
CC DOMAIN 18 294 PROTEIN KINASE.
CC FT DOMAIN 431 523 CARD.
CC FT NP_BIND 24 32 ATP (BY SIMILARITY).
CC FT BINDING 47 47 .ATP (BY SIMILARITY).
CC FT ACT_SITE 146 146 BY SIMILARITY.
CC SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;
CC
CC Query Match 42.9%; Score 39; DB 1; Length 539;
CC Best Local Similarity 33.3%; Pred. No. 48;
CC Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 WRMYFSHRHAHLRSP 15
CC I : : : : :
CC DB 40 WRVRVAVKHLHIHTP 54
CC
CC RESULT 14
CC MASV_CUCMA STANDARD; PRT; 566 AA.
CC ID P24571;
CC DT 01-MAR-1992 (Rel. 21, Created)
CC DT 01-MAR-1992 (Rel. 21, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE Malate synthase, glyoxysomal (EC 4.1.3.2).
CC OS Cucurbita maxima (Pumpkin) (Winter squash).
CC OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
CC NCBI_TaxID=3661;
CC [1]
CC SEQUENCE FROM N.A., AND SEQUENCE OF 83-91: 197-206 AND 417-426.
CC STRAIN-CV. Kurokawa Anakuri Narkin; TISSUE=Etolated cotyledon;
CC MEDLINE-91224123; PubMed=1709098;
CC Mori H., Takeda-Yoshikawa Y., Hara-Nishimura I., Nishimura M.;
CC "Pumpkin malate synthase. Cloning and sequencing of the cDNA and
CC northern blot analysis.";
CC Eur. J. Biochem. 197:331-336(1991).
CC -|- CATALYTIC ACTIVITY: L-malate + CoA -> acetyl-CoA + H(2)O +
CC glyoxylate.
CC -|- PATHWAY: SECOND STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE
CC TRICARBOXYLIC ACID CYCLE (IN BACTERIA, FUNGI AND PLANTS).
CC -|- SUBCELLULAR LOCATION: Glyoxysomal.
CC -|- SIMILARITY: BELONGS TO THE MALATE SYNTHASE FAMILY.
CC -----
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CC -----
CC EMBL: X56948; CAA40262.1; -.
CC PIR: S15387; S15387.
CC PIR: S14601; S14601.
CC InterPro: IPR001465; Malate_synthase.
```

DR Pfam: PF01274; Malate synthase; 1.
DR PROSITE: PS00342; MICROBODIES_CTER; 1.
DR PROSITE: PS00510; MALATE_SYNTHASE; 1.
KW Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
FT SITE 564 566 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 566 AA; 64635 MW; B77F77D1D593834A CRC64;

Query Match 42.9%; Score 39; DB 1; Length 566;
Best Local Similarity 54.5%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 MYFSHRHAHLR 13
Db 209 LYFFHNHANFR 219

RESULT 15

MASY_CUCSA STANDARD: PRT; 568 AA.
AC P08216;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate synthase, glyoxysomal (EC 4.1.3.2).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LONG GREEN RIDGE;
RX MEDLINE=91370851; PubMed=2491683;
RA Graham I.A., Smith L.M., Brown J.W.S., Leaver C.J., Smith S.M.;
RT "The malate synthase gene of cucumber."
RL Plant Mol. Biol. 13:673-684(1989).
RN [2]
RP SEQUENCE OF 475-568 FROM N.A.
RA Smith S.M., Leaver C.J.;
RT "Glyoxysomal malate synthase of cucumber: molecular cloning of a cDNA
and regulation of enzyme synthesis during germination."
RL Plant Physiol. 81:762-767(1986).
CC -!- CATALYTIC ACTIVITY: L-malate + CoA = acetyl-CoA + H(2)O +
glyoxylate.
CC -!- PATHWAY: SECOND STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE
TRICARBOXYLIC ACID CYCLE (IN BACTERIA, FUNGI AND PLANTS).
CC -!- SUBCELLULAR LOCATION: Glyoxysomal.
CC -!- SIMILARITY: BELONGS TO THE MALATE SYNTHASE FAMILY.
CC -----
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CC -----
DR EMBL; X15425; CAA33465.1; -;
DR EMBL; M16219; AAA33123.1; -;
DR PIR; S07550; SYKVMA.
DR InterPro; IPR001465; Malate_synthase.
DR Pfam; PF01274; Malate_synthase; 1.
DR PROSITE; PS00342; MICROBODIES_CTER; 1.
DR PROSITE; PS00510; MALATE_SYNTHASE; 1.
KW Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
FT SITE 566 568 MICROBODY TARGETING SIGNAL (POTENTIAL).
FT CONFLICT 475 475 I -> G (IN REF. 2).
SQ SEQUENCE 568 AA; 64961 MW; 0C25AB66288ECAA4 CRC64;

Query Match 42.9%; Score 39; DB 1; Length 568;
Best Local Similarity 54.5%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 MYFSHRHAHLR 13
Db 210 LYFFHNHANFR 220

Search completed: November 27, 2002, 07:18:52
Job time : 13.1429 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 06:27:07 ; Search time 8.33977 Seconds
(without alignments)
370.599 Million cell updates/sec

Title: US-09-893-615-1

Perfect score: 91

Sequence: 1 WRMYFSHRRAHRLSP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_xvirus.*

16: sp_bacteriaph.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	51.6	757	2 Q9KIB0	Q9kib0 porphyron
2	45	49.5	215	16 Q8ZCP9	Q8zcp9 yersinia pe
3	45	49.5	684	5 Q9VSL7	Q9vsl7 drosophila
4	45	49.5	684	10 Q9LZF4	Q9lzf4 arbidopsis
5	44	48.4	307	16 Q34780	Q34780 bacillus su
6	44	48.4	703	10 Q9ZS84	Q9zsb4 arbidopsis
7	44	48.4	743	10 Q80707	Q80707 arbidopsis
8	43.5	47.8	644	10 Q8S7K3	Q8sbk3 oryza sativ
9	43	47.3	421	10 Q9SB04	Q9sbu4 chlamydomon
10	43	47.3	424	10 Q48663	Q48663 chlamydomon
11	43	47.3	1358	10 Q23887	Q23887 zea mays (m
12	42	46.2	92	16 Q8XVZ0	Q8xvz0 ralstonia s
13	42	46.2	111	6 Q9N0J0	Q9n0j0 bos taurus
14	42	46.2	120	17 Q8TQU6	Q8tqu6 methanosarc
15	42	46.2	134	16 Q31649	Q31649 bacillus su
16	42	46.2	252	16 Q92DC9	Q92dc9 listeria in

17 42 46.2 252 16 Q8Y8P5
18 42 46.2 486 5 Q9VQT3
19 42 46.2 879 4 Q9H3H4
20 42 46.2 917 11 Q99K11
21 42 46.2 935 5 Q17548
22 42 46.2 1435 12 Q9DSQ0
23 42 46.2 1435 12 Q8QVF4
24 42 46.2 2785 4 Q75691
25 41.5 45.6 248 2 Q9AJU8
26 41.5 45.6 267 2 Q8VSA9
27 41.5 45.6 301 2 Q9AFK9
28 41 45.1 208 16 Q8YNI4
29 41 45.1 228 16 Q9CNM1
30 41 45.1 241 16 Q34901
31 41 45.1 285 16 Q9HV33
32 41 45.1 309 5 Q9N9D3
33 41 45.1 310 5 Q9N9D2
34 41 45.1 346 2 Q44165
35 41 45.1 370 16 Q9A7P8
36 41 45.1 378 10 Q942N6
37 41 45.1 452 4 Q96SP6
38 41 45.1 470 16 Q8YTC6
39 41 45.1 552 4 Q9NUG0
40 41 45.1 599 6 Q95LW5
41 41 45.1 692 10 Q9LT62
42 41 45.1 822 10 Q9ZOX3
43 41 45.1 833 12 Q69403
44 41 45.1 838 12 Q65576
45 41 45.1 1063 10 Q80596

ALIGNMENTS

RESULT 1

Q9KIB0
ID Q9KIB0 PRELIMINARY: PRT: 757 AA.
AC Q9KIB0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical tonB-linked outer membrane receptor PG13.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
OC Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W50;
RA Ross B., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,
RA Hocking D., Webb E.;
RT "P. gingivalis polypeptides and nucleic acids."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W50;
RA Ross B.C.;

RT "Genomic analysis of Porphyromonas gingivalis for vaccine discovery."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237558; AAF81416.1; .
DR InterPro; IPR00531; TonB_boxC.
DR Pfam; PF00593; TonB_boxC; 1.
KW Receptor.
SQ SEQUENCE 757 AA; 84517 MW; 224B6D65264F9D62 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 757;

Best Local Similarity 61.5%; Pred. NO.19;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WRMYFSHRRAHRL 13

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Db 700 WRLATSHRFAHFR 712

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RESULT 2
Q8ZCP9          PRELIMINARY;          PRT;      215 AA.
AC Q8ZCP9:
DT 01-WAR-2002 (TREMBlrel. 20, Created)
DT 01-WAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-WAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative membrane protein.
GN YPO2924.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT Nature 413:523-527(2001).
RL "Genome sequence of Yersinia pestis, the causative agent of plague.";
DR EMBL; AJ414154; CAC92172.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 215 AA; 24920 MW; EF312DBBAC15B3BB CRC64;

Query Match          49.5%; Score 45; DB 16; Length 215;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRAHLR 13
    | | | | | | | |
DB 72 WAMTGRRAHLR 84

RESULT 3
Q9VSL7          PRELIMINARY;          PRT;      684 AA.
AC Q9VSL7:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG6817 protein.
GN FOI OR CG6817.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reihert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003555; AAF50401.1; -.
DR FlyBase; FBgn0024236; fol.
DR InterPro; IPR003689; Zn_trnprt.zip.
DR Pfam; PF02535; Zip; 1.
SQ SEQUENCE 684 AA; 75037 MW; A7272B67C342B988 CRC64;

Query Match          49.5%; Score 45; DB 5; Length 684;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 SHRHAHLRSP 15
    | | | | | | | |
DB 505 SHRHGVHSP 514

RESULT 4
Q9LZF4          PRELIMINARY;          PRT;      684 AA.
AC Q9LZF4:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 79.7 kDa protein.
GN F12B4_90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162751; CAB83292.1; -.
DR InterPro; IPR004146; DC1.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF03107; DC1; 3.
DR SMART; SM00184; RING; 2.
KW Hypothetical protein.
SQ SEQUENCE 684 AA; 79746 MW; C872720DD26E133E CRC64;

Query Match          49.5%; Score 45; DB 10; Length 684;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 4 YFSHRAHLR 13
Db 412 HFSHRAHLR 421

RESULT 5
O34780 PRELIMINARY: PRT; 307 AA.
AC O34780;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE RADC homolog.
GN YOFB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_taxid=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita Y., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffey A., Gollightly E.J., Grandi G.,
RA Gulseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF027868; AAB84459.1;
DR EMBL; 299114; CAB13781.1;
KW Complete proteome.
SQ SEQUENCE 307 AA; 35348 MW; BF3974AA51D0F762 CRC64;

Query Match 48.4%; Score 44; DB 16; Length 307;
Best Local Similarity 58.3%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRMYFSHRAHLR 12
Db 412 HFSHRAHLR 421

RESULT 6
Q9ZSB4 PRELIMINARY: PRT; 703 AA.
AC Q9ZSB4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE F3H7.4 protein.
GN F3H7.4 OR T4F9.20 OR AT4G10560.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA WASHU;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Laplant Y., Spalding L.;
RT "The sequence of A. thaliana F3H7.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Wedler E., Wambutt R., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118222; AAD03432.1;
DR EMBL; AL049523; CAB40022.1;
DR EMBL; AL161517; CAB78179.1;
DR InterPro; IPR004146; DCL;
DR InterPro; IPR001841; Znf_ring;
DR Pfam; PF03107; DCL; 3;
DR SMART; SM00184; RING; 2;
KW Hypothetical protein.
SQ SEQUENCE 703 AA; 81396 MW; 6EC241534E870B41 CRC64;

Query Match 48.4%; Score 44; DB 10; Length 703;
Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YFSHRAHLR 13
Db 412 HFSHRAHLR 421

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RESULT 7
O80707 PRELIMINARY; PRT; 743 AA.
AC O80707;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F8K4.22.
GN F8K4.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Kwan A., Yu G., Oji O.,
RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RA "Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.";
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004392; AAC28520.1; -.
DR InterPro; IPR002219; DAG_PE-blind.
DR DR Pfam; PF03107; DC1. 3.
DR SMART; SM00109; CI. 2.
SQ SEQUENCE 743 AA; 85956 MW; 7390A56812CC6F01 CRC64;

Query Match 48.4%; Score 44; DB 10; Length 743;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YFSRHRAHLR 13
DB 418 HFSHQHHLR 427

RESULT 8
Q8S7K3 PRELIMINARY; PRT; 644 AA.
AC Q8S7K3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative protein with similarity to protein phosphatase Pp1 regulatory
DE subunit.
GN OSJNBa0095C06.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
RA Du H., Minx P., de la Bastide M., Nascimento L., Spiegel L.,
RA Preston R., Kirchoff K., Kuit K., Baker J., Vil M.D., Zutavern T.,
RA Santos L., Cunnius D.M., Rodriguez S., Miller B., Bailja V., Shah R.,
RA Bahret A., King L., O'Shaughnessy A., Palmer L., Dedhia N.,
RA McCombie W.R.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNBa0095C06, from Chromosome 10, complete sequence.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC079935; AAM08533.1; -.

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SQ SEQUENCE 644 AA; 67700 MW; D009A65DD8EABC75 CRC64;

Query Match 47.8%; Score 43.5; DB 10; Length 644;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 8; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 WRMY-FSHRHAHLRSP 15
DB 228 WRFLWLSHRNLHRPSP 243

RESULT 9
Q9SBU4 PRELIMINARY; PRT; 421 AA.
AC Q9SBU4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chloroplast w6 desaturase.
GN DES6.
OS Chlamydomonas sp. (strain W80).
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=103365;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W80;
RA Miyasaka H.;
RT "Cloning of chloroplast w6 desaturase of a marine halotolerant
RT Chlamydomonas";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB031546; BAA83822.1; -.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 2.
SQ SEQUENCE 421 AA; 47932 MW; AD48F6039C8EDD57 CRC64;

Query Match 47.3%; Score 43; DB 10; Length 421;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAH 11
DB 176 WRIKHNNHHHAH 186

RESULT 10
O48663 PRELIMINARY; PRT; 424 AA.
AC O48663;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chloroplast w6 desaturase.
GN DES6.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98158334; PubMed=9498569;
RA Sato N., Fujiwara S., Kawaguchi A., Tsuzuki M.;
RT "Cloning of a gene for chloroplast w6 desaturase of a green alga,
RT Chlamydomonas reinhardtii.";
RL J. Biochem. 122:1224-1232(1997).
DR EMBL; AB007640; BAA23881.1; -.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 2.
SQ SEQUENCE 424 AA; 48377 MW; D553054C1CEE6B0D CRC64;

Query Match 47.3%; Score 43; DB 10; Length 424;

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Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAH 11
Db 178 WRIKHHHHAH 188
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RESULT 11
O23887 PRELIMINARY; PRT; 1358 AA.
AC O23887
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Aldehyde oxidase (EC 1.2.3.1).
GN ZMAO-1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=COLEOPTILE;
RX MEDLINE=97326103; PubMed=9182554;
RA Sekimoto H., Seo M., Dohmae N., Takio K., Kamiya Y., Koshiba T.;
RT "Cloning and molecular characterization of plant aldehyde oxidase.";
RL J. Biol. Chem. 272:15280-15285(1997).
CC -1- COFACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL; D88451; BA232236.1; -
DR HSSP; P80457; 1FTQ.
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR000674; Aldxan_dh_C.
DR InterPro; IPR005107; CO_doh_flav_C.
DR InterPro; IPR002346; dehydrog_molyb.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF01315; Ald_xan_dh_C; 1.
DR Pfam; PF02738; Ald_xan_dh_C2; 1.
DR Pfam; PF03450; CO_doh_flav_C; 1.
DR Pfam; PF00941; FAD_binding_5; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF01799; fer2.2; 1.
DR ProDom; PD186071; 2Fe-2S_bind; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Iron-sulfur; Oxidoreductase.
SQ SEQUENCE 1358 AA; 146682 MW; 82449227AFB14861 CRC64;

Query Match 47.3%; Score 43; DB 10; Length 1358;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 MYFSHRHAHLS 14
Db 619 IYSTHPHAHVS 630
II: :|||:|

RESULT 12
O8XV20 PRELIMINARY; PRT; 92 AA.
AC O8XV20
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein RSC2685.
GN RSC2685 OR RS00036.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;

Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646071; CAD16392.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 92 AA; 10226 MW; DB6B4B409C8FC62B CRC64;

Query Match 46.2%; Score 42; DB 16; Length 92;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLS 14
Db 30 WLQFFGDRHGFLRS 43
II: :|||

RESULT 13
Q9NOJ0 PRELIMINARY; PRT; 111 AA.
ID Q9NOJ0
AC Q9NOJ0
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin receptor 2 (Fragment).
GN AT2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Berisha B.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20039923; PubMed=10569984;
RA Acosta T., Berisha B., Ozawa T., Sato K., Schams D., Miyamoto A.;
RT "Evidence for local endothelin-angiotensin atrial natriuretic peptide
RT system in bovine mature follicles in vitro: effects on steroid
RT hormones and prostaglandin secretion.";
RL Biol. Reprod. 61:1419-1425(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ277986; CAB92128.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 13102 MW; 9E8A81D3D580A601 CRC64;

Query Match 46.2%; Score 42; DB 6; Length 111;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLS 15
Db 7 WATYSHRYDWLFGP 21
II: :|||:|
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RESULT 14

Q8TQ06 PRELIMINARY; PRT; 120 AA.
 AC Q8TQ06; 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Predicted protein.
 GN M1443.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Linton N., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hederich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity."
 RL Genome Res. 12:532-542(2002).
 DR EMBL: AE010814; AAM04857.1; -
 KW Complete proteome.
 SQ SEQUENCE 120 AA; 13232 MW; 49AAB649268558FD CRC64;

Query Match 46.2%; Score 42; DB 17; Length 120;
 Best Local Similarity 72.7%; Pred. No. 20;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSHRHAHLRSP 15
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Db 75 FSHRYAQLSP 85

RESULT 15

Q31649 PRELIMINARY; PRT; 134 AA.
 AC Q31649;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE YJH protein.
 GN YJH.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Colightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Key M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie F.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzsaecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 RT subtilis."
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z99110; CAB13062.1; -
 KW Complete proteome.
 SQ SEQUENCE 134 AA; 15340 MW; 80F1E6CFC76B34E3 CRC64;

Query Match 46.2%; Score 42; DB 16; Length 134;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YFSHRHAHLRSP 15
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Db 21 YFSHTNPQRSP 32

Search completed: November 27, 2002, 07:22:39

Job time : 21.3398 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:17:51 ; Search time 2.72201 Seconds
(without alignments)
162.139 Million cell updates/sec

Title: US-09-893-615-1

Perfect score: 91

Sequence: 1 WRMYFSHRHAHLRSP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	40	44.0	264	4	US-09-069-023-7
2	40	44.0	300	4	US-09-099-041A-4
3	40	44.0	300	4	US-09-245-281-4
4	40	44.0	300	4	US-09-207-359B-4
5	40	44.0	531	4	US-09-069-023-1
6	40	44.0	540	3	US-09-018-942-1
7	40	44.0	540	4	US-09-099-041A-2
8	40	44.0	540	4	US-09-069-023-27
9	40	44.0	540	4	US-09-245-281-2
10	40	44.0	540	4	US-09-470-271-1
11	40	44.0	540	4	US-09-207-359B-2
12	39	42.9	1019	1	US-08-271-364A-7
13	39	42.9	1019	2	US-08-222-715B-26
14	38	41.8	305	4	US-09-134-001C-5632
15	37	40.7	29	4	US-09-354-231B-34
16	37	40.7	29	4	US-09-128-602B-34
17	37	40.7	189	2	US-08-837-029-2
18	37	40.7	193	2	US-08-336-031-6
19	37	40.7	193	5	PCT-US95-06725-6
20	37	40.7	224	4	US-08-530-862B-11
21	37	40.7	224	4	US-08-597-313D-11
22	37	40.7	224	4	US-09-133-962A-10
23	37	40.7	355	3	US-08-872-979-7
24	37	40.7	396	1	US-08-229-284A-2
25	37	40.7	411	2	US-08-336-031-2
26	37	40.7	411	2	US-08-902-853-7
27	37	40.7	411	5	PCT-US95-06725-2

28	37	40.7	774	3	US-08-902-632-2	Sequence 2, Appli
29	37	40.7	774	3	US-09-073-354-1	Sequence 1, Appli
30	37	40.7	774	3	US-08-656-005A-1	Sequence 1, Appli
31	37	40.7	774	4	US-09-073-259-1	Sequence 1, Appli
32	37	40.7	774	4	US-09-363-095-1	Sequence 1, Appli
33	37	40.7	774	4	US-09-418-027-1	Sequence 1, Appli
34	37	40.7	921	4	US-09-206-800-9	Sequence 9, Appli
35	37	40.7	1164	2	US-08-589-756-1	Sequence 1, Appli
36	37	40.7	1164	4	US-09-206-800-1	Sequence 1, Appli
37	37	40.7	1164	4	US-09-206-898-1	Sequence 1, Appli
38	37	40.7	1313	4	US-08-989-299-9	Sequence 9, Appli
39	36.5	40.1	840	4	US-08-974-549A-190	Sequence 190, App
40	36.5	40.1	872	3	US-08-851-843A-8	Sequence 8, Appli
41	36.5	40.1	872	3	US-08-851-843A-54	Sequence 54, Appl
42	36.5	40.1	872	4	US-08-974-549A-221	Sequence 221, App
43	36.5	40.1	872	4	US-08-854-050-8	Sequence 8, Appli
44	36.5	40.1	872	4	US-08-854-050-54	Sequence 54, Appl
45	36.5	40.1	872	4	US-09-430-323-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-069-023-7
; Sequence 7, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-7

Query Match 44.0%; Score 40; DB 4; Length 264;
Best Local Similarity 33.3%; Pred. No. 28;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WRMYFSHRHAHLRSP 15
||: :|:|:|:
Db 30 WRVQVAVKHLHTTP 44

RESULT 2
US-09-099-041A-4
; Sequence 4, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-4

Query Match 44.0%; Score 40; DB 4; Length 300;
Best Local Similarity 33.3%; Pred. No. 32;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLRSP 15
||: : || : ||
DB 40 WRVQVAVKHLHIHP 54

RESULT 3

US-09-245-281-4
; Sequence 4, Application US/09245281

; Patent No. 6369196

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

; FILE REFERENCE: 07334/118001

; CURRENT APPLICATION NUMBER: US/09/245,281

; CURRENT FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: US 09/207,359

; EARLIER FILING DATE: 1998-12-08

; EARLIER APPLICATION NUMBER: US 09/099,041

; EARLIER FILING DATE: 1998-06-17

; EARLIER APPLICATION NUMBER: US 09/019,942

; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-245-281-4

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Best Local Similarity 33.3%; Pred. No. 32;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLRSP 15
||: : || : ||
DB 40 WRVQVAVKHLHIHP 54

RESULT 4

US-09-207-359B-4

; Sequence 4, Application US/09207359B

; Patent No. 6469140

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-112001

; CURRENT APPLICATION NUMBER: US/09/207,359B

; CURRENT FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-207-359B-4

Query Match 44.0%; Score 40; DB 4; Length 300;
Best Local Similarity 33.3%; Pred. No. 32;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLRSP 15
||: : || : ||

Db 40 WRVQVAVKHLHIHP 54

RESULT 5

US-09-069-023-1

; Sequence 1, Application US/09069023A

; Patent No. 6348573

; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1

; LENGTH: 531

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-1

Query Match 44.0%; Score 40; DB 4; Length 531;
Best Local Similarity 33.3%; Pred. No. 58;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRHAHLRSP 15
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DB 31 WRVQVAVKHLHIHP 45

RESULT 6

US-09-019-942-1

; Sequence 1, Application US/09019942

; Patent No. 6033855

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

; FILE REFERENCE: 07334-112001

; CURRENT APPLICATION NUMBER: US/09/019,942

; CURRENT FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-019-942-1

; MOLECULE TYPE: protein
US-09-019-942-1

Query Match 44.0%; Score 40; DB 3; Length 540;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WRMYFSHRHAHLRSP 15
||: :| :| :|
Db 40 WRVQVAVKHLHIHTP 54

RESULT 7

US-09-099-041A-2
; Sequence 2, Application US/09099041A
; Patent No. 6340576

GENERAL INFORMATION:

; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001

; CURRENT APPLICATION NUMBER: US/09/099,041A

; CURRENT FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-099-041A-2

Query Match 44.0%; Score 40; DB 4; Length 540;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WRMYFSHRHAHLRSP 15
||: :| :| :|
Db 40 WRVQVAVKHLHIHTP 54

RESULT 8

US-09-069-023-27
; Sequence 27, Application US/09069023A
; Patent No. 6348573

GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-27

Query Match 44.0%; Score 40; DB 4; Length 540;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WRMYFSHRHAHLRSP 15
||: :| :| :|
Db 40 WRVQVAVKHLHIHTP 54

RESULT 9

US-09-245-281-2
; Sequence 2, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

; FILE REFERENCE: 07334/118001

; CURRENT APPLICATION NUMBER: US/09/245,281

; EARLIER FILING DATE: 1999-02-05

; EARLIER FILING DATE: 1998-12-08

; EARLIER FILING DATE: 1998-06-17

; EARLIER FILING DATE: 1998-06-17

; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-245-281-2

Query Match 44.0%; Score 40; DB 4; Length 540;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WRMYFSHRHAHLRSP 15
||: :| :| :|
Db 40 WRVQVAVKHLHIHTP 54

RESULT 10

US-09-470-271-1

; Sequence 1, Application US/09470271

; Patent No. 6410689

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/470,271

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/019,942

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Melklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/068001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 540 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-470-271-1

Query Match 44.0%; Score 40; DB 4; Length 540;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRHRLRSP 15
|| : : || : :
DB 40 WRVQVAVKHLHIHTP 54

RESULT 11

US-09-207-359B-2

; Sequence 2, Application US/09207359B

; Patent No. 6469140

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

; FILE REFERENCE: 07334-112001

; CURRENT APPLICATION NUMBER: US/09/207,359B

; CURRENT FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-207-359B-2

Query Match 44.0%; Score 40; DB 4; Length 540;
Best Local Similarity 33.3%; Pred. No. 59;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WRMYFSHRHRLRSP 15
|| : : || : :
DB 40 WRVQVAVKHLHIHTP 54

RESULT 12

US-08-271-364A-7

; Sequence 7, Application US/08271364A

; Patent No. 5756334

; GENERAL INFORMATION:

; APPLICANT: PERLER, FRANCINE B.

; APPLICANT: SOUTHWORTH, MAURICE W.

; TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA POLYMERASE

; FILE OF INVENTION: FROM ARCHAEABACTERIA

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NEW ENGLAND BIOLABS, INC.

; STREET: 32 TOZER ROAD

; CITY: BEVERLY

; STATE: MASSACHUSETTS

; COUNTRY: US

; ZIP: 01915

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/271,364A

; FILING DATE: 06-JUL-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/811,421

; FILING DATE: 18-DEC-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/686,340
; FILING DATE: 17-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/626,057

; FILING DATE: 11-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/513,994

; FILING DATE: 26-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, GREGORY D.

; REGISTRATION NUMBER: 30901

; REFERENCE/DOCKET NUMBER: NEB-101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 927-5054

; TELEFAX: (508) 927-1705

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1019 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-271-364A-7

Query Match 42.9%; Score 39; DB 1; Length 1019;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WRMYFSH 7
|| : : || : :
DB 83 WRLYFEH 89

RESULT 13

US-08-222-715B-26

; Sequence 26, Application US/08222715B

; Patent No. 5834285

; GENERAL INFORMATION:

; APPLICANT: Comb, Donald G.

; APPLICANT: Perler, Francine

; APPLICANT: Kucera, Rebecca

; APPLICANT: Jack, William E.

; TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA

; FILE OF INVENTION: POLYMERASE FROM ARCHAEABACTERIA

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,

; STREET: 32 TOZER ROAD

; CITY: BEVERLY

; STATE: MASSACHUSETTS

; COUNTRY: US

; ZIP: 01915

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,715B

; FILING DATE: 04-APR-1994

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/167,238

; FILING DATE: 15-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/686,340

; FILING DATE: 17-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/626,057

; FILING DATE: 11-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/513,994
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-054C3FC2
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-222-715B-26

Query Match 42.9%; Score 39; DB 2; Length 1019;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WRMYFSH 7
|||:|
Db 83 WRLYFEH 89

RESULT 14

US-09-134-001C-5632
; Sequence 5632, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 5632
LENGTH: 305
TYPE: PRT

; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5632

Query Match 41.8%; Score 38; DB 4; Length 305;
Best Local Similarity 42.9%; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WRMYFSHRHAHLRS 14
: : |||:
Db 289 YNVVHEDAHIES 302

RESULT 15

US-09-354-231B-34
; Sequence 34, Application US/09354231B
; Patent No. 6342658

GENERAL INFORMATION:

; APPLICANT: DeBonte, Lorin R.
; APPLICANT: Shorosh, Basil S.
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063002
; CURRENT APPLICATION NUMBER: US/09/354,231B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Ricinus communis
US-09-354-231B-34

Query Match 40.7%; Score 37; DB 4; Length 29;
Best Local Similarity 60.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YFSHRHAHLR 13
|||:|
Db 5 YFSWKHSRR 14

Search completed: November 27, 2002, 07:25:10
Job time : 5.72201 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 05:38:32 ; Search time 67.9112 Seconds
(without alignments)
241.342 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 646

Sequence: 1 EWLVBESGGLVQPKGSLK.....SGIDYAMYWGQTSLSFVS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	85.9	115	18	AAW01593
2	549	85.0	119	17	AAW01593
3	549	85.0	599	17	AAW01593
4	536	83.0	333	21	AAW01587
5	532	82.4	110	18	AAW01587
6	519	80.3	117	22	AAW01587
7	519	80.3	117	22	AAW01587
8	519	80.3	148	22	AAW01587
9	514.5	79.6	125	21	AAW01587
10	510	78.9	117	23	AAW01587

11	493	76.3	117	22	AAW09930	Humanised 1D9 heav
12	493	76.3	117	22	AAW09930	Humanised murine 1
13	489	75.7	117	22	AAW09928	Humanised 1D9 heav
14	489	75.7	117	22	AAW09929	Humanised 1D9 heav
15	489	75.7	117	22	AAW09956	Humanised murine 1
16	489	75.7	117	23	AAW014982	Humanised murine h
17	488	75.5	117	22	AAW06955	Humanised murine 1
18	488	75.5	117	23	AAW014981	Humanised murine h
19	487	75.4	117	22	AAW09927	Humanised 1D9 heav
20	487	75.4	117	22	AAW06954	Humanised murine 1
21	487	75.4	117	23	AAW014980	Humanised murine h
22	487	75.4	119	22	AAW07034	Humanised murine a
23	483	74.8	101	22	AAW06971	Murine 1D9 antibod
24	482.5	74.7	118	23	AAW014983	Humanised murine h
25	476	73.7	119	19	AAW046958	Amino acid sequenc
26	471.5	73.0	126	21	AAW07011	Human heavy chain
27	468	72.4	100	22	AAW06972	Mouse germline hea
28	467.5	72.4	256	23	AAW072866	P5-3 single chain
29	467.5	72.4	503	23	AAW072874	3B10P5-23 bispec1
30	463	71.7	127	22	AAW07008	Human heavy chain
31	462.5	71.6	122	21	AAW90812	2G3 hybridoma VH d
32	460.5	71.3	120	18	AAW27553	Human Ab heavy cha
33	460.5	71.3	281	18	AAW27560	Consensus single c
34	456	70.6	123	22	AAW02615	Anti-adipocyte mon
35	455.5	70.5	126	22	AAW07010	Human heavy chain
36	454.5	70.4	120	18	AAW01589	Lead binding Mab 4
37	451.5	69.9	122	21	AAW50973	Human FVIII antibo
38	451.5	69.9	122	21	AAW50975	Human FVIII heavy
39	448.5	69.4	444	21	AAW32263	Humanised anti-CD2
40	448	69.3	121	20	AAW86122	Protein sequence o
41	448	69.3	570	20	AAW39451	Antibody ABX-CBL h
42	447.5	69.3	120	19	AAW23952	Chimeric humanised
43	447.5	69.3	240	19	AAW23954	Chimeric humanised
44	447	69.2	116	20	AAW03869	SM3 heavy chain va
45	447	69.2	142	18	AAW06212	MAB Br-3 heavy cha

ALIGNMENTS

RESULT 1

AAW01593

ID AAW01593 standard; Protein; 115 AA.

AC AAW01593;

DT 22-AUG-1997 (first entry)

DE Lead binding MAB 2B4 heavy chain variable region.

KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.

XX Mus musculus.

OS OS

XX WO9639518-A1.

XX PD 12-DEC-1996.

XX 05-JUN-1996; 96WO-US09258.

XX 10-OCT-1995; 95US-0541373.

XX 05-JUN-1995; 95US-0462798.

XX (BION-) BIONEBRASKA INC.

XX Lopez O, Murray PJ, Wylie DE;

XX WPI; 1997-043140/04.

XX N-PSDB; AAT58267.

XX DNA encoding heavy metal binding polypeptide sequences - used for

PT detecting, removing, adding or neutralising heavy metals, such as
 XX lead cations
 PS Claim 12; Page 89; 125pp; English.
 XX The present sequence represents the heavy chain variable region for
 CC monoclonal antibody (MAb) 2B4, which immunoreacts with a lead cation.
 CC The sequence was derived from RNA isolated from mouse hybridoma cells.
 CC The protein can be used for binding heavy metals, such as lead cations.
 CC It can be used for detecting, removing, adding or neutralising the
 CC heavy metals in biological and inanimate systems. It can be used in
 CC e.g. aqueous liquid systems, in biological or environmental systems or
 CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
 CC care products, skin treatment products, pesticides, herbicides,
 CC solvents used in the production of semi-conductor and integrated
 CC circuit components and production materials for electronic components.
 CC The products can provide for applications involving minute amounts of
 CC specific heavy metals.

XX Sequence 115 AA;
 SQ Query Match 85.9%; Score 555; DB 18; Length 115;
 Best Local Similarity 87.8%; Pred. No. 2.6e-46;
 Matches 108; Conservative 2; Mismatches 5; Indels 8; Gaps 1;
 QY 1 EYLVESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 DB 1 EYLVESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 QY 61 FYADSVKDRFTISRDDSQSMFLYQNNLKTEDTAMYVCVRGASGIDYAMDYWGQGTSLT 120
 DB 61 FYADSVKDRFTISRDDSQSMFLYQNNLKTEDTAMYVCVRGASGIDYAMDYWGQGTSLT 112
 QY 121 VSS 123
 DB 113 VSS 115

RESULT 2
 AAR90829
 ID AAR90829 standard; Protein; 119 AA.
 XX AC AAR90829;
 XX DT 25-JUN-1996 (first entry)
 XX DE 3B1 heavy chain variable region from pCIB4613.
 XX KW delta endotoxin; Bacillus thuringiensis; western corn rootworm;
 KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
 KW antibody.
 XX OS Insecta sp.
 XX PN WO9600783-A1.
 XX PD 11-JAN-1996.
 XX PF 20-JUN-1995; 95WO-IB00497.
 XX PR 28-JUN-1994; 94US-0267641.
 XX PA (CIBA) CIBA GEIGY AG.
 XX PI Carozzi NB, Koziel MG;
 XX DR WPI; 1996-077494/08.
 XX DR N-PSDB; AAT15725.
 XX PT New monoclonal antibodies which bind insect gut proteins - used
 PT partic. with toxin moieties for the control of insect pests, partic.
 PT in plants
 XX

PS Claim 8; Page 50-51; 106pp; English.
 XX AAR90829-39 are monoclonal antibodies or a binding fragments produced by
 CC using insect guts, partic. insect brush border membranes (BBMs), esp.
 CC corn rootworm, as antigen; immunising a donor animal with the antigen;
 CC isolating immunocompetent B cells from the immunised animal; fusing B
 CC cells with a tumour cell line; isolating the fused cells, culturing them
 CC and cloning positive hybrid cells; and screening the hybrid cells for
 CC prodn. of the required MABs. The MABs bind to the gut of a target insect
 CC but do not bind to mammalian BBMs. The DNA sequence can be operably
 CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,
 CC Pseudomonas exotoxin and phytolectin, etc.. The Abs are useful for
 CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
 CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
 CC maize.

XX Sequence 119 AA;
 SQ Query Match 85.0%; Score 549; DB 17; Length 119;
 Best Local Similarity 86.3%; Pred. No. 1e-45;
 Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 2;
 QY 1 EYLVESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 DB 1 QYKLESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 QY 61 FYADSVKDRFTISRDDSQSMFLYQNNLKTEDTAMYVCVRGASGIDY-AMDYWGQGTSL 119
 DB 61 SYGDSVKDRFTISRDDSQSMFLYQNNLKTEDTAMYVCVR- - - - -VYVGAMDYWGQGTSL 115
 QY 120 TVSS 123
 DB 116 TVSS 119

RESULT 3
 AAR90837
 ID AAR90837 standard; Protein; 599 AA.
 XX AC AAR90837;
 XX DT 25-JUN-1996 (first entry)
 XX DE 3B1 single chain antibody from pCIB4631.
 XX KW delta endotoxin; Bacillus thuringiensis; western corn rootworm;
 KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
 KW antibody.
 XX OS Insecta sp.
 XX PN WO9600783-A1.
 XX PD 11-JAN-1996.
 XX PF 20-JUN-1995; 95WO-IB00497.
 XX PR 28-JUN-1994; 94US-0267641.
 XX PA (CIBA) CIBA GEIGY AG.
 XX PI Carozzi NB, Koziel MG;
 XX DR WPI; 1996-077494/08.
 XX DR N-PSDB; AAT15733.
 XX PT New monoclonal antibodies which bind insect gut proteins - used
 PT partic. with toxin moieties for the control of insect pests, partic.
 PT in plants
 PS Claim 8; Page 68-72; 106pp; English.
 XX AAR90829-39 are monoclonal antibodies or a binding fragments produced by
 CC

CC using insect guts, partic. insect brush border membranes (BBMs), esp.
CC corn rootworm, as antigen; immunising a donor animal with the antigen;
CC isolating immunocompetent B cells from the immunised animal; fusing B
CC cells with a tumour cell line; isolating the fused cells, culturing them
CC and cloning positive hybrid cells; and screening the hybrid cells for
CC prodn. of the required MABs. The MABs bind to the gut of a target insect
CC but do not bind to mammalian BBMs. The DNA sequence can be operably
CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,
CC Pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for
CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
CC maize.

XX SQ Sequence 599 AA;

Query Match 85.0%; Score 549; DB 17; Length 599;
Best Local Similarity 86.3%; Pred. No. 6.6e-45;
Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 2;

Qy 1 EYMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNVRQAPGKGLWVARIRKSNYYAT 60
Db 155 QVQLSEGGGLVQPKGSLKLSCAASGFTFNNFAMNVRQAPGKGLWVARIRKSNYYAT 214
Qy 61 FYADSVKDRFTISRDDSQSMLYLQMNLTEDTAMYYCVRGASGIDY-AMDYWGQGTSL 119
Db 215 SYGDSVKDRFTYSRDDSQSMFYLMNLTEDTAMYYCVR----VYTGADYWGQGTSV 269
Qy 120 TVSS 123
Db 270 TVSS 273

RESULT 4

AAW01587
ID AAW01587 standard; Protein: 333 AA.

XX AC AAW01587;
XX DT 05-JUN-2000 (first entry)
XX DE Anti-Her2neu single chain antibody.

XX Retroviral vector; cell specific gene transfer; Spleen Necrosis Virus;
KW SNV; antibody-envelope fusion protein; retroviral envelope protein;
KW gene therapy; antigen binding site; single chain antibody; human;
KW Her2neu cell surface marker.

XX OS Homo sapiens.
XX PN WO200009730-A2.
XX PD 24-FEB-2000.
XX PF 10-AUG-1999; 99WO-US18141.
XX PR 17-AUG-1998; 98US-0135121.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Dornburg RC;

XX WPI: 2000-224358/19.
XX DR N-PSDB; AAZ51115.

XX Cell specific gene transfer using retroviral vectors containing
PT antibody-envelope fusion proteins and wild type envelope proteins -
XX Example; Fig 8; 45pp; English.

XX The patent discloses a novel retroviral vector, particularly Spleen
CC Necrosis Virus (SNV) vector, having target cell specificity. The vector
CC has a targetting envelope which is a chimeric protein consisting of an
CC antigen binding site of an antibody (e.g. anti-DNP-scfv) or another

CC peptide that binds to a specific cell surface protein, fused to the
CC carboxy terminal part of the retroviral envelope protein. The presence
CC of the wild type envelope protein serves as a helper molecule to
CC improve or supplement a functional membrane fusion domain. The
CC antigen binding site replaces the natural viral receptor binding site.
CC The retroviral vector is used for cell specific gene transfer,
CC especially in gene therapy. The invention overcomes the restricted host
CC range limitation of retroviral vectors. The present sequence is an
CC anti-Her2neu single chain antibody (sca). The coding sequence of
CC this antibody was used in the construction of plasmid pAJ7 which
CC contains a targetting vector comprising the anti-Her2neu sca fused to the
CC SNV-Env(envelope)-TM(transmembrane) coding region.

XX SQ Sequence 333 AA;

Query Match 83.0%; Score 536; DB 21; Length 333;
Best Local Similarity 83.3%; Pred. No. 6.2e-44;
Matches 105; Conservative 4; Mismatches 11; Indels 6; Gaps 2;

Qy 1 EYMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNVRQAPGKGLWVARIRKSNYYAT 60
Db 144 EYMLVESGGGLVQPKGSLKLSCAASGFTFNTYAMNVRQAPGKGLWVARIRKSNYYAT 203
Qy 61 FYADSVKDRFTISRDDSQSMLYLQMNLTEDTAMYYCVRGASGIDY---AMDYWGQGT 117
Db 204 YIVDSVKDRFTISRDDSQSMLYLQMNLTEDTAMYYCV---TSYYDYDKVLFAWVGQGT 260
Qy 118 SLTVSS 123
Db 261 TVTVSS 266

RESULT 5

AAW01587
ID AAW01587 standard; Protein: 110 AA.

XX AC AAW01587;
XX DT 22-AUG-1997 (first entry)
XX DE Lead binding MAB 6F5 heavy chain variable region.

XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.

XX OS Mus musculus.
XX PN WO9639518-A1.
XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US09258.
XX PR 10-OCT-1995; 95US-0541373.
XX PR 05-JUN-1995; 95US-0462798.
XX PA (BION-) BIONEERASKA INC.

XX PI Lopez O, Murray PJ, Wylie DE;

XX WPI: 1997-043140/04.
XX DR N-PSDB; AAT58261.

XX DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as
PT lead cations

XX Claim 12; Page 77; 125pp; English.

XX The present sequence represents the heavy chain variable region for
CC monoclonal antibody (MAB) 6F5, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.

CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the
CC heavy metals in biological and inanimate systems. It can be used in
CC e.g. aqueous liquid systems, in biological or environmental systems or
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC care products, skin treatment products, pesticides, herbicides,
CC solvents used in the production of semi-conductor and integrated
CC circuit components and production materials for electronic components.
CC The products can provide for applications involving minute amounts of
CC specific heavy metals.

XX SQ Sequence 110 AA;
Query Match 82.4%; Score 532; DB 18; Length 110;
Best Local Similarity 87.3%; Pred. No. 4.2e-44;
Matches 103; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
QY 6 ESGGGLVQPKGSLKLSCAASGFTFNAYAMNVRQAPGKLEWVARIRKSNNTATFYADS 65
DB 1 ESGGGLVQPKGSLKLSCAASGFTFNAYAMNVRQAPGKLEWVARIRKSNNTATFYADS 60
QY 66 VKDRFTISRDDSQSMYLMQNNLKTEDTAMYYCVRGASGIDYAMDYWGOGTSLTVSS 123
DB 61 VKDRFTISRDDSQSMYLMQNNLKTEDTAMYYCVRGASGIDYAMDYWGOGTSLTVSSA 110

RESULT 6
AAU09919
ID AAU09919 standard; Protein: 117 AA.

XX AC AAU09919;
XX AC
XX DT 18-JUN-2002 (first entry)
XX DE Murine mAb 1D9 heavy chain variable region protein sequence.

XX KW Mouse; mAb 1D9 heavy chain variable region; vasotropic;
KW antiinflammatory; collagen disease; immunosuppressive;
KW antiasthmatic; insulin-dependent diabetes mellitus;
KW inflammatory bowel disease; ulcerative colitis;
KW graft rejection; allergic disease; antipsoriatic;
KW antiarthritic; nephrotropic; antithyroid; restenosis;
KW dermatological; anaphylaxis; cell adhesion inhibitor;
KW vascular injury; autoimmune disease; immunoglobulin;
KW complementarity determining region; CDR; CD18; CCR2;
KW atherosclerosis.

XX OS Mus sp.

XX FH Key Location/Qualifiers
XX FT Region 27..30
XX FT /note= "Part of H1 structure loop"
XX FT Region 31..35
XX FT /note= "Complementarity determining region 1 (CDR1)"
XX FT Region 50..68
XX FT /note= "Complementarity determining region 2 (CDR2)"
XX FT Region 101..106
XX FT /note= "Complementarity determining region 3 (CDR3)"

XX PN WO200170266-A2.

XX XX 27-SEP-2001.

XX XX 15-MAR-2001; 2001WO-US08266.

XX XX 17-MAR-2000; 2000US-0528267.

XX XX (MILL-) MILLENNIUM PHARM INC.

XX PI Horvath CJ, Rao PE;

XX DR WPI; 2001-607511/69.

XX

PT Inhibiting stenosis or restenosis of a blood vessel following vascular
PT injury or angioplasty in a subject by administering agent which
PT inhibits recruitment or adhesion of neutrophils, mononuclear cells to
PT injury site

XX PS Claim 30; Fig 16; 108pp; English.

XX CC The present invention relates to a new method of inhibiting stenosis or
CC restenosis of a blood vessel following vascular injury in a subject. The
CC new method comprises administering to the subject agents which inhibit
CC the adhesion and/or recruitment of neutrophils and mononuclear cells to
CC a site of vascular injury by binding CD18 or CCR2. The method of the
CC invention inhibits stenosis or restenosis of a blood vessel following
CC vascular injury arising from a vascular intervention procedure such as
CC vascular by-pass or transplantation surgery. The method is also useful
CC for treating a subject having an inflammatory disease or condition
CC mediated by neutrophil and mononuclear cell activity e.g. asthma and
CC graft versus host disease. Chronic inflammatory diseases of the lung,
CC collagen diseases, and insulin-dependent diabetes mellitus can also be
CC treated. The method is further useful for treating inflammatory bowel
CC diseases, such as ulcerative colitis. Additional diseases or conditions
CC include inflammatory or allergic diseases and conditions, including
CC systemic anaphylaxis of hypersensitivity responses, drug allergies,
CC psoriasis and inflammatory dermatoses, autoimmune diseases such as
CC arthritis, graft rejection and other diseases including atherosclerosis.
CC The present sequence represents the protein sequence of the mouse mAb
CC 1D9 heavy chain variable region. This sequence contains three CDR's
CC that can be used to inhibit stenosis or restenosis.

XX SQ Sequence 117 AA;

Query Match 80.3%; Score 519; DB 22; Length 117;
Best Local Similarity 80.5%; Pred. No. 8.2e-43;
Matches 99; Conservative 11; Mismatches 7; Indels 6; Gaps 1;

QY 1 EVMVLESGGLVQPKGSLKLSCAASGFTFNAYAMNVRQAPGKLEWVARIRKSNNTAT 60
DB 1 EVQLVESGGGLVQPKGSLKLSCAASGFTFNAYAMNVRQAPGKLEWVARIRKSNNTAT 60
QY 61 FYADSVKDRFTISRDDSQSMYLMQNNLKTEDTAMYYCVRGASGIDYAMDYWGOGTSLT 120
DB 61 FYADSVKDRFTISRDDSQSMYLMQNNLKTEDTAMYYCVRGASGIDYAMDYWGOGTSLT 114

QY 121 VSS 123

DB 115 VSS 117

RESULT 7
AAE06947
ID AAE06947 standard; Protein: 117 AA.

XX AC AAE06947;

XX DT 16-OCT-2001 (first entry)

XX DE Murine 1D9 antibody heavy chain variable (VH) region.

XX KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioptasty; acquired immune deficiency syndrome;
KW AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
KW neointimal hyperplasia; VH; heavy chain variable region.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Region 31..35

XX FT /label= Complementarity_determining_region

```

FT Region 50..68
FT /label= Complementarity_determining_region
FT Region 101..106
FT /label= Complementarity_determining_region
XX
XX WO200157226-A1.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03537.
XX
XX 03-FEB-2000; 2000US-0497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor
XX 2-mediated disorder in a patient, comprises a binding specificity for
XX CCR2, and a non-human antigen binding region and human immunoglobulin
XX
XX Claim 8; Fig 8; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR-2 mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angioplasty and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is the heavy chain variable (VH) region of
XX murine 1D9 antibody.
XX
XX Sequence 117 AA:
XX
XX Query Match 80.3%; Score 519; DB 22; Length 117;
XX Best Local Similarity 80.5%; Pred. No. 8.2e-43;
XX Matches 99; Conservative 11; Mismatches 7; Indels 6; Gaps 1;
XX
XX QY 1 EYVLVSGGGLVQPGSLKLSAASGFTNNYAMWVROAPGKGLWARIKSNVAT 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 1 EYVLVSGGGLVQPGSLKLSAASGFTNNYAMWVROAPGKGLWARIKSNVAT 60
XX
XX QY 61 FYADSVKDRFTISRDDSQSMYLONNLTKETDAMYCYVRRGASGIDYAMDYWGQTSLT 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 61 FYADSVKDRFTISRDDSQSMYLONNLTKETDAMYCYVRRGASGIDYAMDYWGQTSLT 114
XX
XX QY 121 VSS 123
XX |||
XX Db 115 VSS 117
XX
XX RESULT 8
XX AAE07033
XX ID AAE07033 standard; Protein; 148 AA.
XX

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AC AAE07033;
XX
XX 16-OCT-2001 (first entry)
XX
XX Murine antibody 1D9 heavy chain variable region.
XX
XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
XX neuroprotective; immunosuppressive; human immunodeficiency virus;
XX HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
XX multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
XX anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
XX fibrotic disease; angioplasty; acquired immune deficiency syndrome;
XX AIDS; inflammatory glomerulopathy; vascular intervention;
XX neointimal hyperplasia; antibody 1D9 heavy chain variable region.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= Signal_peptide
XX /note= "Murine mature antibody 1D9 kappa
XX light chain variable region"
XX
XX Region 20..137
XX
XX /label= Variable_region
XX Region 138..148
XX /label= constant_region
XX Misc-difference 148
XX /note= "Encoded by Gt"
XX
XX WO200157226-A1.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03537.
XX
XX 03-FEB-2000; 2000US-0497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
XX N-PSDB; AAD13178.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor
XX 2-mediated disorder in a patient, comprises a binding specificity for
XX CCR2, and a non-human antigen binding region and human immunoglobulin
XX
XX Disclosure; Fig 21; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR-2 mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angioplasty and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is the heavy chain variable (VH) region of
XX murine 1D9 antibody.
XX
XX Sequence 117 AA:
XX
XX Query Match 80.3%; Score 519; DB 22; Length 117;
XX Best Local Similarity 80.5%; Pred. No. 8.2e-43;
XX Matches 99; Conservative 11; Mismatches 7; Indels 6; Gaps 1;
XX
XX QY 1 EYVLVSGGGLVQPGSLKLSAASGFTNNYAMWVROAPGKGLWARIKSNVAT 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 1 EYVLVSGGGLVQPGSLKLSAASGFTNNYAMWVROAPGKGLWARIKSNVAT 60
XX
XX QY 61 FYADSVKDRFTISRDDSQSMYLONNLTKETDAMYCYVRRGASGIDYAMDYWGQTSLT 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 61 FYADSVKDRFTISRDDSQSMYLONNLTKETDAMYCYVRRGASGIDYAMDYWGQTSLT 114
XX
XX QY 121 VSS 123
XX |||
XX Db 115 VSS 117
XX
XX RESULT 8
XX AAE07033
XX ID AAE07033 standard; Protein; 148 AA.
XX

```


CC method of the invention is useful for inhibiting graft rejection -
 CC particularly allografts such as kidney, liver, lung, heart-lung,
 CC pancreas, bowel and heart. The method of the invention is also useful for
 CC inhibiting graft versus host disease and for inhibiting chronic rejection
 CC of a transplanted graft. The present amino acid sequence represents a
 CC mouse antibody heavy chain variable region (mAb 1D9).
 XX

SQ Sequence 117 AA;

Query Match 78.9%; Score 510; DB 23; Length 117;

Best Local Similarity 79.7%; Pred. No. 6.1e-42;

Matches 98; Conservative 11; Mismatches 8; Indels 6; Gaps 1;

QY 1 EYMLVSGGLVQPKSLKSCAASGFTFNNAVMMNRQAPGKGLWVARIRKSNYYAT 60

DB 1 EYMLVSGGLVQPKSLKSCAASGFTFNNAVMMNRQAPGKGLWVARIRKSNYYAT 60

QY 61 FYADSVKDRFTISRDDSQSMYLMNNLKTEDTAMYYCVRGASGIDYAMDYWGQTSLT 120

DB 61 FYADSVKDRFTISRDDSQSMYLMNNLKTEDTAMYYCVRGASGIDYAMDYWGQTSLT 114

QY 121 VSS 123

DB 115 VSS 117

RESULT 11

AAU09930

ID AAU09930 standard; Protein; 117 AA.

XX

AC AAU09930;

XX

DT 18-JUN-2002 (first entry)

XX

DE Humanised 1D9 heavy chain variable region, 1D9RH protein sequence.

XX

KW Human; mouse; 4B4'CL heavy chain variable region; vasotropic;

KW antiinflammatory; collagen disease; immunosuppressive;

KW antiasthmatic; insulin-dependent diabetes mellitus;

KW inflammatory bowel disease; ulcerative colitis; 1D9RH;

KW graft rejection; allergic disease; antipsoriatic;

KW antiarthritic; nephrotropic; antithyroid; restenosis;

KW dermatological; anaphylaxis; cell adhesion inhibitor;

KW vascular injury; autoimmune disease; immunoglobulin;

KW complementarity determining region; CDR; CD18; CCR2;

KW atherosclerosis; mutant; mutein.

XX

OS Chimeric - Homo sapiens.

OS Chimeric - Mus sp.

OS Chimeric - Synthetic.

XX

FH Key Location/Qualifiers

FT Region 27..30

FT

FT Misc-difference 28

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT residue normally present in mouse mAb 1D9 heavy
 FT chain sequence (AAU09919)."
 FT
 FT Region 50..68
 FT /note- "Complementarity determining region 2 (CDR2),
 FT grafted from mouse mAb 1D9 heavy chain
 FT sequence (AAU09919)."
 FT
 FT Misc-difference 70
 FT /note- "Substitution of Phe residue normally present
 FT in human 4B4'CL sequence (AAU09926) by Tyr
 FT residue normally present in mouse mAb 1D9 heavy
 FT chain sequence (AAU09919)."
 FT
 FT Misc-difference 99
 FT /note- "Substitution of Thr residue normally present
 FT in human 4B4'CL sequence (AAU09926) by Val
 FT residue normally present in mouse mAb 1D9 heavy
 FT chain sequence (AAU09919)."
 FT
 FT Region 101..108
 FT /note- "Complementarity determining region 3 (CDR3),
 FT grafted from mouse mAb 1D9 heavy chain
 FT sequence (AAU09919)."
 FT
 XX

PN WO200170266-A2.

XX

XX 27-SEP-2001.

XX

XX 15-MAR-2001; 2001WO-US08266.

XX

XX 17-MAR-2000; 2000US-0528267.

PR

XX (MILL-) MILLENNIUM PHARM INC.

PA

XX Horvath CJ, Rao PE;

XX

XX WPI; 2001-607511/69.

DR

XX

PT Inhibiting stenosis or restenosis of a blood vessel following vascular

PT injury or angioplasty in a subject by administering agent which

PT inhibits recruitment or adhesion of neutrophils, mononuclear cells to

PT injury site

XX

PS Claim 32; Fig 18; 108pp; English.

XX

CC The present invention relates to a new method of inhibiting stenosis or

CC restenosis of a blood vessel following vascular injury in a subject. The

CC new method comprises administering to the subject agents which inhibit

CC the adhesion and/or recruitment of neutrophils and mononuclear cells to

CC a site of vascular injury by binding CD18 or CCR2. The method of the

CC invention inhibits stenosis or restenosis of a blood vessel following

CC vascular injury arising from a vascular intervention procedure such as

CC vascular by-pass or transplantation surgery. The method is also useful

CC for treating a subject having an inflammatory disease or condition

CC mediated by neutrophil and mononuclear cell activity e.g. asthma and

CC graft versus host disease. Chronic inflammatory diseases of the lung,

CC collagen diseases, and insulin-dependent diabetes mellitus can also be

CC treated. The method is further useful for treating inflammatory bowel

CC diseases, such as ulcerative colitis. Additional diseases or conditions

CC include inflammatory or allergic diseases and conditions, including

CC systemic anaphylaxis of hypersensitivity responses, drug allergies,

CC psoriasis and inflammatory dermatoses, autoimmune diseases such as

CC arthritis, graft rejection and other diseases including atherosclerosis.

CC This sequence represents the variable region of one of several humanised

CC 1D9 heavy chains (AAU09927-AAU09930). These heavy chains were used in

CC the invention for the production of anti-CCR2 antibody or antigen-binding

CC fragment.

XX

SQ Sequence 117 AA;

Query Match 76.3%; Score 493; DB 22; Length 117;

Best Local Similarity 76.4%; Pred. No. 2.7e-40;

Matches 94; Conservative 14; Mismatches 9; Indels 6; Gaps 1;

QY 1 EYMLVSGGLVQPKSLKSCAASGFTFNNAVMMNRQAPGKGLWVARIRKSNYYAT 60

DB 1 EYMLVSGGLVQPKSLKSCAASGFTFNNAVMMNRQAPGKGLWVARIRKSNYYAT 60

XX


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Db      1  EVLVESGGGLVPGGSLRLSCAASGFSFNAYAMNVRQAPGKGLIEWARIETKNNYAT 60
Qy      61  FYADSVKDRFTISRDDSSQSMLYLQMNKLKTDETAMTYCYCVRGASGIDYAMDYWGQGTSLT 120
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  YYADSVKDRYTIISRDDSKNTLYLQMNLSLKTDETFAYTYCTTFYGVNGV-----WGQGTLLVT 114
Qy      121 VSS 123
       |||
Db      115 VSS 117

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Job time : 70.9112 secs

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OW protein - protein search, using sw model

Run on: November 27, 2002, 07:15:05 ; Search time 33.7181 Seconds
(without alignments)
350.688 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 646

Sequence: 1 EVMLVSGGGLVQPKGSLK.....SGIDYAMDYWGQGTSLTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528.5	81.8	141	2 I32513	Ig heavy chain pre
2	526.5	81.5	137	2 S42467	Ig heavy chain V r
3	522	80.8	121	2 A41940	Ig heavy chain V r
4	494.5	76.5	110	2 PH1091	Ig heavy chain V r
5	489	75.7	119	2 A27630	Ig heavy chain pre
6	480.5	74.4	110	2 PH1092	Ig heavy chain V r
7	477	73.8	110	2 PH1093	Ig heavy chain V r
8	467.5	72.4	101	2 B42575	Ig heavy chain V r
9	463	71.7	127	2 S58213	Ig heavy chain V r
10	456	70.5	100	2 S26452	Ig heavy chain V r
11	450	69.7	123	2 S32186	Ig heavy chain V r
12	449.5	69.6	124	2 S20775	Ig heavy chain V r
13	446	69.0	115	1 AVMS06	Ig heavy chain V-I
14	444	68.7	143	2 S23624	Ig heavy chain V r
15	443.5	68.7	115	2 S38714	Ig heavy chain V r
16	442.5	68.5	122	2 S20642	Ig heavy chain V r
17	441.5	68.3	118	2 A31485	Ig heavy chain V r
18	441	68.0	119	2 D30540	Ig heavy chain V r
19	439.5	68.0	111	1 MHMS76	Ig heavy chain V-I
20	439	68.0	119	2 S31107	Ig heavy chain V-I
21	439	68.0	121	2 H36005	Ig heavy chain - h
22	439	68.0	139	2 S31678	Ig heavy chain V r
23	438.5	67.9	126	2 S44107	Ig heavy chain V r
24	438.5	67.9	140	2 S70442	Ig heavy chain V-D
25	438	67.8	113	1 AVMSB7	Ig heavy chain pre
26	438	67.8	121	2 S31106	Ig heavy chain V-I
27	438	67.8	124	2 PT0388	Ig heavy chain V r
28	437	67.6	115	2 A25803	Ig heavy chain V r
29	436	67.5	113	1 AVMSAB	Ig heavy chain V-I

ALIGNMENTS

RESULT 1

I32513

Ig heavy chain precursor V region (MRL4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999

C:Accession: I32513

R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization a

A:Reference number: A94689; MUID:88331394; PMID:3138286

A:Accession: I32513

A:Molecule type: DNA

A:Residues: 1-141 <KOF>

A:Cross-references: GB:M20829; NID:g196951; PIDN:AAA38849.1; PID:g196952

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 528.5; DB 2; Length 141;

Best Local Similarity 83.7%; Pred. No. 9.5e-42;

Matches 103; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EVMLVSGGGLVQPKGSLKSCAAGFTFNYYAMNWRQAPKGLEWVARISKSNYYAT 60

Db 20 EVQLVETGGGLVQPKGSLKSCPASGFSFNTNMMWRQAPKGLEWVARISKSNYYAT 79

Qy 61 FYADSVKDRFTISRDDSSMLYLQNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120

Db 80 YYADSVKDRFTISRDDSSMLYLQNNLKTEDTAMYYCVRDAANWSAN-FAYWGQGTSLT 138

Qy 121 VSS 123

Db 139 VSA 141

RESULT 2

S42467

Ig heavy chain V region precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S42467

R:Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.

submitted to the EMBL Data Library, March 1994

A:Reference number: S42466

A:Accession: S42467

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137 <SHI>

A:Cross-references: EMBL:X78107; NID:g460798; PIDN:CAA54997.1; PID:g460799

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 526.5; DB 2; Length 137;
Best Local Similarity 82.9%; Pred. No. 1.4e-41;
Matches 102; Conservative 6; Mismatches 10; Indels 5; Gaps 1;

QY 1 EYVLVSGGGLVQPKGSLKLSAASGFTNNYAMNVVRQAPGKLEWVARIRSKSNYYAT 60
DB 20 EVQLVETGGGLVQPKGSLKLSAASGFTNTYAMNVVRQAPGKLEWVARIRSKSNYYAT 79
QY 61 FYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
DB 80 YFGNSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVYG-----NFGFYWGQGTSLT 134
QY 121 VSS 123
DB 135 VSA 137

RESULT 3
A:1940
Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)
N:Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C:Accession: A41940; PLO201
R:Herron, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss J
Proteins 11, 159-175, 1991
A:Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional str
A:Reference number: A41940; MUID:92086633; PMID:1749770
A:Accession: A41940
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-121 <HER>
A:Note: sequence extracted from NCBI backbone (NCBIP:70715)
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A:Reference number: PLO198; MUID:90309768; PMID:2114528
A:Accession: PLO201
A:Molecule type: mRNA
A:Residues: 1-118 <SMI>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-68/Region: complementarity-determining 2
F:101-110/Region: complementarity-determining 3
F:101-106/Region: D region
F:107-115/Region: JH region

Query Match 80.8%; Score 522; DB 2; Length 121;
Best Local Similarity 82.9%; Pred. No. 3.2e-41;
Matches 102; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 EYVLVSGGGLVQPKGSLKLSAASGFTNNYAMNVVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EVQPVETGGGLVQPKGSLKLSAASGFTNTYAMNVVRQAPGKLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
DB 61 FYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVRRDGTGTAWFA--YWGQGTSLT 118
QY 121 VSS 123
DB 119 VSA 121

RESULT 4
PH1091
Ig heavy chain V region (clone P17.79) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1091

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1091
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-110 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 494.5; DB 2; Length 110;
Best Local Similarity 84.3%; Pred. No. 1e-38;
Matches 97; Conservative 4; Mismatches 7; Indels 7; Gaps 2;

QY 1 EYVLVSGGGLVQPKGSLKLSAASGFTNNYAMNVVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EVQLVETGGGLVQPKGSLKLSAASGFTNTYAMNVVRQAPGKLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVRRGASGIDYA--MDYW 113
DB 61 YYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYCHRD-----DYVAVFAYW 110

RESULT 5
A27630
Ig heavy chain precursor V-10 region (MRL-DNA4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 23-Jul-1999
C:Accession: A27630
R:Kofler, R.
J. Immunol. 140, 4031-4034, 1988
A:Title: A new murine Ig V-H gene family.
A:Reference number: A27630; MUID:88229103; PMID:3131427
A:Accession: A27630
A:Molecule type: DNA
A:Residues: 1-119 <KOF>
A:Cross-references: GB:M21470; NID:g196220; PIDN:AAA38634.1; PID:g196221; GB:M20825
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 489; DB 2; Length 119;
Best Local Similarity 93.0%; Pred. No. 3.5e-38;
Matches 93; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EYVLVSGGGLVQPKGSLKLSAASGFTNNYAMNVVRQAPGKLEWVARIRSKSNYYAT 60
DB 20 EVQLVETGGGLVQPKGSLKLSAASGFTNTYAMNVVRQAPGKLEWVARIRSKSNYYAT 79
QY 61 FYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVR 100
DB 80 YYADSVKDRFTISRDDSQSMVLYLQNNLTKTDTAMYCYVR 119

RESULT 6
PH1092
Ig heavy chain V region (clone P17.80) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1092
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1092
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-110 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 480.5; DB 2; Length 110;
Best Local Similarity 82.6%; Pred. No. 1.9e-37;
Matches 95; Conservative 3; Mismatches 10; Indels 7; Gaps 2;

Qy 1 EVMLVESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKSNYYAT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVETGGGLVQPKGSLKLSAASGTSFTNMYAMNVRQAPKGLWVARIRSKSNYYAT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 FYADSVKDRFTISRDDSOSMLYLQNNLKTEDTAMYYCVRRGASGIDYA--MDYW 113
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YYADSVKDRFTISRDDSOSMLYLQNNLKIEDTAMYYCVRD-----DYVAFAYW 110
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7

PH1093

Ig heavy chain V region (clone S17.161) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1093

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1093

A;Status: nucleic acid sequence not shown.

A:Molecule type: mRNA

A:Residues: 1-110 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 477; DB 2; Length 110;
Best Local Similarity 90.0%; Pred. No. 4.1e-37;
Matches 90; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EVMLVESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKSNYYAT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVETGGGLVQPKGSLKLSAASGTSFTNMYAMNVRQAPKGLWVARIRSKTNYYAT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 FYADSVKDRFTISRDDSOSMLYLQNNLKTEDTAMYYCVR 100

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 YYADSVKDRFTISRDDSOSMLYLQNNLKTDTDAMYYCVR 100

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8

B42575

Ig heavy chain V region (anti-angiotensin II) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C;Accession: B42575

R;Garcta, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.

Science 257, 528-531, 1992

A;Title: Recognition of angiotensin II: antibodies at different levels of an idiotypic r

A;Reference number: A42575; MUID:92342952; PMID:1636087

A;Accession: B42575

A:Molecule type: mRNA

A:Residues: 1-101 <GAR>

A;Cross-references: GB:540679; NID:9252098; PIDN:AAB22669.1; PID:g252099

A:Experimental source: BALB/c mice, myeloma cell line NS-1

A;Note: sequence extracted from NCBI backbone (NCBIN:109337, NCBIIP:109338)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;7-92/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 467.5; DB 2; Length 101;
Best Local Similarity 87.6%; Pred. No. 2.8e-36;
Matches 92; Conservative 2; Mismatches 6; Indels 5; Gaps 2;

Qy 9 GGLVQPKGSLKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKSNYYATFYADSVKD 68

Db 1 GGLVQPKGSLKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKGYTYTYVADSVKD 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 69 RFTISRDDSOSMLYLQNNLKTEDTAMYYCVRRGASGID-YAMDY 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFTISRDDSOSMLYLQNNLKTEDTAMYYCVR---GYDGYAMDY 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9

S58213

Ig heavy chain V region (anti-F(ab')2) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999

C;Accession: S58213; S58212

R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitlin

submitted to the EMBL Data Library, July 1995

A;Description: Characterization of heavy and light chain immunoglobulin variable regi

A;Reference number: S58206

A;Accession: S58213

A:Molecule type: mRNA

A:Residues: 1-127 <WEL>

A;Cross-references: EMBL:X89055; NID:g929638; PIDN:CAA61442.1; PID:g929639; EMBL:X890

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 463; DB 2; Length 127;
Best Local Similarity 71.9%; Pred. No. 9.2e-36;
Matches 92; Conservative 11; Mismatches 19; Indels 6; Gaps 2;

Qy 1 EVMLVESGGGLVQPKGSLKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKSNYYAT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPKGSLKLSAASGFTFSGTHHWVRQASGKGLWVGRIKRNDSYAT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 FYADSVKDRFTISRDDSOSMLYLQNNLKTEDTAMYYCVR-----RGASGIDYAMDYWGQ 115
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AYAASVKGRTISRDDSSENTAYLQNNLSLKIEDTAVYYCTRGSSMVRGVNGY-YGMDVWGQ 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 116 GTSLTVSS 123

Db 120 GTTVTVSS 127

|||:|||||

RESULT 10

S26462

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

C;Accession: S26462

R;Kavaler, J.

submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S26462

A;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-100 <KAV>

A;Cross-references: EMBL:X59104; NID:g51920; PID:g51921

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-92/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 456; DB 2; Length 100;
Best Local Similarity 84.3%; Pred. No. 3.2e-35;
Matches 91; Conservative 4; Mismatches 3; Indels 10; Gaps 3;

Qy 11 LVQPKGS--LKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKSNYYATFYADSVKD 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LVQPKGSLLKLSAASGFTFNMYAMNVRQAPKGLWVARIRSKSNYYATFYADSVKD 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 69 RFTISRDDSOSMLYLQNNLKTEDTAMYYCVRRGASGIDYAMDYWGQ 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFTISRDDSOSMLYLQNNLKTEDTAMYYCVS-----DFG--HWGOG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11

S32186
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C:Accession: S32186
R:Zul, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32186
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <I2>
A:Cross-references: EMBL:X70093; NID:g288249; PIDN:CAA49698.1; PID:g288250
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 450; DB 2; Length 123;
Best Local Similarity 69.9%; Pred. No. 1.4e-34;
Matches 86; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 EYLVESGGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EVKLVEGGGLVQPGGSLKSCATSGFTFTDYMSWVRQPPGKALEWLGFIIRKANGYTT 60
QY 61 FYADSVKDRFTISRDDSQSMVLYQMNNLKTEDTAMYYCVRRGASGIDYANDYWGQGTSLT 120
DB 61 EYASVKGKFTISRDNQSILYQMNNLRAEDSATYICARSYYGSSRYANDYWGQGTSVT 120
QY 121 VSS 123
DB 121 VSS 123

RESULT 12

S20775
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20775
R:Morcarl, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A:Reference number: S20764
A:Accession: S20775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <MOR>
A:Cross-references: EMBL:Z11950; NID:g33882; PIDN:CAA78007.1; PID:g33883
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 449.5; DB 2; Length 124;
Best Local Similarity 71.0%; Pred. No. 1.6e-34;
Matches 88; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

QY 1 EYLVESGGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EYLVESGGGLVQPGGSLKSCAASGFTFSDYMDVMVRQAPAKGLEWLAIRNKANSYTT 60
QY 61 FYADSVKDRFTISRDDSQSMVLYQMNNLKTEDTAMYYCVRRGASGID-YANDYWGQGTSL 119
DB 61 EYASVKGKFTISRDNQSMVLYQMNNLKTEDTAIYYCVTRCHGMDVWGQGTTV 120
QY 120 TVSS 123
DB 121 TVSS 124

RESULT 13

AVMS06

Ig heavy chain V-III region (J606) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C92811; A02072
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding pro
A:Reference number: A92811; MUID:82099361; PMID:6798111
A:Accession: C92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 69.0%; Score 446; DB 1; Length 115;
Best Local Similarity 70.7%; Pred. No. 3.1e-34;
Matches 87; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

QY 1 EYLVESGGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EVKLVEGGGLVQPGGSLKSCVSGFTFSNYYMMNVRQSPKLEWVAEIRLKSNNYAT 60
QY 61 FYADSVKDRFTISRDDSQSMVLYQMNNLKTEDTAMYYCVRRGASGIDYANDYWGQGTSLT 120
DB 61 HTAESVKGKFTISRDDSSVLYQMNNLRAEDTGIIYCTGTGFA-----YWGQGTSLT 112
QY 121 VSS 123
DB 113 VSA 115

RESULT 14

S23624
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23624
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deflos, M.; Kozin, F.; Carson, D.A.
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <OLE>
A:Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 444; DB 2; Length 143;
Best Local Similarity 70.7%; Pred. No. 5.9e-34;
Matches 87; Conservative 14; Mismatches 16; Indels 6; Gaps 2;

QY 1 EYLVESGGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EYLVESGGGLVQPGGSLKSCAASGFTFSNYSMMNVRQAPGKLEWVSTISSSS--TI 58
QY 61 FYADSVKDRFTISRDDSQSMVLYQMNNLKTEDTAMYYCVRRGASGIDYANDYWGQGTSLT 120
DB 59 YYADSVKGRFTISRDNKNSLYQMNNLRAEDTAVYYCARSYRG----GDYWGQGTSLT 114
QY 121 VSS 123
DB 115 VSS 117

RESULT 15

S38714

Search completed: November 27, 2002, 07:24:15
Job time : 35.7181 secs

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DE Ig heavy chain V-III region HPC76 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81013937; PubMed=6251474;
 RA Bernard O., Gough N.M.;
 RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
 between translocated VH and mu constant regions genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
 REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
 CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
 DR PIR: A02074; MMS76.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv; 1.
 DR Immunoglobulin V region.
 FT NON_TER 1 111
 FT SEQUENCE 111 111
 SQ SEQUENCE 111 AA; 12304 MW; 0BDE98EC7348056A CRC64;
 Query Match 68.0%; Score 439.5; DB 1; Length 111;
 Best Local Similarity 72.9%; Pred. No. 3.1e-40;
 Matches 86; Conservative 9; Mismatches 16; Indels 7; Gaps 2;
 Qy 6 EGGGLVQPKGSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 65
 Db 1 EGGGLVQPGGSMKLSVASGFTFSNYMNMVVRQSPKGLWVAEIRLKS-GYATHYAES 59
 Qy 66 VKDFTISRDDQSOMLYLQMNLLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLTVSS 123
 Db 60 VKGRTISRDDSKSVYLQMNLLRAEDTGIIYCTTGPV-----DYWGQGTSLTVSS 111
 RESULT 3
 HV30_MOUSE
 ID HV30_MOUSE STANDARD; PRT; 113 AA.
 AC P01799;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region ABE-47N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77134726; PubMed=402936;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
 protein.";
 RL Biochemistry 16:1170-1175(1977).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS INULIN.
 DR PIR: A90400; AVMSB7.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv; 1.
 DR Immunoglobulin V region.
 FT DISULFID 22 98
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;
 Query Match 67.8%; Score 438; DB 1; Length 113;
 Best Local Similarity 70.2%; Pred. No. 4.5e-40;
 Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;
 Qy 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 Db 1 EVKLEESGGGLVQPGGSMKLSVASGFTFSNYMNMVVRQSPKGLWVAEIRLKSNNYAT 60
 Qy 61 FYADSVKDRFTISRDDQSOMLYLQMNLLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
 Db 61 HYAESVKGRTISRDDSKSVYLQMNLLRAEDTGIIYCTTGFA-----YWGQGTSLT 112
 Qy 121 V 121
 Db 113 V 113
 RESULT 5
 HV33_MOUSE
 ID HV33_MOUSE STANDARD; PRT; 115 AA.
 AC P01802;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region W3082.
 OS Mus musculus (Mouse).
 Query Match 67.8%; Score 438; DB 1; Length 113;
 Best Local Similarity 70.2%; Pred. No. 4.5e-40;
 Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;
 Qy 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 Db 1 EVKLEESGGGLVQPGGSMKLSVASGFTFSNYMNMVVRQSPKGLWVAEIRLKSNNYAT 60
 Qy 61 FYADSVKDRFTISRDDQSOMLYLQMNLLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
 Db 61 HYAESVKGRTISRDDSKSVYLQMNLLRAEDTGIIYCTTGFA-----YWGQGTSLT 112
 Qy 121 V 121
 Db 113 V 113
 RESULT 4
 HV27_MOUSE
 ID HV27_MOUSE STANDARD; PRT; 113 AA.
 AC P01796;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region A4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78158406; PubMed=417344;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Sequence variation among heavy chains from inulin-binding myeloma
 proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS INULIN.
 DR PIR: A93818; AVMSAB.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv; 1.
 DR Immunoglobulin V region.
 FT DISULFID 22 98
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;
 Query Match 67.5%; Score 436; DB 1; Length 113;
 Best Local Similarity 70.2%; Pred. No. 7.4e-40;
 Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;
 Qy 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRSKSNYYAT 60
 Db 1 EVKLEESGGGLVQPGGSMKLSVASGFTFSNYMNMVVRQSPKGLWVAEIRLKSNNYAT 60
 Qy 61 FYADSVKDRFTISRDDQSOMLYLQMNLLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
 Db 61 HYAESVKGRTISRDDSKSVYLQMNLLRAEDTGIIYCTTGFA-----YWGQGTSLT 112
 Qy 121 V 121
 Db 113 V 113
 RESULT 5
 HV33_MOUSE
 ID HV33_MOUSE STANDARD; PRT; 115 AA.
 AC P01802;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region W3082.
 OS Mus musculus (Mouse).
 Query Match 67.5%; Score 436; DB 1; Length 113;
 Best Local Similarity 70.2%; Pred. No. 7.4e-40;
 Matches 85; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR: D92811; AVMS82.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;
SQ
Query Match 67.5%; Score 436; DB 1; Length 115;
Best Local Similarity 69.1%; Pred. No. 7.6e-40;
Matches 85; Conservative 12; Mismatches 18; Indels 8; Gaps 1;

Oy 1 EVMLVESGGGLVQPKGSLKSCAASGFTFNMYAMNWRQAPGKGLWVAIRTSKNVAT 60
Db 1 EVKLEESGGGLVQPGSMKLSVAGSFTFSYWMNWRQSPKGLWVAIRLKSNNAT 60

Oy 61 FYADSVKDRFTISRDDSSMLYLQNNLKTEDTAMNYCVRRGASGIDYAMDYWGOGTSLT 120
Db 61 HYAESVKGKRTISRDDSSKSVYLQNNLRPDTGIYCTTGA-----YWGOGTLVT 112

Oy 121 VSS 123
Db 113 VSA 115

RESULT 6
HV28_MOUSE
ID HV28_MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR: B93818; AVMS61.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;
SQ
Query Match 66.6%; Score 430; DB 1; Length 113;

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Best Local Similarity 69.4%; Pred. No. 3.3e-39;
Matches 84; Conservative 10; Mismatches 19; Indels 8; Gaps 1;

Oy 1 EVMLVESGGGLVQPKGSLKSCAASGFTFNMYAMNWRQAPGKGLWVAIRTSKNVAT 60
Db 1 EVKLEESGGGLVQPGSMKLSVAGSFTFSYWMNWRQSPKGLWVAIRLKSNNAT 60

Oy 61 FYADSVKDRFTISRDDSSMLYLQNNLKTEDTAMNYCVRRGASGIDYAMDYWGOGTSLT 120
Db 61 HYAESVKGKRTISRDDSSKSVYLQNNLRPDTGIYCTTGA-----YWGOGTLVP 112

Oy 121 V 121
Db 113 V 113

RESULT 7
HV01_RAT
ID HV01_RAT STANDARD; PRT; 142 AA.
AC P01805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region IR2 precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Petterson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
RT E."
RL Nucleic Acids Res. 10:6041-6049(1982).
CC -1- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
CC IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
DR PIR: A02075; EVTR2.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
FT NON_TER 142 142
FT SEQUENCE 142 AA; 16024 MW; DE29B6CFE745DF3B CRC64;
SQ
Query Match 66.1%; Score 427; DB 1; Length 142;
Best Local Similarity 65.9%; Pred. No. 8.9e-39;
Matches 83; Conservative 18; Mismatches 19; Indels 6; Gaps 3;

Oy 1 EVMLVESGGGLVQPKGSLKSCAASGFTFNMYAMNWRQAPGKGLWVAIRTSKNVAT 60
Db 20 EVKLEESGGGLVQPGSMKLSVAGSFTFSYDMWWRQAPGKGLWVAIRLKSNNAT 79

Oy 61 FYADSVKDRFTISRDDSSMLYLQNNLKTEDTAMNYCVRRGASGIDYAMDYWGOGT 117
Db 80 YGKSLKGRFTLSRDDSSKSVYLQNNLRPDTGIYCTTGA-----YSENFVYWGOGT 136

Oy 118 SLTVSS 123
Db 137 LVTVSS 142

RESULT 8
HV29_MOUSE
ID HV29_MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR: C93818; AVMS09.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Query Match 65.9%; Score 426; DB 1; Length 113;
Best Local Similarity 67.8%; Pred. No. 8.7e-39;
Matches 82; Conservative 13; Mismatches 18; Indels 8; Gaps 1;

QY 1 EYVLVSGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKGLKLEWVARIRSKSNYYAT 60
DB 1 EVKLEESGGGLVQPGGSKMLSCVSGFTFSNYMNMVVRQSPKGLKLEWVAEIRLKSHTY 60
QY 61 FYADSVKDRFTTSRDSQSMVLYOMNNLKTEDTAMYYCYVRRGASGIDYAMDYWGQTSLT 120
DB 61 HYAESVKGRTTSRDDSKSVLYOMNNLRAEDTGIHYCTGFA-----YWGQGTLYT 112
QY 121 V 121
DB 113 V 113

RESULT 9
HV31_MOUSE
ID HV31_MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR: A92810; AVMS57.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Ig heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR: C93818; AVMS09.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Query Match 65.9%; Score 426; DB 1; Length 113;
Best Local Similarity 67.8%; Pred. No. 8.7e-39;
Matches 82; Conservative 13; Mismatches 18; Indels 8; Gaps 1;

QY 1 EYVLVSGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKGLKLEWVARIRSKSNYYAT 60
DB 1 EVKLEESGGGLVQPGGSKMLSCVSGFTFSNYMNMVVRQSPKGLKLEWVAEIRLKSHTY 60
QY 61 FYADSVKDRFTTSRDSQSMVLYOMNNLKTEDTAMYYCYVRRGASGIDYAMDYWGQTSLT 120
DB 61 HYAESVKGRTTSRDDSKSVLYOMNNLRAEDTGIHYCTGFA-----YWGQGTLYT 112
QY 121 V 121
DB 113 V 113

RESULT 9
HV31_MOUSE
ID HV31_MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR: A92810; AVMS57.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 65.3%; Score 422; DB 1; Length 113;
Best Local Similarity 68.6%; Pred. No. 2.3e-38;
Matches 83; Conservative 10; Mismatches 20; Indels 8; Gaps 1;

QY 1 EYVLVSGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKGLKLEWVARIRSKSNYYAT 60
DB 1 EVKLEESGGGLVQPGGSKMLSCVSGFTFSNYMNMVVRQSPKGLKLEWVAEIRLKSHTY 60
QY 61 FYADSVKDRFTTSRDSQSMVLYOMNNLKTEDTAMYYCYVRRGASGIDYAMDYWGQTSLT 120
DB 61 HYAESVKGRTTSRDDSKSVLYOMNNLRAEDTGIHYCTGFA-----YWGQGTLYT 112
QY 121 V 121
DB 113 V 113

RESULT 10
HV25_MOUSE
ID HV25_MOUSE STANDARD; PRT; 123 AA.
AC P01794;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region HPGC14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS75.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;

Query Match 65.2%; Score 421; DB 1; Length 123;
Best Local Similarity 65.9%; Pred. No. 3.3e-38;
Matches 81; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

QY 1 EYVLVSGGLVQPGKSLKSCAASGFTFNYYAMNVRQAPGKGLKLEWVARIRSKSNYYAT 60
DB 1 EVKLEESGGGLVQPGGSKRLSCATSGTFSAFYMEVVRQPPGKRLKLEWVAASRANKANDYTT 60
QY 61 FYADSVKDRFTTSRDSQSMVLYOMNNLKTEDTAMYYCYVRRGASGIDYAMDYWGQTSLT 120
DB 61 EYSASVKGRTTSRDDTSQSYLYOMNNLRAEDTAIIYCARDYVYGYDFWVWGAGTTVT 120
QY 121 VSS 123
DB 121 VSS 123

RESULT 11
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

Query Match 63.5%; Score 410.5; DB 1; Length 122;
Best Local Similarity 64.5%; Pred. No. 4.3e-37;
Matches 80; Conservative 18; Mismatches 23; Indels 3; Gaps 2;

QY 1 EYMLVSGGLVQPKGSLKSLCAASGFTFNAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EYMLVSGGLVQPKGSLKSLCAASGFTFNAMNVRQAPGKLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMLYLQMNKLKTEDTAMYYCVRRGASGIDYAMDYWGQTSLSL 120
DB 61 FYADSVKDRFTISRDDSQSMLYLQMNKLKTEDTAMYYCVRRGASGIDYAMDYWGQTSLSL 120
QY 121 VSS 123
DB 121 VSS 123

RESULT 14
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE=8019926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "Ig antibodies to phosphorylcholine exhibit more diversity than
their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
DR PIR; A02070; AMST5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123
FT SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 63.0%; Score 407; DB 1; Length 123;
Best Local Similarity 63.4%; Pred. No. 1e-36;
Matches 78; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

QY 1 EYMLVSGGLVQPKGSLKSLCAASGFTFNAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EYMLVSGGLVQPKGSLKSLCAASGFTFNAMNVRQAPGKLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMLYLQMNKLKTEDTAMYYCVRRGASGIDYAMDYWGQTSLSL 120
DB 61 FYADSVKDRFTISRDDSQSMLYLQMNKLKTEDTAMYYCVRRGASGIDYAMDYWGQTSLSL 120
QY 121 VSS 123
DB 121 VSS 123

RESULT 15
HV34_MOUSE
ID HV34_MOUSE STANDARD; PRT; 113 AA.
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region AMPL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR; A02073; HVMSAM.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;

Query Match 62.8%; Score 406; DB 1; Length 113;
Best Local Similarity 66.1%; Pred. No. 1.2e-36;
Matches 80; Conservative 10; Mismatches 23; Indels 8; Gaps 1;

QY 1 EYMLVSGGLVQPKGSLKSLCAASGFTFNAMNVRQAPGKLEWVARIRSKSNYYAT 60
DB 1 EYMLVSGGLVQPKGSLKSLCAASGFTFNAMNVRQAPGKLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMLYLQMNKLKTEDTAMYYCVRRGASGIDYAMDYWGQTSLSL 120
DB 61 FYADSVKDRFTISRDDSQSMLYLQMNKLKTEDTAMYYCVRRGASGIDYAMDYWGQTSLSL 120
QY 121 V 121
DB 113 V 113

Search completed: November 27, 2002, 07:18:56
Job time : 18.5714 secs


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RESULT 2
Q8WU38      PRELIMINARY;      PRT;      573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 63.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC021276; AAH21276.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match      66.3%; Score 428.5; DB 4; Length 573;
Best Local Similarity 66.7%; Pred. No. 3.7e-36;
Matches 84; Conservative 17; Mismatches 20; Indels 5; Gaps 2;

QY 1 EYVLVESGGGLVQPGKSLKSLCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 EVLVESGGGLVQPGKSLKSLCAASGFTDDYAMHVRQAPGKLEWVGISWNSGSIG- 78

QY 61 FYADSVKDRFTISRDSQSMLYLQNNLKTEDTAMYCYVRRGAS---GIDYAMDYWGQGT 117
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 79 -YADSVKGRFTISRDNKNSLYLQNNLSRAEDTALYYCAKHGSGSYIGYYGMDVWGQGT 137

QY 118 STVSS 123
  ::|||
DB 138 TVTVSS 143

RESULT 3
Q9UL90      PRELIMINARY;      PRT;      113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match      64.9%; Score 419.5; DB 4; Length 118;
Best Local Similarity 68.0%; Pred. No. 4.4e-36;
Matches 83; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 EYVLVESGGGLVQPGKSLKSLCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 EVLVESGGGLVQPGKSLKSLCAASGFTFSYSMNVRQAPGKLEWVSYI--SSTIIPI 58

QY 61 FYADSVKDRFTISRDSQSMLYLQNNLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 59 YIADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAK-----DLNYWGQGTSLT 110

QY 121 VSS 123
  |||
DB 111 VSS 113

RESULT 4
Q9UL91      PRELIMINARY;      PRT;      118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match      64.9%; Score 419.5; DB 4; Length 118;
Best Local Similarity 68.0%; Pred. No. 4.4e-36;
Matches 83; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 EYVLVESGGGLVQPGKSLKSLCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 EVLVESGGGLVQPGKSLKSLCAASGFTFSYSMNVRQAPGKLEWVSYI--SSTIIPI 58

QY 61 FYADSVKDRFTISRDSQSMLYLQNNLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 59 YIADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAK-----EAFDIWGQGTWVT 115

QY 121 VS 122
  ||
DB 116 VS 117

RESULT 5
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match      65.2%; Score 421; DB 4; Length 113;
Best Local Similarity 66.7%; Pred. No. 2.9e-36;
Matches 82; Conservative 17; Mismatches 14; Indels 10; Gaps 2;

QY 1 EYVLVESGGGLVQPGKSLKSLCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 EVLVESGGGVQPGKSLKSLCAASGFTFSYGMHVRQAPGKLEWVAFIRYDGSN--K 58

QY 61 FYADSVKDRFTISRDSQSMLYLQNNLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 59 YIADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAK-----DLNYWGQGTSLT 110

QY 121 VSS 123
  |||
DB 111 VSS 113

RESULT 4
Q9UL91      PRELIMINARY;      PRT;      118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match      64.9%; Score 419.5; DB 4; Length 118;
Best Local Similarity 68.0%; Pred. No. 4.4e-36;
Matches 83; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 EYVLVESGGGLVQPGKSLKSLCAASGFTFNYYAMNVRQAPGKLEWVARIRSKSNYYAT 60
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 EVLVESGGGLVQPGKSLKSLCAASGFTFSYSMNVRQAPGKLEWVSYI--SSTIIPI 58

QY 61 FYADSVKDRFTISRDSQSMLYLQNNLKTEDTAMYCYVRRGASGIDYAMDYWGQGTSLT 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 59 YIADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAK-----EAFDIWGQGTWVT 115

QY 121 VS 122
  ||
DB 116 VS 117

RESULT 5
```



```
RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY GLAND;
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Takatsuma M., Hosofiri T., Raku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027379; BAB5072.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 494 AA; 5308 MW; 9A1D7AEBSAEE4C0E CRC64;

Query Match 64.0%; Score 413.5; DB 4; Length 494;
Best Local Similarity 65.3%; Pred. No. 1.1e-34;
Matches 81; Conservative 18; Mismatches 22; Indels 3; Gaps 2;

QY 1 EYMLVSGGGLVQPKGSLKSLCAASGFTFNYYAMNVRQAPGKGLWVARIKSKSNYYAT 60
DB 20 EVOLVESGGGLVQPKGSLKSLCAASGFTFNYYAMNVRQAPGKGLWVARIKSKSNYYAT 77
QY 61 FYADSVKDRFTISRDSQSMVLYLQMNLLKTEDTAMYYCVRRGASG-IDYAMDYWGQGTSL 119
DB 78 YYRDSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARR-----RYALDYWGQGT 137
QY 120 TVSS 123
DB 138 TVSS 141

RESULT 9
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FOHSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 64.0%; Score 413.5; DB 4; Length 613;
Best Local Similarity 65.0%; Pred. No. 1.5e-34;
Matches 80; Conservative 19; Mismatches 21; Indels 3; Gaps 2;

QY 1 EYMLVSGGGLVQPKGSLKSLCAASGFTFNYYAMNVRQAPGKGLWVARIKSKSNYYAT 60
DB 20 QVOLVESGGVQPKGSLKSLCAASGFTFNYYAMNVRQAPGKGLWVARIKSKSNYYAT 77
QY 61 FYADSVKDRFTISRDSQSMVLYLQMNLLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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DB 78 YYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAKDWSEGVETFDIWGQGTWVT 136
QY 121 VSS 123
DB 137 VSS 139

RESULT 10
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update).
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : isolation from a
human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG-like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 63.7%; Score 411.5; DB 4; Length 112;
Best Local Similarity 67.5%; Pred. No. 2.8e-35;
Matches 79; Conservative 17; Mismatches 14; Indels 7; Gaps 2;

QY 1 EYMLVSGGGLVQPKGSLKSLCAASGFTFNYYAMNVRQAPGKGLWVARIKSKSNYYAT 60
DB 1 EVOLVESGGGVVQPKGSLKSLCAASGFTFDYGMVVRQAPGKGLWVSGI--NNNGGST 58
QY 61 FYADSVKDRFTISRDSQSMVLYLQMNLLKTEDTAMYYCVRRGASGIDYAMDYWGQGT 117
DB 59 GYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARR-----RYALDYWGQGT 110

RESULT 11
Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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Db 1 EVLVESGGVQVPGRSLRSLCAASFTFSNYGMHWVRQAPGKLEWVAASNDGSN--K 58
QY 61 FYADSVKDRFTISRDSQSMVLYLQNNLKTEDTAMYYCVR--RGASSIDYAMDYWGQGTG 118
Db 59 FYADSVKGRFTIFRDNKNNMDLQMSLRRAEDTAVYICAKDERGLVGY-FDYWGQGTG 117
QY 119 LTVSS 123
Db 118 VTVSS 122
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RESULT 15

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Q91WPS
ID Q91WPS PRELIMINARY: PRT: 479 AA.
AC Q91WPS:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1;
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
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Query Match 62.4%; Score 403; DB 11; Length 479;
Best Local Similarity 64.2%; Pred. No. 1.3e-33;
Matches 79; Conservative 18; Mismatches 18; Indels 8; Gaps 2;

QY 1 EVMLVESGGGLVQPKGSLKSLCAASGFTFNMYAMNVRQAPGKLEWVARIRSKSNYYAT 60
Db 20 EVLVESGGGLVQPKGSLKSLCAASGLTFSNYAMSVMVRQSPKRLWVAASNDGSN--T 77
QY 61 FYADSVKDRFTISRDSQSMVLYLQNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
Db 78 YYSDTMKGRFTISRDNKNNMDLQMSLRRAEDTAVYICAKDERGLVGY-FDYWGQGTG 131
QY 121 VSS 123
Db 132 VSS 134
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Search completed: November 27, 2002, 07:22:53
Job time : 74.3861 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:17:51 : Search time 22.3205 Seconds
(without alignments)
162.139 Million cell updates/sec

Title: US-09-893-615-87

Perfect score: 646

Sequence: 1 EYMLVSGGLVQPKGSLK.....SGIDYAMDYWGQTSLSVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	85.9	115	3	US-08-767-128-36
2	549	85.0	119	1	US-08-442-542-2
3	549	85.0	119	3	US-08-765-469-2
4	549	85.0	599	1	US-08-442-542-18
5	549	85.0	599	3	US-08-765-469-18
6	532	82.4	110	3	US-08-767-128-24
7	462.5	71.6	122	3	US-08-483-749A-2
8	460.5	71.3	120	4	US-09-025-769B-38
9	460.5	71.3	120	4	US-09-025-769B-63
10	460.5	71.3	281	4	US-09-025-769B-178
11	454.5	70.4	120	3	US-08-767-128-28
12	446	69.0	119	3	US-08-767-128-26
13	444.5	68.8	114	3	US-08-483-749A-10
14	444.5	68.8	124	3	US-08-767-128-38
15	444.5	68.8	263	4	US-09-069-821-3
16	444.5	68.8	283	4	US-09-420-592A-6
17	444	68.7	117	4	US-09-025-769B-24
18	443.5	68.7	130	1	US-08-478-039-70
19	443.5	68.7	130	1	US-08-478-039-93
20	443.5	68.7	130	1	US-08-476-349A-70
21	443.5	68.7	130	1	US-08-476-349A-93
22	441.5	68.3	120	2	US-07-934-373C-4
23	441.5	68.3	120	3	US-08-437-642B-4
24	441.5	68.3	120	4	US-08-146-206C-4
25	441.5	68.3	140	4	US-08-983-607-32
26	441.5	68.3	250	2	US-08-392-338A-15
27	441.5	68.3	250	3	US-09-166-750-15

Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 14, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 13, Appl
Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-08-767-128-36
Sequence 36, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:

US-08-767-128-36

Query Match 85.9%; Score 555; DB 3; Length 115;
Best Local Similarity 87.8%; Pred. No. 1.6e-49;
Matches 108; Conservative 2; Mismatches 5; Indels 8; Gaps 1;

QY 1 EYVLVESGGGLVQPKGSLKLSCAASGFTFNYYAMNVRQAPKGLEWVARIRSKSNYYAT 60
|||
DB 1 EYVLVESGGGLVQPKGSLKLSCAASGFTFNYYAMNVRQAPKGLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMFLQNMNLTEDTAMYYCVRRCASGIDYAMDYWGQGTSLT 120
DB 61 FYADSVKDRFTISRDDSQSMFLQNMNLTEDTAMYYCVRRCASGIDYAMDYWGQGTSLT 112

QY 121 VSS 123
|||
DB 113 VSS 115

RESULT 2

US-08-442-542-2
Sequence 2, Application US/08442542
Patent No. 5686600

GENERAL INFORMATION:

APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,542
FILING DATE: 16-MAY-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sprull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-442-542-2

Query Match 85.0%; Score 549; DB 1; Length 119;
Best Local Similarity 86.3%; Pred. No. 6.8e-49;
Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 2;

QY 1 EYVLVESGGGLVQPKGSLKLSCAASGFTFNYYAMNVRQAPKGLEWVARIRSKSNYYAT 60
:|||
DB 1 QVKLQESGGGLVQPKGSLKLSCAASGFTFNFMNVRQAPKGLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMFLQNMNLTEDTAMYYCVRRCASGIDYAMDYWGQGTSL 119
DB 61 SYGDSVKDRFTVSRDSSQSMFLQNMNLTEDTAMYYCVR-----VYGCAMDYWGQGTSLV 115
QY 120 TVSS 123
|||
DB 116 TVSS 119

RESULT 3

US-08-765-469-2
Sequence 2, Application US/08765469
Patent No. 6069301

GENERAL INFORMATION:

APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Sprull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-765-469-2

Query Match 85.0%; Score 549; DB 3; Length 119;
Best Local Similarity 86.3%; Pred. No. 6.8e-49;
Matches 107; Conservative 5; Mismatches 6; Indels 6; Gaps 2;

QY 1 EYVLVESGGGLVQPKGSLKLSCAASGFTFNYYAMNVRQAPKGLEWVARIRSKSNYYAT 60
:|||
DB 1 QVKLQESGGGLVQPKGSLKLSCAASGFTFNFMNVRQAPKGLEWVARIRSKSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMFLQNMNLTEDTAMYYCVRRCASGIDYAMDYWGQGTSL 119
DB 61 SYGDSVKDRFTVSRDSSQSMFLQNMNLTEDTAMYYCVR-----VYGCAMDYWGQGTSLV 115

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE: 05-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-767-128-24

Query Match 82.4%; Score 532; DB 3; Length 110;
Best Local Similarity 87.3%; Pred. No. 3.3e-47;
Matches 103; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
QY 6 EGGGLVQPKGSLKLSAASGFTFNYYAMNVRQAPGKGLWVARIRSKSNYYATFYADS 65
DB 1 EGGGLVQPKGSLKLSAASGFTFNYYAMNVRQAPGKGLWVARIRSKSNYYATFYADS 60
QY 66 VKDRFTISRDDSQSMLYLQNMNLTEDTAMYYCVRRGASGIDYAMDYWGQGTSLTVSS 123
DB 61 VKDRFTISRDDSQSMLYLQNMNLTEDTAMYYCVRREA-----YWAQGTILVTYSA 110

RESULT 7
US-08-483-749A-2
Sequence 2, Application US/08483749A
Patent No. 6034561
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508.008
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-2
Query Match 71.6%; Score 462.5; DB 3; Length 122;
Best Local Similarity 73.2%; Pred. No. 4.4e-40;
Matches 90; Conservative 10; Mismatches 22; Indels 1; Gaps 1;
QY 1 EYMLVESGGGLVQPKGSLKLSAASGFTFNYYAMNVRQAPGKGLWVARIRSKSNYYAT 60
DB 1 EVKLEESGGGLVQPKGSRMKLSVASGFTFSNNYNNWVROSPEKGLWVAIRKLSNYYAT 60
QY 61 FYADSVKDRFTISRDDSQSMLYLQNMNLTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
DB 61 HYAESVKGRETISRDDSQSMVYLQNLNLRADTGIIYCAREYLY-YYTMDYWGQGTSTV 119
QY 121 VSS 123
DB 120 VSS 122
RESULT 8
US-09-025-769B-38
Sequence 38, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

```
;
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-38

Query Match 71.3%; Score 460.5; DB 4; Length 120;
Best Local Similarity 72.4%; Pred. No. 6.9e-40;
Matches 89; Conservative 14; Mismatches 17; Indels 3; Gaps 2;

QY 1 EVMVLVESGGGLVQPGKSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRKSNYYAT 60
Db 1 EVOLVESGGGLVQPGKSLKLSCAASGFTFSSYAMNVRQAPGKGLWVSATSGSGG--ST 58

QY 61 FYADSVKDRFTISRDSOSMLYLQNNLKTEDTAMYYCVRRCASGIDYAMDYWGQGTSLT 120
Db 59 YYADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYYCARWGGDGF-YAMDYWGQGTSLT 117

QY 121 VSS 123
Db 118 VSS 120

RESULT 9
US-09-025-769B-63
; Sequence 63, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid

QY 1 EVMVLVESGGGLVQPGKSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRKSNYYAT 60
Db 1 EVOLVESGGGLVQPGKSLKLSCAASGFTFSSYAMNVRQAPGKGLWVSATSGSGG--ST 58

QY 61 FYADSVKDRFTISRDSOSMLYLQNNLKTEDTAMYYCVRRCASGIDYAMDYWGQGTSLT 120
Db 59 YYADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYYCARWGGDGF-YAMDYWGQGTSLT 117

QY 121 VSS 123
Db 118 VSS 120

RESULT 10
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 71.3%; Score 460.5; DB 4; Length 281;
Best Local Similarity 72.4%; Pred. No. 1.8e-39;
Matches 89; Conservative 14; Mismatches 17; Indels 3; Gaps 2;

QY 1 EVMVLVESGGGLVQPGKSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRKSNYYAT 60
Db 1 EVOLVESGGGLVQPGKSLKLSCAASGFTFSSYAMNVRQAPGKGLWVSATSGSGG--ST 58

QY 61 FYADSVKDRFTISRDSOSMLYLQNNLKTEDTAMYYCVRRCASGIDYAMDYWGQGTSLT 120
Db 59 YYADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYYCARWGGDGF-YAMDYWGQGTSLT 117

QY 121 VSS 123
Db 118 VSS 120

RESULT 9
US-09-025-769B-63
; Sequence 63, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid

QY 1 EVMVLVESGGGLVQPGKSLKLSCAASGFTFNMYAMNVRQAPGKGLWVARIRKSNYYAT 60
Db 1 EVOLVESGGGLVQPGKSLKLSCAASGFTFSSYAMNVRQAPGKGLWVSATSGSGG--ST 58

QY 61 FYADSVKDRFTISRDSOSMLYLQNNLKTEDTAMYYCVRRCASGIDYAMDYWGQGTSLT 120
Db 59 YYADSVKGRFTISRDNKNTLYLQNNLSRAEDTAVYYCARWGGDGF-YAMDYWGQGTSLT 117

QY 121 VSS 123
Db 118 VSS 120
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Db 26 EVLVESGGGLVQPGKSLRSLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGGG--ST 83
QY 61 FYADSVKDRFTISRDSQSMLYLQMNLLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
Db 84 YYADSVKGRFTISRDSKNTLYLQMSLRADTAVYICARWGGDGF-YANDYWGQGTSLT 142
QY 121 VSS 123
Db 143 VSS 145
RESULT 11
US-08-767-128-28
; Sequence 28, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 NO. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-28

Query Match 70.4%; Score 454.5; DB 3; Length 120;
Best Local Similarity 70.7%; Pred. No. 2.8e-39;
Matches 87; Conservative 11; Mismatches 22; Indels 3; Caps 1;
QY 1 EVMVLVSGGGLVQPGKSLKSLSCAASGFTFNMYAMNVRQAPGKLEWVAIRSKSNYYAT 60
Db 1 EVKTEESGGGLVQPGGSKLSVASGFTFSYWNWVRQSPKGLWVAEIRLKSNNYAT 60
QY 61 FYADSVKDRFTISRDSQSMLYLQMNLLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
Db 61 HYAESVKGRTISRDSKSSVYLQMNLLRAEDTGIIYCTYGRGK---GAYWGEGLT 117
QY 121 VSS 123
Db 118 VSA 120
RESULT 12
US-08-767-128-26
; Sequence 26, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 NO. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

[illegible]

RESULT 15

US-09-069-821-3
: Sequence 3, Application US/09069821
: Patent No. 6323322
: GENERAL INFORMATION:
: APPLICANT: FILPULA, DAVID
: APPLICANT: WANG, MAOLIANG
: APPLICANT: SHORR, ROBERT
: APPLICANT: WHITLOW, MARC
: APPLICANT: LEE, LIHSYNG S.
: TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
: CAPABILITY OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVE., NW, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/069,821
: FILING DATE: 30-APR-1998
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/067,341
: FILING DATE: 02-DEC-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/063,074
: FILING DATE: 27-OCT-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/050,472
: FILING DATE: 23-JUN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/044,449
: FILING DATE: 30-APR-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: KIM, JUDITH U.
: REGISTRATION NUMBER: 40,679
: REFERENCE/DOCKET NUMBER: 0977.2280003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 263 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: US-09-069-821-3

[illegible]

Search completed: November 27, 2002, 07:25:12
Job time : 24.3205 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:36:38 ; Search time 1460.96 seconds
(without alignments)
7350.598 Million cell updates/sec

Title: US-09-893-615-86
Perfect score: 369
Sequence: 1 GAAGTGATGCTGGTGGAGTC.....CCTCACTACCGTCCTCTCA 369

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl : *

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 20: em_on.*
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- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sv.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	309.8	84.0	370	10	S65980	S65980 Ig VH193020
2	305	82.7	366	10	MUSIGH339A	L30140 Mus Musculu
3	304	82.4	475	10	MUSIGHAAAC	M60022 Mouse Ig he
4	303.4	82.2	499	10	MUSIGHAAAB	M60021 Mouse Ig he
5	301	81.6	443	10	MUSIGHXS	M21469 Mouse Ig un
6	301	81.6	444	10	MMIGHRF2	X16801 Mouse MRL-R
7	300.4	81.4	357	6	I73737	I73737 Sequence 1
8	300.4	81.4	1797	6	I73745	I73745 Sequence 17
9	298.6	80.9	366	10	AF178591	AF178591 Mus muscu
10	297	80.5	366	10	AF178595	AF178595 Mus muscu
11	297	80.5	366	10	AF178596	AF178596 Mus muscu
12	291	78.9	408	10	AF045483	AF045483 Mus muscu
13	289.6	78.5	366	10	MUSIGH125A	L31512 Mus musculu
14	288.8	78.3	360	10	MUSIHCVRA	D50376 Mouse mRNA
15	288.6	78.2	345	6	ARI08686	ARI08686 Sequence
16	287.8	78.0	351	10	AF006586	AF006586 Mus muscu
17	286.2	77.6	663	10	AF064445	AF064445 Mus muscu
18	285.8	77.5	474	10	MUSIGKCLT	M20829 Mouse Igg2a
19	284.4	77.1	330	6	ARI08680	ARI08680 Sequence
20	283.8	76.9	375	6	AX025327	AX025327 Sequence
21	283.4	76.8	18591	2	AC073561	AC073561 Mus muscu
22	283.4	76.8	661	10	AF064446	AF064446 Mus muscu
23	282.4	76.5	357	10	MUSIGHUHF	M5948 Mouse Ig ac
24	282.2	76.5	348	10	AF468835	AF468835 Mus muscu
25	280.6	76.0	360	10	AF006574	AF006574 Mus muscu
26	279.4	75.7	357	10	MUSIGHXT	M21470 Mouse Ig ac
27	279.2	75.7	360	10	MDIGMVAQ	Z22080 M.domesticu
28	279.2	75.7	360	10	AF118969	AF118969 Mus muscu
29	279	75.6	316	10	S63182	S63182 Ig VH-anti-
30	277.8	75.3	375	10	S63182	S63182 Ig VH-anti-
31	276.4	74.9	353	10	AF321939	AF321939 Mus muscu
32	276.2	74.9	421	10	MMIGGIHV	X78107 M.musculus
33	276	74.8	360	10	MDIGMVAR	Z22082 M.domesticu
34	274.4	74.4	202704	10	AC090843	AC090843 Mus muscu
35	274	74.3	312	10	MUSIGHACT	M34735 Mouse Ig H-
36	273.8	74.2	337	10	MMU55546	U55546 Mus musculu
37	273.2	74.0	337	10	MMU55545	U55545 Mus musculu
38	272.8	73.9	663	10	AF064442	AF064442 Mus muscu
39	272.8	73.9	663	10	AF064444	AF064444 Mus muscu
40	272.4	73.8	783	10	MMSCFVCP	Z70661 Artificial
41	269.6	73.1	360	10	MDIGGVAT	Z22093 M.domesticu
42	269.2	73.0	443	6	AX208064	AX208064 Sequence
43	269.2	73.0	443	6	AX208067	AX208067 Sequence
44	264.8	71.8	381	10	S72511	S72511 anti-estradi
45	264.6	71.7	333	10	MMU55544	U55544 Mus musculu

ALIGNMENTS

RESULT 1
S65980
LOCUS
DEFINITION
Ig VH193020-anti-insulin 193020 monoclonal antibody heavy chain
variable region [mice, NOD spleen and myeloma cells, nonobese
diabetic, mRNA Partial, 370 nt].
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 370)
Pleau,J.M., Marche,P.N., Serrano,M.P., Boitard,C. and Bach,J.F.

S65980 370 bp mRNA linear ROD 24-NOV-1993
Ig VH193020-anti-insulin 193020 monoclonal antibody heavy chain
variable region [mice, NOD spleen and myeloma cells, nonobese
diabetic, mRNA Partial, 370 nt].
S65980
S65980.1 GI:425687
Mus sp. nonobese diabetic NOD spleen and myeloma cells.
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 370)
Pleau,J.M., Marche,P.N., Serrano,M.P., Boitard,C. and Bach,J.F.

ORGANISM	SOURCE
Mus musculus	Mouse (strain C57BL/6) spleen cell hybridoma Z22, cDNA to mRNAs

Db	255	TATTATCCGGATTTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTACAAGCATG	314
QY	241	CTCTATCTGCAAAATGAACAACTTGAAGAACTGAGGACACAGCCATGATTACTGTGTGAGA	300
Db	315	CTCTATCTGCAAAATGAACAACTTGAAGAACTGAGGACACAGCCATGATTACTGTGTGATC	374
QY	301	CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTTGGGGTCAAGAACCTCACTCACC	360
Db	375	CTCTATGGTAACACAGCCCTCTATGCTATGGACTACTTGGGGTCAAGAACCTCACTCACC	434
QY	361	GTCTCCTCA 369	
Db	435	GTCTCCTCA 443	
RESULT 6			
MMIGHRF2			
LOCUS	MMIGHRF2 444 bp mRNA linear ROD 07-MAY-1992		
DEFINITION	Mouse MRL-RF24BG nonfunctional Ig heavy chain transcript.		
ACCESSION	X16801		
VERSION	X16801.1 GI:52049		
KEYWORDS	Ig D-segment; Ig heavy chain; immunoglobulin; joining region; pseudogene; variable region.		
SOURCE	Mus musculus.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 444)		
TITLE	Kofler,R.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (24-JUL-1989) Kofler,R., General and Experimental		
AUTHORS	Pathology, University of Innsbruck,, Fritz-Pregl-Str. 3, A-6020		
TITLE	Innsbruck		
JOURNAL	2 (bases 2 to 444)		
MEDLINE	Kroemer,G., Faessler,R., Strohal,R., Wick,G. and Kofler,R.		
PUBMED	Evidence for a new murine immunoglobulin heavy chain variable		
COMMENT	region gene family		
FEATURES	Immunol. Invest. 16 (2), 107-116 (1987)		
SOURCE	8/308735		
FEATURES	MRL-RF24		
FEATURES	hybridoma produces an anti-Ig(RF)autoantibody Data kindly		
FEATURES	(30-JAN-1990) by Kofler R.		
FEATURES	Location/Qualifiers		
FEATURES	1..444		
FEATURES	/organism="Mus musculus"		
FEATURES	/strain="MRL-Mp-lpr/lpr."		
FEATURES	/db_xref="taxon:10090"		
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FEATURES	/note="(pseudo) Ig heavy chain precursor: protein"		
FEATURES	77..>444		
FEATURES	/note="(pseudo) Ig heavy chain mature protein"		
FEATURES	77..375		
FEATURES	/note="(pseudo) Ig heavy chain variable region"		
FEATURES	106..107		
FEATURES	/note="(deletion site (1 bp))"		
FEATURES	128..130		
FEATURES	/note="(premature stop"		
FEATURES	376..396		
FEATURES	/note="(DSP2.7 diversity region"		
FEATURES	397..444		
FEATURES	/note="(JH4 joining region"		
FEATURES	BASE COUNT 118 a 92 c 108 g 126 t		
FEATURES	ORIGIN		
FEATURES	Query Match 81.6%; Score 301; DB 10; Length 444;		
FEATURES	Best Local Similarity 90.2%; Pred. No. 4.8e-83;		
FEATURES	Matches 333; Conservative 0; Mismatches 35; Indels 1; Gaps 1;		
QY	1	GAGTGTGCTGGTGGAGTCTGGTGGAGGATTGGTGGAGCTTAAGGGTCATTGAAACTC	60
Db	77	GAGTGGAGCTGTGTAGTCTGGTGGAGTA-TGGTGGAGCTTAAGGATCATTTGAAACTC	135

QY 61 TCATGTGCAGCCTCTGGATTACCTTCAATAAATACCGCATGAATGGGTCCGCCAGGCT 120
Db 136 TCATGTGCAGCCTCTGGTTTCACTTCAATACCTATGCCATGAATGGGTCCGCCAGGCT 195
QY 121 CCAGGAAGGGTTTGAATGGGTTCCTCGATAAAGTAAGTAATAATATATGCAACA 180
Db 196 CCAGGAAGGGTTTGAATGGGTTCCTCGATAAAGTAAGTAATAATATATGCAACA 255
QY 181 TTTATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 240
Db 256 TATATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 315
QY 241 CTCATCTGCAATGAACAACTTGAAGAACTGAGGACACAGCCATGATTACTGTGTGAGA 300
Db 316 CTCATCTGCAATGAACAACTTGAAGAACTGAGGACACAGCCATGATTACTGTGTGATC 375
QY 301 CGGGGGGCTTCAGGATTCAGTATGCTATGGACTACTGGGTCAAGAACCTCACTCACC 360
Db 376 CTCATGCGTAACCTACCCCTCTATGCTATGGACTACTGGGTCAAGGAACCTCAGTCACC 435
QY 361 GTCTCCTCA 369
Db 436 GTCTCCTCA 444

RESULT 7
LOCUS I73737 357 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 1 from patent US 5686600.
ACCESSION I73737
VERSION I73737.1 GI:3009878
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 357)
AUTHORS Carozzi,N.B. and Koziel,M.G.
TITLE Antibodies which bind to insect gut proteins and their use
JOURNAL Patent: US 5686600-A 11-NOV-1997;
FEATURES Location/Qualifiers
source 1..357
BASE COUNT 102 a 76 c 91 g 88 t
ORIGIN

Query Match 81.4%; Score 300.4; DB 6; Length 357;
Best Local Similarity 91.0%; Pred. No. 7.3e-83;
Matches 335; Conservative 0; Mismatches 21; Indels 12; Gaps 1;
QY 2 AGTGTATGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTCT 61
Db 2 AGTCAAACTGCAGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTCT 61
QY 62 CATGTGCAGCCTCTGGATTACCTTCAATAAAGTAAGTAATAATATATGCAACAT 181
Db 62 CATGTGCAGCCTCTGGATTACCTTCAATAAAGTAAGTAATAATATATGCAACAT 181
QY 122 CAGGAAGGGTTTGAATGGGTTCCTCGATAAAGTAAGTAATAATATATGCAACAT 241
Db 122 CAGGAAGGGTTTGAATGGGTTCCTCGATAAAGTAAGTAATAATATATGCAACAT 241
QY 182 TTTATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 361
Db 182 TTTATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 361
QY 242 TCATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 703
Db 242 TCATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 703
QY 302 GGGGGGCTTCAGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 811
Db 302 GGGGGGCTTCAGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 811

QY 362 TCTCCTCA 369
Db 350 TCTCCTCA 357

RESULT 8
LOCUS I73745 1797 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 17 from patent US 5686600.
ACCESSION I73745
VERSION I73745.1 GI:3009886
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1797)
AUTHORS Carozzi,N.B. and Koziel,M.G.
TITLE Antibodies which bind to insect gut proteins and their use
JOURNAL Patent: US 5686600-A 17-11-NOV-1997;
FEATURES Location/Qualifiers
source 1..1797
BASE COUNT 455 a 488 c 452 g 402 t
ORIGIN

Query Match 81.4%; Score 300.4; DB 6; Length 1797;
Best Local Similarity 91.0%; Pred. No. 8e-83;
Matches 335; Conservative 0; Mismatches 21; Indels 12; Gaps 1;
QY 2 AAGTGTATGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTCT 61
Db 464 AGGTCAAACTGCAGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTCT 523
QY 62 CATGTGCAGCCTCTGGATTACCTTCAATAAAGTAAGTAATAATATATGCAACAT 121
Db 524 CATGTGCAGCCTCTGGATTACCTTCAATAAAGTAAGTAATAATATATGCAACAT 583
QY 122 CAGGAAGGGTTTGAATGGGTTCCTCGATAAAGTAAGTAATAATATATGCAACAT 181
Db 584 CAGGAAGGGTTTGAATGGGTTCCTCGATAAAGTAAGTAATAATATATGCAACAT 643
QY 182 TTTATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 241
Db 644 CTTATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 703
QY 242 TCATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 301
Db 704 TCATGCGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 761
QY 302 GGGGGGCTTCAGGATTCAGTGAAGACAGTTCCACATCTCCAGAGATGATTCACAAAGCATG 361
Db 762 -----GGTAGTATACGGTGTCTATGGACTACTGGGTCAAGGAACCTCACTCACC 811
QY 362 TCTCCTCA 369
Db 812 TCTCCTCA 819

RESULT 9
LOCUS AF178591 366 bp mRNA linear ROD 22-MAY-2000
DEFINITION Mus musculus 23-7 immunoglobulin heavy chain variable region mRNA, partial cds.
ACCESSION AF178591
VERSION AF178591.1 GI:5853171
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 366)
AUTHORS Puterman,C., Deocharan,B. and Diamond,B.
TITLE Molecular analysis of the autoantibody response in peptide-induced

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autoimmunity
J. Immunol. 164 (5), 2542-2549 (2000)
JOURNAL MEDLINE 20143847
PUBMED 10679092
REFERENCE 2 (bases 1 to 366)
AUTHORS Puttermann,C., Deocharan,B. and Diamond,B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
FEATURES
source
Location/Qualifiers
1..366
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="8-3"
/cell_type="hybridoma"
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/translation="DVKVESGGGLVQPKSLKSCAASGFTENTYAMNVRQAPKGG
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GSRYWFDVWGAGTTVTSS"
BASE COUNT 101 a 84 c 95 g 86 t
ORIGIN

Query Match 80.9%; Score 298.6; DB 10; Length 366;
Best Local Similarity 90.0%; Pred. No. 2.7e-82;
Matches 332; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

Qy 1 GAAGTGATGCTGGGAGTCTGGTGGAGGATTTGGTGCAGGCTAAAGGTCATTGAAACTC 60
Db 1 GACGTCAAGGTGGTGGAGTCTGGAGGAGGATTTGGTGCAGGCTAAAGGTCATTGAAACTC 60

Qy 61 TCATGTGCAGCCTCGGATTCACCTTCAATAACTTACGCCATGAATTTGGTCCGCGCAGGCT 120
Db 61 TCATGTGCAGCCTCGGATTCACCTTCAATAACTTACGCCATGAATTTGGTCCGCGCAGGCT 120

Qy 121 CCAGGAAGGGTTTGGAAATGGTGTCTGCATTAAGAAGTAAAGTAATAATATATGCAACA 180
Db 121 CCAGGAAGGGTTTGGAAATGGTGTCTGCATTAAGAAGTAAAGTAATAATATATGCAACA 180

Qy 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 TATTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240

Qy 241 CTCATCTGCAAAATGAACAACCTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
Db 241 CTCATCTGCAAAATGAACAACCTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300

Qy 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
Db 301 CACAGCGGTTCCCGC---CTACTGGTACTTCGATGCTCTGGGCGCGAGGACACCGGTCACC 357

Qy 361 GTCCTCTCA 369
Db 358 GTCCTCTCA 366

RESULT 10
AF178595
LOCUS Mus musculus 8-3 immunoglobulin heavy chain variable region mRNA,
DEFINITION partial cds.
ACCESSION AF178595
VERSION AF178595.1 GI:5853179
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

autoimmunity
J. Immunol. 164 (5), 2542-2549 (2000)
JOURNAL MEDLINE 20143847
PUBMED 10679092
REFERENCE 2 (bases 1 to 366)
AUTHORS Puttermann,C., Deocharan,B. and Diamond,B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
FEATURES
source
Location/Qualifiers
1..366
/organism="Mus musculus"
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LEWVARIRKSNNTATYYADSVDRFTISRDDSQSMLYLQMNLLKTEDTAMYYCVRHS
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BASE COUNT 101 a 84 c 95 g 86 t
ORIGIN

Query Match 80.9%; Score 298.6; DB 10; Length 366;
Best Local Similarity 90.0%; Pred. No. 2.7e-82;
Matches 332; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

Qy 1 GAAGTGATGCTGGGAGTCTGGTGGAGGATTTGGTGCAGGCTAAAGGTCATTGAAACTC 60
Db 1 GACGTCAAGGTGGTGGAGTCTGGAGGAGGATTTGGTGCAGGCTAAAGGTCATTGAAACTC 60

Qy 61 TCATGTGCAGCCTCGGATTCACCTTCAATAACTTACGCCATGAATTTGGTCCGCGCAGGCT 120
Db 61 TCATGTGCAGCCTCGGATTCACCTTCAATAACTTACGCCATGAATTTGGTCCGCGCAGGCT 120

Qy 121 CCAGGAAGGGTTTGGAAATGGTGTCTGCATTAAGAAGTAAAGTAATAATATATGCAACA 180
Db 121 CCAGGAAGGGTTTGGAAATGGTGTCTGCATTAAGAAGTAAAGTAATAATATATGCAACA 180

Qy 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 TATTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240

Qy 241 CTCATCTGCAAAATGAACAACCTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
Db 241 CTCATCTGCAAAATGAACAACCTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300

Qy 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
Db 301 CACAGCGGTTCCCGC---CTACTGGTACTTCGATGCTCTGGGCGCGAGGACACCGGTCACC 357

Qy 361 GTCCTCTCA 369
Db 358 GTCCTCTCA 366

RESULT 10
AF178595
LOCUS Mus musculus 8-3 immunoglobulin heavy chain variable region mRNA,
DEFINITION partial cds.
ACCESSION AF178595
VERSION AF178595.1 GI:5853179
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 366)
Puttermann,C., Deocharan,B. and Diamond,B.
Molecular analysis of the autoantibody response in peptide-induced
autoimmunity
J. Immunol. 164 (5), 2542-2549 (2000)
JOURNAL MEDLINE 20143847
PUBMED 10679092
REFERENCE 2 (bases 1 to 366)
AUTHORS Puttermann,C., Deocharan,B. and Diamond,B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
/strain="BALB/c"
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/notes="anti-peptide antibody"
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/product="immunoglobulin heavy chain variable region"
/protein_id="A054351.1"
/db_xref="GI:5853180"
/translation="DVRVVEGGGLVQPKSLKSCAASGFTENTYAMNVRQAPKGG
LEWVARIRKSNNTATYYADSVDRFTISRDDSQSMLYLQMNLLKTEDTAMYYCVRHG
LGRWYFDVWGAGTTVTSS"
BASE COUNT 99 a 82 c 99 g 86 t
ORIGIN

Query Match 80.5%; Score 297; DB 10; Length 366;
Best Local Similarity 89.7%; Pred. No. 8.4e-82;
Matches 331; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

Qy 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGGCTAAAGGTCATTGAAACTC 60
Db 1 GACGTCAAGGTGGTGGAGTCTGGAGGAGGATTTGGTGCAGGCTAAAGGTCATTGAAACTC 60

Qy 61 TCATGTGCAGCCTCGGATTCACCTTCAATAACTTACGCCATGAATTTGGTCCGCGCAGGCT 120
Db 61 TCATGTGCAGCCTCGGATTCACCTTCAATAACTTACGCCATGAATTTGGTCCGCGCAGGCT 120

Qy 121 CCAGGAAGGGTTTGGAAATGGTGTCTGCATTAAGAAGTAAAGTAATAATATATGCAACA 180
Db 121 CCAGGAAGGGTTTGGAAATGGTGTCTGCATTAAGAAGTAAAGTAATAATATATGCAACA 180

Qy 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 TATTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240

Qy 241 CTCATCTGCAAAATGAACAACCTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
Db 241 CTCATCTGCAAAATGAACAACCTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300

Qy 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
Db 301 CATGGG---CTGGGCGCGCTACTGTGATGCTCTGGGCGCGAGGACACCGGTCACC 357

Qy 361 GTCCTCTCA 369
Db 358 GTCCTCTCA 366

RESULT 11
AF178596
LOCUS Mus musculus 39-9 immunoglobulin heavy chain variable region mRNA,
DEFINITION partial cds.
ACCESSION AF178596
VERSION AF178596.1 GI:5853181
```



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Matches 293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GAAGTGATGCTGGTGGAGCTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Db 4 GAGGTGAAGCTGAAGGAGCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTC 63
Qy 61 TCATGTGCAGCCTCTGGGATTCACCTTTCAATTAACGACCATGAATTTGGTCCGCCAGGCT 120
Db 64 TCATGTGCAGCCTCTGGGATTCACCTTTCAATTAACGACCATGAATTTGGTCCGCCAGGCT 123
Qy 121 CCAGGAAAGGGTTTGGGATTTGGGTTGCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
Db 124 CCAGGAAAGGGTTTGGGATTTGGGTTGCTCGCATAGAAGTAAAGTAATAATTATGCAACA 183
Qy 181 TTTATGCGGATTCAGTCAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATG 240
Db 184 TATTATGCGGATTCAGTCAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATG 243
Qy 241 CTCATCTGCAAAATGAACAACCTTGAAGTCTGAGGACAGGACATGATTTACTGTGTGAGA 300
Db 244 CTCATCTGCAAAATGAACAACCTTGAAGTCTGAGGACAGGACATGATTTACTGTGTGAGA 303

RESULT 15
ARI08686
LOCUS ARI08686 345 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 35 from patent US 611079.
ACCESSION ARI08686
VERSION ARI08686.1 GI:12824173
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 345)
AUTHORS Wylie,D.E., Lopez,O., Murray,P.Joseph. and Goebel,P.
TITLE Lead binding polypeptides and nucleotides coding therefore
JOURNAL Patent: US 611079-A 35 29-AUG-2000;
FEATURES
source 1..345
BASE COUNT 100 a 75 c 87 g 83 t
ORIGIN

Query Match 78.2%; Score 288.6; DB 6; Length 345;
Best Local Similarity 89.7%; Pred. No. 3.6e-79;
Matches 331; Conservative 0; Mismatches 14; Indels 24; Gaps 1;
Qy 1 GAAGTGATGCTGGTGGAGCTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Db 1 GAGGTGCAGCTTGTAGCTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Qy 61 TCATGTGCAGCCTCTGGGATTCACCTTTCAATTAACGACCATGAATTTGGTCCGCCAGGCT 120
Db 61 TCATGTGCAGCCTCTGGGATTCACCTTTCAATTAACGACCATGAATTTGGTCCGCCAGGCT 120
Qy 121 CCAGGAAAGGGTTTGGGATTTGGGTTGCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
Db 121 CAAGGAAAGGGTTTGGGATTTGGGTTGCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
Qy 181 TTTATGCGGATTCAGTCAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 TATTATGCGGATTCAGTCAAGACAGGTTCCACATCTCCAGAGATGATTCACAAAGCATG 240
Qy 241 CTCATCTGCAAAATGAACAACCTTGAAGTCTGAGGACAGGACATGATTTACTGTGTGAGA 300
Db 241 CTCATCTGCAAAATGAACAACCTTGAAGTCTGAGGACAGGACATGATTTACTGTGTGAGA 300
Qy 301 CGGGGGGGTTCAGGATTTGACTATGCTATGGAAGTCAAGGAGCAACCTCACTCACC 360
Db 301 CGG-----AGGGACTACTGGGGTCAAGGAGCAACCTCACTCACC 336
Qy 361 GTCTCCTCA 369
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Db 337 GTCTCCTCA 345

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Job time : 1478.46 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:34:25 ; Search time 198.734 Seconds
(without alignments)
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Title: US-09-893-615-86
Perfect score: 369
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	300.4	81.4	357	AAT15725	3B1 heavy chain va
2	300.4	81.4	1797	AAT15733	3B1 single chain a
3	293.8	79.6	1079	21 AAZ51115	Anti-Her2neu singl
4	288.6	78.2	345	AAT58267	Lead binding MAb 2
5	284.4	77.1	330	AAT58261	Lead binding MAB 6
6	283.8	76.9	375	21 AAA40202	H. pylori 26 kda p
7	269.2	73.0	443	AAD13178	Murine antibody 1D
8	249.2	67.5	357	22 AAD13179	Humanised murine a
9	227.2	61.6	366	21 AAA38896	2G3 hybridoma VH d

10	225.8	61.2	359	21	AAA44338	Human secreted exp
11	215.4	58.4	5227	18	AAT79537	Plasmid pTERMSC2H1
12	214.6	58.2	369	22	AAS03515	DNA encoding anti-
13	214.6	58.2	761	24	ABK47271	Insulin/insulin-11
14	213.6	57.9	372	18	AAT58268	Lead binding MAB 2
15	212.8	57.7	768	24	AAS97139	P5-2 single chain
16	212.8	57.7	1509	24	AAS97147	3B10XP5-2 bispecif
17	212.2	57.5	375	24	ABK88128	DNA encoding mouse
18	210.6	57.1	761	24	ABK47275	Insulin/insulin-11
19	210.2	57.0	357	19	AAF22331	Nucleic acid encod
20	209	56.6	378	22	AAF29062	Human HIV-1 monoc
21	205	55.6	361	13	AAQ29148	WN1 222-5 antibody
22	204.4	55.4	379	22	AAI68772	Human autoantibody
23	204.2	55.3	738	14	AAQ43293	Sequence encoding
24	204.2	55.3	738	15	AAQ66841	CC49 VL / 217 / 4-
25	204.2	55.3	738	20	AAQ47477	DNA encoding a pro
26	204.2	55.3	738	20	AAV99764	Fusion polypeptide
27	204.2	55.3	738	21	AAV95090	DNA encoding bival
28	204.2	55.3	738	21	AAAS9622	DNA encoding a sin
29	204.2	55.3	738	21	AAZ57095	4-4-20 Vh region a
30	204.2	55.3	738	21	AAZ90344	DNA (SEQ ID NO:22)
31	204.2	55.3	738	21	AAZ37393	Antibody CC49/anti
32	204.2	55.3	744	14	AAQ43288	Sequence encoding
33	204.2	55.3	744	20	AAQ04742	DNA encoding a pro
34	204.2	55.3	744	21	AAAS9085	Bivalent antigen b
35	204.2	55.3	744	21	AAAS9617	DNA encoding a het
36	204.2	55.3	744	21	AAZ57090	4-4-20 Vh region a
37	204.2	55.3	744	21	AAZ90339	DNA (SEQ ID NO:12)
38	204.2	55.3	752	24	ABK47272	Insulin/insulin-11
39	203	55.0	345	14	AAQ40046	BW 835 Vh. Synthe
40	202.6	54.9	1172	20	AAZ87209	AGA2-HA-4-4-20 gen
41	202.6	54.9	1172	22	AAZ15339	Yeast AGA2 aggluti
42	202.6	54.9	1172	24	AAZ27164	Yeast cell wall pr
43	202.2	54.8	357	22	AAS03439	DNA encoding anti-
44	202.2	54.8	360	22	AAH47724	Nucleotide sequenc
45	201.8	54.7	1774	20	AAZ20419	Antibody ABX-CBL h

ALIGNMENTS

RESULT 1

AAT15725
ID AAT15725 standard; cDNA; 357 BP.

XX AAT15725;

XX AAT15725;

DT 25-JUN-1996 (first entry)

DE 3B1 heavy chain variable region DNA from pCIB4613.

XX delta endotoxin; Bacillus thuringiensis; western corn rootworm;
KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
KW antibody; ss.

XX Insecta sp.

XX WO9600783-A1.

XX 11-JAN-1996.

PF 20-JUN-1995; 95WO-IB00497.

PR 28-JUN-1994; 94US-0267641.

XX (CIBA) CIBA GEIGY AG.

PI Carozzi NB, Koziel MG;

XX WPI; 1996-077494/08.

DR P-PSDB; AAR90829.

XX New monoclonal antibodies which bind insect gut proteins - used


```
Query Match      78.2%; Score 288.6; DB 18; Length 345;
Best Local Similarity 89.7%; Pred. No. 1.3e-76;
Matches 331; Conservative 0; Mismatches 14; Indels 24; Gaps 1;

QY 1 GAAGTGATGCTGGAGTCTGGTGGAGGATTGGTGACGCTAAAGGGTCAATTGAAACTC 60
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Db 1 GAGGTGCAGCTTGTGTGAGTCTGGTGGAGGATTGGTGACGCTAAAGGGTCAATTGAAACTC 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TCATGTGCAGGCTCTGGATTCACTTCAATAAAGTACGCCATGAATTTGGTCCGCCAGGCT 120
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Db 61 TCATGTGCAGGCTCTGGATTCACTTCAATAAAGTACGCCATGAATTTGGTCCGCCAGGCT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CCAGGAAGGGTTGGATGGGTTGCTCGCATAGAAAGTAAAGTAATAATTATGCAACA 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CAAGGAAGGGTTGGATGGGTTGCTCGCATAGAAAGTAAAGTAATAATTATGCAACA 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TATTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 CTCTATCTGCAAAATCAACAACCTTCAAAAGTACGAGCAGCATGTATTACTGTGTGAGA 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CTCTATCTGCAAAATCAACAACCTTCAAAAGTACGAGCAGCATGTATTACTGTGTGAGA 300
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QY 301 CGGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGGTCAAGGAACCTCACTCACC 360
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QY 361 GTCCTCTCA 369
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Db 337 GTCCTCTCA 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
AAT58261
ID AAT58261 standard; CDNA; 330 BP.
AC AAT58261;
XX
DT 22-AUG-1997 (first entry)
DE Lead binding MAB 6F5 heavy chain variable region encoding cDNA.
XX
KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..330
FT /tag= a
FT /note= "no stop codon given"
XX
PN WO9639518-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US09258.
XX
PR 10-OCT-1995; 95US-0541373.
PR 03-JUN-1995; 95US-0462798.
XX
PA (BION-) BIONEERASKA INC.
XX
PI Lopez O, Murray PJ, Wylie DE;
XX
DR WPI; 1997-043140/04.
DR P-PSDB; AAW01587.
XX
PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as
PT lead cations
```

```
XX Claim 1; Page 76; 125pp; English.
PS
CC The present sequence encodes the heavy chain variable region for
CC monoclonal antibody (MAB) 6F5, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from hybridoma cells from
CC mouse spleen cells. The protein can be used for binding heavy metals,
CC such as lead cations. It can be used for detecting, removing, adding
CC or neutralising the heavy metals in biological and inanimate systems.
CC It can be used in e.g. aqueous liquid systems, in biological or
CC environmental systems or in such compositions as perfumes, cosmetics,
CC pharmaceuticals, health care products, skin treatment products,
CC pesticides, herbicides, solvents used in the production of semi-
CC conductor and integrated circuit components and production materials
CC for electronic components.
XX
SQ Sequence 330 BP; 93 A; 73 C; 82 G; 82 T; 0 other;
Query Match      77.1%; Score 284.4; DB 18; Length 330;
Best Local Similarity 93.4%; Pred. No. 2.4e-75;
Matches 297; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 16 GAGTCTGGTGGAGGATTGGTGACGCTAAAGGGTCAATTGAAACTCTCATGTGCAAGCTCT 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAGTCTGGTGGAGGATTGGTGACGCTAAAGGGTCAATTGAAACTCTCATGTGCAAGCTCT 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 76 GGATTCACTTCAATAACTACGCCCATGAATTTGGTCCGCCAGGCTCCAGGAAGGGTTTG 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GGATTCACTTCAATAACTACGCCCATGAATTTGGTCCGCCAGGCTCCAGGAAGGGTTTG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 GAATGGGTGCTCGCATAGAAGTAAAGTAATAATTATGCAAGCTTTTATGCCGATTC 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GAATGGGTGCTCGCATAGAAGTAAAGTAATAATTATGCAAGCTTTTATGCCGATTC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 196 GTGAAGACAGGTTCAACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTCAAAATG 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GTGAAGACAGGTTCAACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTCAAAATG 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 AACAACTTGAAGAACTGAGGACACAGCCATGATTACTGTGTGAGCGGGGCTTCAGGG 315
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AACAACTTGAAGAACTGAGGACACAGCCATGATTACTGTGTGAGCGGGGCTTCAGGG 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 316 ATTGACTATGCTATGGAC 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GCCCAAGGACTCTGGTC 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
AAA40202
ID AAA40202 standard; DNA; 375 BP.
XX
AC AAA40202;
XX
DT 01-NOV-2000 (first entry)
DE
DE H. pylori 26 kDa protein-binding antibody heavy chain encoding DNA.
XX
KW Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; heavy chain; ds.
XX
OS Unidentified.
XX
PN WO200026671-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-EP08212.
XX
PR 29-OCT-1998; 98EP-0120517.
PR 06-NOV-1998; 98EP-0120687.
XX
PA (CONN-) CONNEX GMBH.
XX
```


CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is a DNA encoding murine antibody 1D9 heavy chain
 CC variable region.

XX SQ Sequence 443 BP; 117 A; 97 C; 108 G; 121 T; 0 other;

Query Match 73.0%; Score 269.2; DB 22; Length 443;
 Best Local Similarity 94.0%; Pred. No. 9.4e-71;
 Matches 280; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGACGCTAAAGGTCATTGAAACTC 60
 DB 58 GAGGTGCAGCTTGTAGCTGGAGGAGGATTGGTGACGCTAAAGGTCATTGAAACTC 117
 QY 61 TCATGTGCAGCTCTGGATTACCTTCAATAACTACGCCATGAATTTGGTCCGCGAGCT 120
 DB 118 TCATGTGCAGCTCTGGATTACCTTCAATAACTACGCCATGAATTTGGTCCGCGAGCT 177
 QY 121 CCAGGAAGGGTTTGGAAATGGTCTGCATAGAGTAAAGTAAATAATTATGCAACA 180
 DB 178 CCAGGAAGGGTTTGGAAATGGTCTGCATAGAGTAAAGTAAATAATTATGCAACA 237
 QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCTCTCCAGAGATGATTCACAAAGCATG 240
 DB 238 TATTATGCCGATTCAGTGAAGACAGATACACCATCTCCAGAGATGATTCACAAAGCATG 297
 QY 241 CTCATCTGCAATGACAACTTGAATACTGAGGACAGCCATGTTACTGTGTGA 298
 DB 298 CTCATCTGCAATGACAACTTGAATACTGAGGACAGCCATGTTACTGTGTGA 355

RESULT 8

AAD13179

ID AAD13179 standard; DNA; 357 BP.

XX AC AAD13179;

DT 16-OCT-2001 (first entry)

DE Humanised murine antibody heavy chain 1D9RHA DNA.

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disease; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; antibody 1D9 heavy chain; 1D9RHA; ds.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT CDS

FT 1..357

FT /*tag= a

FT /product= "Humanised murine antibody heavy chain

FT region, 1D9RHA"

FT /note= "CDS does not include start and stop codon"

FT /partial

XX W0200157226-A1.

PN

PD 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03537.

XX 03-FEB-2000; 2000US-0497625.

XX (MILL-) MILLENNIUM PHARM INC.

PA Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX WPI; 2001-488888/53.

DR P-PSDB; AAE07034.

XX Humanized immunoglobulin for treating a CC-chemokine receptor

PT 2-mediated disorder in a patient, comprises a binding specificity for

PT CCR2, and a non-human antigen binding region and human immunoglobulin

PT -

XX Claim 64; Fig 23; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is a DNA encoding humanised murine antibody heavy
 CC chain region, 1D9RHA. 1D9RHA sequence consist of the complementarity
 CC determining regions (CDRs) of the murine 1D9 antibody heavy chain
 CC variable (VH) region genetically inserted into the framework regions
 CC (FRs) of the human 4B4/CL antibody VH region.

XX Sequence 357 BP; 99 A; 79 C; 95 G; 84 T; 0 other;

QY Query Match 67.5%; Score 249.2; DB 22; Length 357;

DB Best Local Similarity 90.5%; Pred. No. 8.6e-65;

DB Matches 266; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGACGCTAAAGGTCATTGAAACTC 60

DB 1 GAGGTGCAATTTGGTGTAGTCTGGAGGAGGATTGGTGAAGCTGGGGGTCATTGAGACTC 60

QY 61 TCATGTGCAGCTCTGGATTACCTTCAATAACTACGCCATGATTTGGTCCGCGAGCT 120

DB 61 TCATGTGCAGCTCTGGATTACCTTCAATAACTACGCCATGATTTGGTCCGCGAGCT 120

QY 121 CCAGGAAGGGTTTGGAAATGGTCTGCATAGAGTAAAGTAAATAATTATGCAACA 180

DB 121 CCAGGAAGGGTTTGGAAATGGTCTGCATAGAGTAAAGTAAATAATTATGCAACA 180

QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCTCTCCAGAGATGATTCACAAAGCATG 240

DB 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCACAAAGCATG 240

QY 241 CTCATCTGCAATGACAACTTGAATACTGAGGACAGCCATGTTACTGT 294

DB 241 CTCATCTGCAATGACAACTTGAATACTGAGGACAGCCATGTTACTGT 294

CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the sESTs. Proteins encoded by the sESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AA45946 to AA45931 represent linker variants which are given
CC in the exemplification of the present invention.

XX
SQ Sequence 359 BP; 91 A; 66 C; 93 G; 109 T; 0 other;

Query Match 61.2%; Score 225.8; DB 21; Length 359;
Best Local Similarity 95.1%; Pred. No. 8.9e-58;
Matches 233; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATGGTGAGGCTAAAGGGTCAATGAAATC 60
DB 114 GAGTGCAGCTGTTGAGTCTGGTGGAGGATGGTGAGGCTAAAGGGTCAATGAAATC 173
QY 61 TCATGTGCAGCCTCTGGATTCACCTCAATAACTACCCATGAATGGGTCCGCCAGGCT 120
DB 174 TCATGTGCAGCCTCTGGATTCACCTCAATAACTACCCATGAATGGGTCCGCCAGGCT 233
QY 121 CCAGGAAGGGTTGGAAATGGTGGTTCGCATAGAAAGTAAAGTAAATATGCAACA 180
DB 234 CCAGGAAGGGTTGGAAATGGTGGTTCGCATAGAAAGTAAAGTAAATATGCAACA 293
QY 181 TTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
DB 294 TATTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 353
QY 241 CTCTCA 245
DB 354 CTCGA 358

RESULT 11
AAT79537
ID AAT79537 standard; DNA: 5227 BP.

XX
AC AAT79537;
XX
DT 06-MAR-1998 (first entry)
XX
DE Plasmid pTERMSC2H10myc3sCAM.
XX
KW Protein-protein interaction; interacting polypeptide;
KW polyphage principle; plasmid pTERMSC2H10myc3sCAM; vector;
KW Escherichia coli display; peptide library; ds.
XX
OS Synthetic.

XX
PN WC9732017-A1.
XX
PD 04-SEP-1997.
XX
PF 26-FEB-1997; 97WO-EP00931.
XX
PR 26-FEB-1996; 96EP-0102852.
XX
PA (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX
PI Ge L, Ilag V;
XX
DR WPI; 1997-448687/41.

XX
PT Identification of interacting polypeptide encoding nucleic acid
PT sequences - e.g. to identify protein-protein interactions, which
PT play an important role in biological processes

XX
PS
XX
CC Example 8; Fig 25; 105pp; English.

CC Plasmid pTERMSC2H10myc3sCAM (AAT79537) can be used in a novel method
CC for identifying nucleic acid sequences (NAS), which encode
CC polypeptides capable of interacting with at least 1 of their fellow
CC polypeptides. This comprises: (a) providing a 1st library of
CC recombinant vectors containing genetically diverse NAS comprising a
CC variety of NAS encoding polypeptides; (b) providing a 2nd library of
CC recombinant vectors containing genetically diverse NAS comprising a
CC variety of NAS encoding polypeptides capable of interacting with
CC the polypeptides of (a), where the vectors employed for production
CC of the recombinant vectors and/or recombinant inserts display
CC properties that are phenotypically distinguishable from those used
CC in (a), and where at least 1 of the properties displayed by the
CC vectors and/or recombinant inserts used in steps (a) and (b), upon
CC the interaction of a polypeptide from the 1st library with a
CC polypeptide from the 2nd library, together generate a screenable or
CC selectable property; (c) expressing members of the libraries of
CC recombinant vectors or nucleic acid sequences of (a) and (b), in
CC appropriate host cells so that at least 1 interaction is
CC established; and (d) selecting for the generation of the
CC screenable or selectable property representing the interaction of
CC the polypeptides. The method can be used to identify protein-protein
CC interactions.

XX
SQ Sequence 5227 BP; 1232 A; 1265 C; 1355 G; 1375 T; 0 other;

Query Match 58.4%; Score 215.4; DB 18; Length 5227;
Best Local Similarity 76.7%; Pred. No. 2.9e-54;
Matches 283; Conservative 0; Mismatches 71; Indels 15; Gaps 1;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATGGTGAGGCTAAAGGGTCAATGAAATC 60
DB 1830 GAAGTTAAACTGGTTCGAGTCTGGAGGAGGCTGGTGAACCTCGAGGATCCATGAAATC 1889
QY 61 TCATGTGCAGCCTCTGGATTCACCTCAATAACTACCCATGAATGGGTCCGCCAGGCT 120
DB 1890 TCCTGTGTTGCCCTCGGAATCACTTTTCAGTAATACCGGATGAATGGGTCCGCCAGTCT 1949
QY 121 CCAGGAAGGGTTGGAAATGGTGGTTCGCATAGAAAGTAAAGTAAATATGCAACA 180
DB 1950 CCAGGAAGGGGGCTTGAGTGGTTCGTAATAGATTGAATCTAATAATATGCAACA 2009
QY 181 TTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
DB 2010 CATATGCGGAGTCTGTGAAGGGAGGTTCCACCATCTCAAGAGATGATTCACAAAGTAGT 2069
QY 241 CTCTATCTGCAAAATGAACAACTTGAAACCTGAGGACACAGCCATCTATTCTGTGTGAGA 300
DB 2070 GTCTACCTGCAATGAACAACTTAAGAGCTGAAGACACTGGCATTTTATTACTG----- 2122
QY 301 CGGGGGGCTTCAGGGATTTGACTATGCTATGGACTACTGGGGTCCANGAACTCTACTCACC 360
DB 2123 -----TAGAGGGGTTTCATATACATAGACTACTGGGGTCCANGAACTCTAGTCACA 2174
QY 361 GTCTCTCTCA 369
DB 2175 GTCTCTCTCA 2183

RESULT 12
AAS03515
ID AAS03515 standard; cDNA; 369 BP.

XX
AC AAS03515;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 103.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.

```
XX OS Homo sapiens.
XX PN WO200127279-A1.
XX PD 19-APR-2001.
XX PF P-PSDB; RAU02615.
XX PR 11-OCT-2000; 2000WO-GB03900.
XX PR 12-OCT-1999; 99US-0158812.
XX PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Edwards BM, Main SH, Vaughan TJ;
XX WPI: 2001-282031/29.
XX DR P-PSDB; RAU02615.
XX PT Panel of specific binding members of antibody molecules which bind to
XX related diseases -
XX PS Disclosure; Page 164; 182pp; English.
XX AA503401-AAS03535 represent anti-adipocyte monoclonal antibody heavy
XX and light chain coding sequences of the invention. The antibodies can be
XX used in the treatment of obesity and obesity related diseases. The
XX antibodies can be used to deliver drugs or pro-drugs directly to the fat
XX mass of an obese patient or the antibody can be used as a therapeutic
XX itself. Antibodies binding specifically to adipocytes can be used to
XX activate the immune system to destroy the cells by complement mediated
XX lysis. The antibodies may be labeled with a detectable label such as
XX radiolabel, fluorescent or chemical group and used in methods of
XX diagnosis in human subjects e.g. to determine the presence of adipocyte
XX antigen on the surface of an adipocyte to detect or determine the
XX presence or level of adipocytes in a cell or tissue sample. The
XX antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease.
XX SQ Sequence 369 BP; 81 A; 90 C; 122 G; 76 T; 0 other;

Query Match 58.2%; Score 214.6; DB 22; Length 369;
Best Local Similarity 74.2%; Pred. No. 2e-54;
Matches 271; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1 GNAAGTGATCGTGGTGGAGTCTGGTGGAGGATTGGTGGACGCTTAAGGGTCAATTGAAACTC 60
DB 1 GAGGTCCAGCTGGTGCAGCTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAAACTC 60
QY 61 TCATGTGCGAGCCTCTGGATTACCTTACCTTAATTAAGTACGCGCATGAATTTGGTCCGCCAGGCT 120
DB 61 TCTGTGAGCCTCTGGGTTCACCTTCAGTGGCTCTGTATGTCATGGTCCGCCAGGCT 120
QY 121 CCAGGAAAGGGTTTGGAAATGGGTTGCTCGCATAGAAAGTAAAGTAATAATATATCAACA 180
DB 121 TCCGGAAAGGGCTGGAGTGGGTTGGCCGCTATTAGAACAAGCTAACAGTTTACCGGACA 180
QY 181 TTTTATGCGGATTGAGTGAAGACAGGTTTACCATTCTCCAGAGATGATTCACAAAGCATG 240
DB 181 GCATATGTGCTGCGTGGTGAAGGAGGTTCCACCTCTCCAGAGATGATTCACAAAGACAG 240
QY 241 CTCATCTGCAATCAACAACTTGAACCTTGAACCTGAGGACAGCCATCTATTACTGTGTGAGA 300
DB 241 GGTATCTGCAATGAACAGCCTTGAACCCGAGGACAGCGGCTGTATTACTATTACTAGA 300
QY 301 CCGGGGGGTTTACAGGATTGACTATGCTATGGACTACTGGGGTCAAGGAACCTCACTACC 360
DB 301 CCTGAGATAGCAGTGGCGGTATGGGGAGGAGGACTACTGGGGAGGCGGCCCTGTGTACC 360
QY 361 GTCTC 365
DB 11111
```

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Db 361 GTCTC 365

RESULT 13
ABK47271
ID ABK47271 standard; DNA; 761 BP.
XX AC ABK47271;
XX DT 18-JUN-2002 (first entry)
XX DE Insulin/insulin-like growth factor receptor, DNA sequence #25.
XX KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
XX KW ophthalmological; insulin; receptor; gene therapy; diabetes;
XX KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
XX KW diabetic retinopathy; neurological diseases; stroke;
XX KW diabetic neuropathy; gene; ss.
XX OS Synthetic.
XX PN WO200172771-A2.
XX PD 04-OCT-2001.
XX PF 29-MAR-2000; 2000WO-US08528.
XX PR 29-MAR-2000; 2000WO-US08528.
XX PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX PI (NOVO) NOVO NORDISK AS.
XX PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
XX PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
XX PI Hansen PH, Ravera M, Hsiao K;
XX WPI: 2002-025774/03.
XX DR Modulating insulin activity in mammalian cells, for treating e.g.
XX PT diabetes and tumours, comprises using peptides that bind to insulin or
XX PT insulin-like growth factor receptors
XX PS Example 1; Figure 19; 390pp; English.
XX The invention relates to a method of modulating insulin activity in
XX mammalian cells by administering a peptide that binds the insulin
XX receptor (IR). A composition containing a peptide, optionally expressed
XX from gene therapy vectors, that binds to Site 1 of IR and an insulin
XX agonist are useful for treating diabetes. Also, peptides that are
XX antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
XX useful for treating insulin-like growth factor (IGF)-sensitive tumours
XX (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
XX receptor agonists are useful for treating neurological diseases,
XX including stroke and diabetic neuropathy. The peptides are also useful in
XX screening for compounds that bind to IR or IGF-1 receptor, potential
XX therapeutics and research reagents. ABK47246-ABK47277 represent IR
XX and/or IGF-1 receptor DNA sequences of the invention.
XX SQ Sequence 761 BP; 179 A; 201 C; 219 G; 162 T; 0 other;

Query Match 58.2%; Score 214.6; DB 24; Length 761;
Best Local Similarity 74.2%; Pred. No. 2.6e-54;
Matches 271; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 5 TCATCTGCTGGTGGAGTCTGGTGGAGGATTGGTCCAGCCTTAAGGGTCAATTGAAACTCTCAT 64
DB 23 TGCACCTGCTGGAGTCTGGGGGAGGCTTGGTAAAGCTGGGGGGTCCCTTAGACTCTCTCT 82
QY 65 GTGACGCTCTGGATTACCTTCAATACTACGCCATGAATTTGGTCCGCCAGGCTCCAG 124
DB 83 GTGACGCTCTGGATTACCTTTCAGTACGCCCTGGATGAGTGGGTCCGCCAGGCTCCAG 142
QY 125 GAAAGGGTTTGAATGGGTTGCTCGCATAGAAGTAAAGTAATAATATATGCAACATTTT 184
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DR P-PSDB; AAU72865.

XX Multifunctional polypeptides comprising binding sites that specifically
XX recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -

XX Example 7; Fig 16; 114pp: English.

XX The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. The sequences represent DNA encoding the
XX polypeptides of the invention.

SQ Sequence 768 BP; 179 A; 192 C; 203 G; 194 T; 0 other;

Query Match 57.7%; Score 212.8; DB 24; Length 768;
Best Local Similarity 76.4%; Pred. No. 9e-54;
Matches 278; Conservative 0; Mismatches 77; Indels 9; Gaps 1;

QY	6	GATGCTGGTGGAGTCTGGTGGAGGATTTGGTCGAGCTAAAGGTCATTGAAACTCTCATG	65
DB	9	GCTGCTCGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCCTG	68
QY	66	TGCAGCCTCTGGATTCACTTCAATAACTACGCCCATGAATTGGTCCGCCAGCTCCAGG	125
DB	69	TGTTGCTCTGGATTCACTTTCAGTAACACTACTGGATGAACCTGGTCCGCCAGCTCCAGA	128
QY	126	AAAGGTTTGGAAATGGGTTGCTCGCATAGAAGTAAAGTAATAATATGCAACATTTTA	185
DB	129	GAAGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTAATAATTATGCAACACATTA	188
QY	186	TGCCGATTCCAGTGAAGACAGCTTACCACATCTCCAGAGATGATTCACAAGCATGCTCTA	245
DB	189	TGCGGAGTCTGTGAAGGAGGAGTTCCACCATCTCAAGAGATGATTCAAAAGTAGTGTCTA	248
QY	246	TCTGAAATGAACAACTTGAAACTGAGGACACAGCCATGTATTACTGTGTGAGACGGGG	305
DB	249	CCTGCAATGAACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTACCAGGC----	304
QY	306	GGCTTCAGGGATTGACTATGCTATGAGCTACTGGGGTCAAGGAACCTCACTCACCGTCTC	365
DB	305	-----TCCCTACGGCTTTGCTATGACTACTGGGGCCCAAGGACACCGGTCAACGCTCTC	359
QY	366	CTCA	369
DB	360	CTCA	363

Search completed: November 27, 2002, 03:53:36
Job time : 213.234 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:45:51 ; Search time 1529.71 Seconds
(without alignments)
3906.706 Million cell updates/sec

Title: US-09-893-615-86

Perfect score: 369

Sequence: 1 GAAGTATGCTGGTGAGTC.....CCTCACTACCGTCTCTCTCA 369

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_estl.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_othr.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284.4	77.1	865	13	BI150936 602916745
2	230.4	62.4	932	12	BF135929 601781259
3	229.8	62.3	700	12	BG757291 602715276
4	220.2	59.7	1039	14	BQ937972 AGENCOURT
5	218.4	59.2	522	10	AW401500 UI-HF-BK0
6	212.8	57.7	552	17	BH319627 CH230-119

ALIGNMENTS

RESULT 1
BI150936
LOCUS 602916745F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5067346 5',
DEFINITION mRNA sequence.
ACCESSION BI150936
VERSION BI150936.1 GI:14610937
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L2AM1181 row: 1 column: 11
High quality sequence stop: 797.
Location/Qualifiers 1. .865

7	212	57.5	359	10	BB843560
8	203	55.0	711	12	BG759283
9	202.2	54.8	560	12	BF581663
10	201.4	54.6	861	12	BG754897
11	201.2	54.5	966	14	BQ711793
12	200.8	54.4	693	12	BG684987
13	199.4	54.0	548	12	BF119726
14	198.2	53.7	909	14	BQ706843
15	198.2	53.7	931	14	BQ712530
16	197.8	53.6	483	10	AW402331
17	197.4	53.5	1526	11	BC011342
18	197.2	53.4	503	10	AW402572
19	197.2	53.4	907	14	BQ708724
20	197.2	53.4	1001	14	BM914366
21	197	53.4	430	10	AW402433
22	196.8	53.3	830	12	BG756192
23	196.6	53.3	476	17	BH114467
24	196.6	53.3	837	13	BG966355
25	196.4	53.2	446	10	AW504516
26	195.8	53.1	625	17	BH021344
27	194.6	52.7	476	10	AW404015
28	193.4	52.4	866	14	BQ707524
29	192.4	52.1	565	12	BG686641
30	190.4	51.6	516	10	AW402430
31	190.2	51.5	618	14	BM713479
32	190.2	51.5	870	12	BG684039
33	190.2	51.5	987	12	BF577496
34	190	51.5	898	14	BQ711108
35	189.8	51.4	932	12	BG341370
36	189.2	51.3	1164	12	BF974771
37	187.8	50.9	861	13	BI455668
38	187	50.7	880	14	BQ709039
39	187	50.7	914	12	BF163883
40	187	50.7	915	14	BQ707232
41	187	50.7	957	14	BQ709536
42	186.4	50.5	864	13	BM008425
43	185.8	50.4	613	13	BM007656
44	185.2	50.2	452	14	BM818764
45	185	50.1	1012	12	BF142302

BB843560 BB843560
BG759283 602710970
BF581663 602099628
BG754897 602714288
BQ711793 AGENCOURT
BG684987 602636738
BF119726 601758583
BQ706843 AGENCOURT
BQ712530 AGENCOURT
AW402331 UI-HF-BK0
BC011342 Mus muscu
AW402572 UI-HF-BK0
BQ708724 AGENCOURT
BM914366 AGENCOURT
AW402433 UI-HF-BK0
BG756192 602713494
BH114467 RPCI-24-3
BG966355 602832843
AW504516 UI-HF-BN0
BH021344 CT7-463K1
AW404015 UI-HF-BK0
BQ707524 AGENCOURT
BG686641 602637877
AW402430 UI-HF-BK0
BM713479 UI-E-EJ0-
BG684039 602635646
BF577496 602092343
BQ711108 AGENCOURT
BG341370 602463849
BF974771 602245420
BI455668 603173862
BQ709039 AGENCOURT
BF163883 601772396
BQ707232 AGENCOURT
BQ709536 AGENCOURT
BM008425 603617419
BM007656 603617080
BM818764 K-EST0086
BF142302 601791844

Plate: LLC1704 row: h column: 20

High quality sequence stop: 696.

FEATURES

Location/Qualifiers

source

1..700
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:485363"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 140 a 199 c 209 g 152 t

Query Match 62.3%; Score 229.8; DB 12; Length 700;
Best Local Similarity 76.4%; Pred. No. 4.4e-56;
Matches 282; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 1 GAAGTGATGCTGGTGAGTCTGGTGAGGATTGGTGACGCTAAAGGGTCAATTGAAACTC 60
DB 103 GAGGTGCACCTGGTGAGTCTGGGGAGGCTTGGTCCACCCCTGGGGGGTCCCTGAAACTC 162
QY 61 TCATGTGACGCTCTGGATTCACTTCAATAACTAGCCCAATTAATGGTCCGCCAGGCT 120
DB 163 TCCTGTGACGCTCTGGGTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 222
QY 121 CCAGGAAAGGCTTGGAAATGGGTTGCTCCGTAAGAAAGTAAAGTAATTAATATGCAACA 180
DB 223 TCCGGGAAGGCTGGAGTGGGTTGGCCGCTAGAGCAAACTAAGAAATTAACGGACA 282
QY 181 TTTTATGCGGATTCAGTGAAGACAGGTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 240
DB 283 GAATATATTCGCTGGTGAAGGAGGTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 342
QY 241 CTCATCTCAATGAACAACTTGAACACTGAGGACACAGCCATGATTTACTGTGTGAGA 300
DB 343 CGGTTTCTGCAATGATAGCTGGAACCGAGGACACGCGCTGATTTACTGTGTGAGA 402
QY 301 CGGGGGCTTCAGGATTCATCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360
DB 403 GCGGTTCACGAGGGGTATTATTACGGTATGGACGCTCGGGGCCAAGGGACACGCTCACC 462
QY 361 GTCTCCTCA 369
DB 463 GTCTCCTCA 471

RESULT 4
BO937972
LOCUS BO937972 1039 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8952769 NCI_CGAP_C024 Mus musculus cDNA clone
IMAGE:6474993 5', mRNA sequence.
ACCESSION BO937972
VERSION BO937972.1 GI:22353438
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1039)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC14013 row: a column: 10
High quality sequence stop: 612.

FEATURES

source

1..1039
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6474993"
/clone_lib="NCI_CGAP_C024"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 263 a 263 c 257 g 242 t 14 others

Query Match 59.7%; Score 220.2; DB 14; Length 1039;
Best Local Similarity 74.8%; Pred. No. 3.1e-53;
Matches 276; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 1 GAAGTGATGCTGGTGAGTCTGGTGAGGATTGGTGACGCTAAAGGGTCAATTGAAACTC 60
DB 116 GAAGTGAACCTTGAAGAGGCTGGAGGAGCTTGGTGCAACCTGGAGGATCCATGAAACTC 175
QY 61 TCATGTGACGCTCTGGATTCACTTCAATAACTAGCCCAATTAATGGTCCGCCAGGCT 120
DB 176 TCCTGTGCTCTGGTTCAGTTCATTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 235
QY 121 CCAGGAAAGGCTTGGAAATGGGTTGCTCCGTAAGAAAGTAAAGTAATTAATATGCAACA 180
DB 236 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTAGATTGAGATCTAATAATATGCAACA 295
QY 181 TTTTATGCGGATTCAGTGAAGACAGGTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 240
DB 296 CATTATGCGGAGTCTGTGAAGGGAGGTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 355
QY 241 CTCATCTCAATGAACAACTTGAACACTGAGGACACAGCCATGATTTACTGTGTGAGA 300
DB 356 GTCTACCTCAATGAACAACTTGAAGCTGAGGACACTGGCATTATTTACTGTACCAGG 415
QY 301 CGGGGGCTTCAGGGATTGACTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360
DB 416 AGGGGTATGGTGACCCCTAACTGGTACTTCTGGGGCCGAGGACACGCTCACC 475
QY 361 GTCTCCTCA 369
DB 476 GTCTCCTCA 484
RESULT 5
AW401500
LOCUS AW401500 522 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BK0-aaU-b-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055046 5', mRNA sequence.
ACCESSION AW401500
VERSION AW401500.1 GI:6920108
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

musculus cDNA clone F430102008 5', mRNA sequence.

BB843560
 VERSION BB843560.1 GI:17081927
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS 1 (bases 1 to 359)
 Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

JOURNAL
 COMMENT Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 , M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
 e mouse tissues.

FEATURES
 source
 1. 359
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="F430102008"
 /clone.lib="RIKEN full-length enriched, 6 days neonate spleen"
 /tissue_type="spleen"
 /dev_stages="6 days neonate"
 /note="vector: pSPORT1; Site:1: SalI; Site:2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dt)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000,

Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

Mol Genet 7: 1967-1978."

BASE COUNT 90 a 69 c 91 g 109 t
 ORIGIN

Query Match 57.5% Score 212; DB 10; Length 359;
 Best Local Similarity 93.6%; Pred. No. 5,3e-51;
 Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCCTAAAGGCTCATTTGAACATC 60
 II III III III III III III III III III III III III III III III III III III
 Db 124 GAGGTGCAGCTTGTGTTGAGTCTGGTGGAGGATTGGTGCAGCCCTAAAGGATCATTTGAACATC 183
 QY 61 TCATGTGCAGCCTCGGATTTCACCTTCAATTAAGTACCTAGGCATCAATTTGGTCCGCCAGGCT 120
 III III III III III III III III III III III III III III III III III III III
 Db 184 TCATGTGCCGCTCTGGTTTCACTTCAATCACTATGCATGCATCTGGTCCGCCAGGCT 243
 QY 121 CCAGGAAAGGGTTTGAATGGTTCTCGCTAAGAAAGTAAAGCTAAATTAATTTATGCAACA 180
 III III III III III III III III III III III III III III III III III III III
 Db 244 CCAGGAAAGGGTTTGAATGGTTCTCGCTAAGAAAGTAAAGTAGTAGTAATTTATGCAACA 303
 QY 181 TTTTATGCCGATTCAGTGAAGACAGAGTTTCCACCTCTCCAGAGATCATTTCAACAAG 236
 I III III III III III III III III III III III III III III III III III III
 Db 304 TATTATGCCGATTCAGTGAAGACAGAGTTTCCACCTCTCCAGAGATCATTTCAACAAG 359

RESULT 8
 BG759283
 LOCUS 602710970F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851232 5',
 DEFINITION mRNA sequence.
 ACCESSION BG759283
 VERSION BG759283.1 GI:14069936
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 711)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone-distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1693 row: 1 column: 17
 High quality sequence stop: 711.
 Location/Qualifiers
 1. 711
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 /db_xref="taxon:9606"
 /clone="IMAGE:4851232"
 /clone.lib="NIH_MGC_48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DHI0B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."									
BASE COUNT	154 a	209 c	201 g	145 t	2 others				
ORIGIN									
Query Match	55.0%; Score 203; DB 12; Length 711;								
Best Local Similarity	73.4%; Pred. No. 2.8e-48;								
Matches	273;	Conservative	0;	Mismatches	96;	Indels	3;	Gaps	1;
QY	1	GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGTCATTGAAACTC	60						
DB	80	GAGGTGCAGGTGGTGGAGTCTGGGAGGCCCTGAAAAAGCCAGGTCGGTCCCTGAGACTC	139						
QY	61	TCATGTGCAGCCTCTGGATTCACCTTCATATACTACGCCATGAATTTGGTCCGCCAGGCT	120						
DB	140	TCCTGCACAGTTTCTGGATTCACCTTTCCTGACTATGCCATGAATTTGGTCCGCCAGGCT	199						
QY	121	CCAGGAAAGGTTTGAATGGTGTCTGCATTAAGAAGTAAAGTAAATTAATATGCAACA	180						
DB	200	CCANGNAGGGCTGAGTGGGTAGGTCTCATTAAGACAGAGGTCAAGGTGAGACACA	259						
QY	181	TTTTATGCGATTCAGTGAAGACAGGTTCCACTCTCCAGAGATGATTCACAAAGCATG	240						
DB	260	GAATACGCCGCTCTGTAAGAGCAGATTCACCATCTCAAGAGATGATTTCCAAAAGCATC	319						
QY	241	CTCTATTCGAATGACAACTTGAACACTGAGGACAGCCATGTATCTGTGTGAGA	300						
DB	320	GCCTATCTGCAATGAACAGCCTGAGACCGAGGACACAGCGGTGCTACTGTCTGCGC	379						
QY	301	CGGGGGCTTCAGG---GATTGACTATGTATGGACTACTGGGGTCAAGGAACCTCACTC	357						
DB	380	CCGTGGGTGACGGTCTCAGGCTATATGATGTAGGACCTGTGGGGCCAGGACCCAGGTC	439						
QY	358	ACCGTCTCTCA	369						
DB	440	ACCGTCTCTCA	451						
RESULT 9									
BF581663	560, bp mRNA linear EST 12-DEC-2000								
LOCUS	602099628F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4219447 5',								
DEFINITION	mRNA sequence.								
ACCESSION	BF581663								
VERSION	BF581663.1 GI:11655375								
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.								
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)								
JOURNAL	Unpublished (1999)								
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9801 row: h column: 08 High quality sequence stop: 555. Location/Qualifiers								
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source									

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/notes=Organ; B-cells; Vector: pOM7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACAGCAG(C). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGSC Library.

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BASE COUNT	ORIGIN
198 a	255 c 231 g 177 t

Query Match	54.6%	Score	201.4;	DB	12;	Length	861;
Best Local Similarity	73.7%	Pred. No.	8.6e-48;				

[illegible]

RESULT 11

BO711793	BO711793	966 bp	linear	EST 16-JUL-2002		
LOCUS	AGENCOURT-B487710	NIH_MGC_113	Homo sapiens	cdna clone IMAGE:6300705		
DEFINITION	5', mRNA sequence.					
ACCESSION	BO711793					
VERSION	BO711793.1	GI:21850692				
KEYWORDS	EST.					
SOURCE	human.					

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 966)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

ncnp://image.llnl.gov
Plate: LLM2515 row: g column: 10
High quality sequence stop: 561.
Location/Qualifiers

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1. .966
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6300705"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
213 a 260 g 202 t
BASE COUNT

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BASE COUNT	213 a	291 c	260 g	202 t	
ORIGIN					
Query Match	54.5%	Score 201.2;	DB 14;	Length 966;	
Best Local Similarity	79.18;	Pred. No. 1e-47;			
Matches 239;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;	
Qy	1	GAAGTGATGCTGGTGGAGCTCTGGTGGAGGATTTGGTGCAGCCTAAAGGTCATTTGAAACTC	60		
Db	120	GAAGTGCAGCTGGTGGAGCTCCGGGGAGGCTTGGTCCAGCCTTGGGGGTCCTTGAAACTC	179		
Qy	61	TCATGTGCAGGCTCTGGAGTTCACCTTCAATTAACACGCCATGAATTGGGTCGCCCAGGCT	120		
Db	180	TCCGTGCAGGCTCTGGGTTACCTTCACTAGTGGCTCTACTATGCACCTGGGTCGCCCAGGCT	239		
Qy	121	CCAGGAAAGGGTTTGGAAATGGGTTGCTCGCATAGAAGTAAAGCTAATTAATTATCAACA	180		
Db	240	TCCGGGAAAGGGCTGGAGTGGGTTGGCCGTATTAGACGCAAGCTTCACAGTTTACCGGACA	299		
Qy	181	TTTTATGCCGATTTCAGTCAAGACAGAGGTTTACCATTCTCCAGAGATGATTTACAAAGCATG	240		
Db	300	TCATATGTCGGTCGGTGAAGGACAGGTTCAACATCTCCAGAGATGATTTCAAGAACAACG	359		
Qy	241	CTCTATCTGCAAAATGAACAACCTTGAAGAACTTGAGGACACAGCCATCTATTACTGTGTGAGA	300		
Db	360	CGGTATCTGCAATGAACAACCTGAAGACCAGGACACGGCCGTCTATTACTGTGCTAGA	419		
Qy	301	CG 302			
		+			
Db	420	GG 421			

RESULT 12	
BG684987	
LOCUS	693 bp mRNA linear EST 01-MAY-2001
DEFINITION	602636739f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764440 5',
ACCSSION	BG684987
VERSION	BG684987.1 GI:13916384
KEYWORDS	mRNA sequence.
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Carnivora; Insectivora; Hominoidea; Mammalia; Eutheria; Primates; Carnivora; Insectivora; Hominoidea;
JOURNAL	1 (bases 1 to 693)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: ccapbs@email.nih.gov Tissue Procurement: Louis W. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI621 row: 1 column: 09 High quality sequence stop: 691.

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2476 row: 1 column: 19
High quality sequence stop: 653.

FEATURES

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6282330"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 190 a 274 c 250 g 195 t

Query Match 53.7%; Score 198.2; DB 14; Length 909;
Best Local Similarity 73.2%; Pred. No. 7.5e-47;
Matches 270; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

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QY 1 GAAGTGTGCTGGTGGAGTCTGGTGAGGATTGGTCAGCCTAAAGGGGTCATTGAAACATC 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTCGAGACTC 177

QY 61 TCATGTGCAGCCTCTGGATTCACTTCAATACTAGCCATGATGGTGGTCCGCCAGGCT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 TCTGTGTAGCCTCTGGACTCACCTTAAATAGCTATGCCATGACCTGGGTCCGCCAGGCT 237

QY 121 CCAGGAAAGGGTTTGAATGGGTTGCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 CCAGGAAAGGGTTGAGTGGGTTCTCAAGTATGAGTGGTGGTGTGCTA-----GGACA 291

QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCCAGAGATGATTCACAAAGCATG 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 TACTACCGACACTCCCTGAGGCGCGTTCACCATCTCCAGACACAATTCACAGACATG 351

QY 241 CTCATCTGCAATGAACAACCTTGAACACTGAGGACACAGCCCATGTATTACTGTGTGAGA 300
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Db 352 TTGTTTCTGCAATGAGCAGCCTGAGAACCGAGGACACGCCCATATATTACTGTGGGAAA 411

QY 301 CGGGGGGCTTCAGGGATTGACTATGCTATGAGTCTACTGGGTCAAGGAACCTCACTCACC 360
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Db 412 GCAAGCGCCCACTGGGAACACTACTGTTGGACTCTCTGGGGCCAGGAACGGTGGTCACC 471

QY 361 GTCTCCTCA 369
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Db 472 GTCTCCTCA 480
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RESULT 15
B0712530
LOCUS B0712530 931 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8354768 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281345
5', mRNA sequence.

ACCESSION B0712530
VERSION B0712530.1 GI:21851429
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)

REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2473 row: p column: 18
High quality sequence stop: 597.

FEATURES

Location/Qualifiers
1..931
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6281345"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 190 a 283 c 269 g 189 t

Query Match 53.7%; Score 198.2; DB 14; Length 931;
Best Local Similarity 73.2%; Pred. No. 7.6e-47;
Matches 270; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

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QY 1 GAAGTGTGCTGGTGGAGTCTGGTGAGGATTGGTCAGCCTAAAGGGTTCATTGAAACATC 60
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Db 118 GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTCGAGACTC 177

QY 61 TCATGTGCAGCCTCTGGATTCACTTCAATACTAGCCATGATGGTGGTCCGCCAGGCT 120
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Db 178 TCTGTGTAGCCTCTGGACTCACCTTAAATAGCTATGCCATGACCTGGGTCCGCCAGGCT 237

QY 121 CCAGGAAAGGGTTTGAATGGGTTGCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
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Db 238 CCAGGAAAGGGTTGAGTGGGTTCTCAAGTATGAGTGGTGGTGTGCTA-----GGACA 291

QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
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Db 292 TACTACCGACACTCCCTGAGGCGCGTTCACCATCTCCAGACACAATTCCAAGAACATG 351

QY 241 CTCATCTGCAATGAACAACCTTGAACACTGAGGACACAGCCCATGTATTACTGTGTGAGA 300
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Db 352 TTGTTTCTGCAATGAGCAGCCTGAGAACCGAGGACACGCCCATATATTACTGTGGGAAA 411

QY 301 CGGGGGGCTTCAGGGATTGACTATGCTATGAGTCTACTGGGTCAAGGAACCTCACTCACC 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 GCAAGCGCCCACTGGGAACACTACTGTTGGACTCTCTGGGGCCAGGAACGGTGGTCACC 471

QY 361 GTCTCCTCA 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 GTCTCCTCA 480
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Search completed: November 27, 2002, 05:29:29
Job time : 1554.71 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:35:53 ; Search time 41.3581 Seconds
(without alignments)
2736.194 Million cell updates/sec

Title: US-09-893-615-86

Perfect score: 369

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued_Patents_NA.*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300.4	81.4	357	1 US-08-442-542-1	Sequence 1, Appli
2	300.4	81.4	357	3 US-08-765-469-1	Sequence 1, Appli
3	300.4	81.4	1797	1 US-08-442-542-17	Sequence 17, Appl
4	300.4	81.4	1797	3 US-08-765-469-17	Sequence 17, Appl
5	288.6	78.2	345	3 US-08-767-128-35	Sequence 35, Appl
6	284.4	77.1	330	3 US-08-767-128-23	Sequence 23, Appl
7	227.2	61.6	366	3 US-08-483-749A-1	Sequence 1, Appli
8	213.6	57.9	372	3 US-08-767-128-37	Sequence 37, Appl
9	205	55.6	361	2 US-08-647-144-1	Sequence 1, Appli
10	204.2	55.3	738	2 US-08-224-591-13	Sequence 13, Appl
11	204.2	55.3	738	2 US-08-392-338A-22	Sequence 22, Appl
12	204.2	55.3	738	2 US-08-926-789-13	Sequence 13, Appl
13	204.2	55.3	738	3 US-09-166-750-22	Sequence 22, Appl
14	204.2	55.3	738	3 US-09-166-093-22	Sequence 22, Appl
15	204.2	55.3	738	3 US-09-172-019-22	Sequence 22, Appl
16	204.2	55.3	738	3 US-09-166-094-22	Sequence 22, Appl
17	204.2	55.3	738	5 PCT-US93-11138-13	Sequence 13, Appl
18	204.2	55.3	744	2 US-08-392-338A-12	Sequence 12, Appl
19	204.2	55.3	744	3 US-09-166-750-12	Sequence 12, Appl
20	204.2	55.3	744	3 US-09-166-093-12	Sequence 12, Appl
21	204.2	55.3	744	3 US-09-172-019-12	Sequence 12, Appl
22	204.2	55.3	744	3 US-09-166-094-12	Sequence 12, Appl
23	203	55.0	345	1 US-08-468-661-2	Sequence 2, Appli
24	203	55.0	345	1 US-08-466-272A-2	Sequence 2, Appli
25	203	55.0	345	1 US-08-478-857-2	Sequence 2, Appli
26	203	55.0	345	2 US-08-471-771-2	Sequence 2, Appli
27	203	55.0	345	3 US-09-130-783-2	Sequence 2, Appli

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Sequence 3, Appl
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Sequence 59, Appl
Sequence 33, Appl
Sequence 43, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-08-442-542-1

; Sequence 1, Application US/08442542

; Patent No. 5686600

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine B.

; TITLE OF INVENTION: Antibodies which Bind to Insect Gut

; TITLE OF INVENTION: Proteins and their Use

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ciba-gelgy Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: NY

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/442,542

; FILING DATE: 16-MAY-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/267,641

; FILING DATE: 28-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: CGC 1750

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8615

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..357

; OTHER INFORMATION: /note= "3B1 heavy chain variable

; OTHER INFORMATION: region from pCIB4613"

US-08-442-542-1

;; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
;; NUMBER OF SEQUENCES: 46
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
;; STREET: 3100 No. 6111079west Center, 90 South Seventh St
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/767,128
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/09258
;; FILING DATE: 05-JUN-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/541,373
;; FILING DATE: 10-OCT-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/462,798
;; FILING DATE: 05-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Carter, Charles G.
;; REGISTRATION NUMBER: 35,093
;; REFERENCE/DOCKET NUMBER: 8648.49USF1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612/371-5278
;; TELEFAX: 612/332-9081
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 35:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 345 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 1..345
;; OTHER INFORMATION:
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Best Local Similarity 89.7%; Pred. No. 2.2e-85;
Matches 331; Conservative 0; Mismatches 14; Indels 24; Gaps 1;
QY 1 GAAGTCATGCTGGTGAGTCTGGTGAGGATTGGTGCAGCCCTAAAGGGTCATTGAAATC 60
DB 1 GAGGTGCAGCTGTTGAGTCTGGTGAGGATTGGTGCAGCCCTAAAGGGTCATTGAAATC 60
QY 61 TCATGTGACGCTCTCGATTACCTCAATACTAGCCATGAATGGTCCGCCAGGCT 120
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DB 121 CAAGGAAAGGGTTGGAATGGTGTGCTGCATAAAGTAAGTAATTAATTATGCAACA 180
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DB 301 CGG-----AGGGACTACTGGGGTCAAGGAACCTCACTCACC 336
QY 361 GTCTCTCTCA 369
DB 337 GTCTCTCTCA 345
RESULT 6
US-08-767-128-23
; Sequence 23, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...330
OTHER INFORMATION:
US-08-767-128-23

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Best Local Similarity 93.4%; Pred. No. 5.2e-84;
Matches 297; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 16 GAGTCTGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTCT 75
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Qy 76 GGATTCACCTCAATAACTAGCCATGAATTTGGTCCGCCAGGCTCCAGGAAGGGTTTG 135
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Qy 136 GAATGGTGTCTCGCATAGAGTAAAGTAATAATTATGCAACATTTTATGCCGATTCA 195
Db 121 GAATGGTGTCTCGCATAGAGTAAAGTAATAATTATGCAACATTTTATGCCGATTCA 180
Qy 196 GTGAAGACAGGTTTCCACCATCTCCAGAGATGATTCACAAAGCATCTCTATCTGCAAAATG 255
Db 181 GTGAAGACAGGTTTCCACCATCTCCAGAGATGATTCACAAAGCATCTCTATCTGCAAAATG 240
Qy 256 ACAACTGTAAACTGAGGACACACCCATGATTTACTGTGTGAGAGGGGGCTTCAGGG 315
Db 241 ACAACTGTAAACTGAGGACACACCCATGATTTACTGTGTGAGAGGGGGCTTCAGGG 300
Qy 316 ATTGACTATGCTATGGAC 333
Db 301 GCCCAAGGAGCTCTGGTC 318

RESULT 7
US-08-483-749A-1
; Sequence 1, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CITRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..366
US-08-483-749A-1

Query Match 61.6%; Score 227.2; DB 3; Length 366;
Best Local Similarity 78.0%; Pred. No. 3.2e-65;
Matches 287; Conservative 0; Mismatches 78; Indels 3; Gaps 1;
Qy 1 GAAATGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Db 1 GAAATGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Qy 61 TCATGTGAGCCTCTGGATTACCTTCAATAACTAGCCATGAATTTGGGTCGCCAGGCT 120
Db 61 TCCTGTGTGCTCTGGATTCACTTTTCAGTAATACTACTGGATGAACCTGGGTCGCCAGGCT 120
Qy 121 CCAGGAAAGGGTTTGAATGGTGTCTGCATGAAGAAGTAAAGTAATAATTATGCAACA 180
Db 121 CCAGGAAAGGGTTTGAATGGTGTCTGCATGAAGAAGTAAAGTAATAATTATGCAACA 180
Qy 181 TTTTATGCCGATTTCAGTGAAGACAGAGTTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 CATTATGCCGAGTCTGTGAAGGGAGGTTTCCACCATCTCAAGAGATGATTCACAAAGCATG 240
Qy 241 CTCATCTGCAANTGAACAACTTGAAGTGAAGGACAGACAGCCATGATTTACTGTGTGAGA 300
Db 241 GTCTACCTGCAACTGAACAACTTGAAGTGAAGGACAGCTGGCATTTTATTTACTGTGCCA 298
Qy 301 CGGGGGCTTTCAGGATTGACTATGCTATGGGACTACTGGGGTCAAGGAACCTTCACCTACC 360
Db 299 -GGGAGAGGTACCTCTATTTACTATATGAGTACTGGGGTCAAGGAACCTTCAGTCCACA 357
Qy 361 GTCTCCTC 368
Db 358 GTATCCTC 365

RESULT 8
US-08-767-128-37
; Sequence 37, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079 West Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767.128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1..372

OTHER INFORMATION:

US-08-767-128-37

Query Match 57.9%; Score 213.6; DB 3; Length 372;
Best Local Similarity 75.3%; Pred. No. 9.2e-61;
Matches 280; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGGCTAAAGGTCATTGAAACTC 60
DB 1 GAGTGAAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGGCTGGGGTCTCTGAGACTC 60
QY 61 TCATGTGACGCTCTGGATTACCTTCAATAACTTACCCCATGAATTTGGTCCGCGAGGCT 120
DB 61 TCCTGTGCAACTTCTGGGTTACCTTCACTGATTACTACATGAGCTGGTCCGCGAGGCT 120
QY 121 CCAGGAAGGCTTGGGATGGTGGTCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
DB 121 CCAGGAAGGCACTTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
QY 181 TTTTATGCCGATTCAGTGAAGACAGAGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
DB 181 GAGTACAGTGCATCTGTGAAGGTCGGTTCACCATCTCCAGAGATGATTCACAAAGCATC 240
QY 241 CTCATCTGCAAAATGAACAACCTTGAACAACCTGAGGACACAGCCATGATTTACTGTGTGAGA 300
DB 241 CTCATCTTCAAAATGAACAACCTTGAACAACCTGAGGACAGTGCCTACTTATTTACTGTGCAAGA 300
QY 301 CGGGGGGCTTCAGGAGTTG---ACTATGCTTGGACTTGGGCTCAAGGACCTCACTC 357
DB 301 GATATCTACTGATTAACGACTACTATGCTATGAGTACTGGGCTCAAGGACCTCACTC 360
QY 358 ACCGCTCTCCTCA 369
DB 361 ACCGCTCTCCTCA 372

RESULT 9

US-08-647-144-1

Sequence 1, Application us/08647144

Patent No. 5858728

GENERAL INFORMATION:

APPLICANT: Gram, Hermann

APPLICANT: Di Padova, Franco
APPLICANT: Barclay, George R.
APPLICANT: Poxton, Ian R.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
CITY: Charlotte
STATE: No. 5858728th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,144
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US 08/119,046
APPLICATION NUMBER: 10-SEP-1993
FILING DATE: 22-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 1749-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..361
US-08-647-144-1

Query Match 55.6%; Score 205; DB 2; Length 361;
Best Local Similarity 74.5%; Pred. No. 6e-58;
Matches 275; Conservative 0; Mismatches 85; Indels 9; Gaps 1;

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QY 121 CCAGGAAGGCTTGGGATGGTGGTCTCGCATAGAAGTAAAGTAATAATTATGCAACA 180
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DB 241 CTCATCTTCAAAATGAATGCCCTGAGAACCTGAGGACAGTGCCTACTTATTTACTGTGTAAGA 300
QY 301 CGGGGGGCTTCAGGAGTTGACTATGCTATGAGTACTGGGCTCAAGGACCTCACTCACC 360
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Db 301 CAG-----GGAGGGGGCTATACCTTGGACTATTGGGGTCAAGGAACCTCAGTCACC 351

QY 361 GTCTCCTCA 369
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Db 352 GTCTCCTCA 360

RESULT 10
US-08-224-591-13
; Sequence 13, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..726)
US-08-224-591-13

Query Match 55.3%; Score 204.2; DB 2; Length 738;
Best Local Similarity 74.8%; Pred. No. 1.5e-57;
Matches 276; Conservative 0; Mismatches 78; Indels 15; Gaps 1;

QY 1 GAAGTGATGCTGGTGAGTCTGGTGAGGATGGTGCAGCCCTAAAGGGTCATTGAAACTC 60
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Db 376 GAAGTAAACTGGATGAGACTGGAGGCTGGTGCAACCTGGGAGGCCCATGAAACTC 435

QY 61 TCATGTGACGCTCTGGATTCACCTCAATAACTAGCCCATGAATGGGTCCGCCAGGCT 120
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Db 436 TCGTGTGGCTCTGGATTCATCTTTAGTGACTACTGTGTAACCTGGGTCCGCCAGTCT 495
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QY 121 CCAGGAAGGGTTTGAATGGGTGCTCGCTAAGAAAGTAAATTAATATGCAACA 180
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Db 616 GTCTACCTGCAATGAACAACCTTAAGAGTTGAAGACATGGTATCTATTACTG----- 668

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Db 669 -----TACGGGTCTTACTATGATGGACTACTGGGGTCAAGGAACCTCAGTCACC 720

QY 361 GTCTCCTCA 369
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Db 721 GTCTCCTAA 729

RESULT 11
US-08-392-338A-22
; Sequence 22, Application US/08392338A
; Patent No. 5869620
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,338A
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
US-08-392-338A-22

Query Match 55.3%; Score 204.2; DB 2; Length 738;
Best Local Similarity 74.8%; Pred. No. 1.5e-57;
Matches 276; Conservative 0; Mismatches 78; Indels 15; Gaps 1;

QY 1 GAAGTGATGCTGGTGAGTCTGGTGAGGATGGTGCAGCCCTAAAGGGTCATTGAAACTC 60
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Db 376 GAAGTTAACTGGATGAGACTGGAGGAGCTTGGTGCACACCTGGGAGGCCCATGAAACTC 435
Qy 61 TCATGTCAGCCTCGGATTCACCTCAATAACTACGCCATGAATTTGGTCCGCCAGGCT 120
Db 436 TCCTGTGTGGCTCGGATTCACCTTTAGTGACTACTGGATGAACCTGGTCCGCCAGTCT 495
Qy 121 CCAGGAAGGTTTGGATGGTTCGCGATAGAAAGTAAAGTAATAATATGCAACA 180
Db 496 CCAGGAAGGACTGGAGTGGGTAGCACAAATAGAACAAACCTTATATATGAACA 555
Qy 181 TTTTATCCGATTCAGTGAAGACAGCTTCCACCTCCAGAGATGATTCACAAAGCATG 240
Db 556 TATTATTACAGATTCGTGAAGGAGAGATTCACCATCTCAAGAGATGATTCACAAAGTAGT 615
Qy 241 CTCTATCTGCAAACTTGAACACTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 300
Db 616 GTCTACCTGCAATGAACACTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 668
Qy 301 CGGGGGCTTCAGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 360
Db 669 -----TAGGGTTCTTACTATGGTATGGACTTGGGTCAGGAGTGAAGAGTGAAGAGT 720
Qy 361 GTCTCCTCA 369
Db 721 GTCTCCTAA 729

RESULT 12
US-09-826-789-13
; Sequence 13, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..726)
US-08-926-789-13
Query Match 55.3%; Score 204.2; DB 2: Length 738;
Best Local Similarity 74.8%; Pred. No. 1.5e-57;
Matches 276; Conservative 0; Mismatches 78; Indels 15; Gaps 1;

Qy 1 GAAGTATGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGTCATTGAAACTC 60
Db 376 GAAGTTAACTGGATGAGACTGGAGGAGCTTGGTGCACACCTGGGAGGCCCATGAAACTC 435
Qy 61 TCATGTCAGCCTCGGATTCACCTTCAATAACTACGCCATGAATTTGGTCCGCCAGGCT 120
Db 436 TCCTGTGTGGCTCGGATTCACCTTTAGTGACTACTGGATGAACCTGGTCCGCCAGTCT 495
Qy 121 CCAGGAAGGTTTGGATGGTTCGCGATAGAAAGTAAAGTAATAATATGCAACA 180
Db 496 CCAGGAAGGACTGGAGTGGGTAGCACAAATAGAACAAACCTTATATATGAACA 555
Qy 181 TTTTATCCGATTCAGTGAAGACAGCTTCCACCTCCAGAGATGATTCACAAAGCATG 240
Db 556 TATTATTACAGATTCGTGAAGGAGAGATTCACCATCTCAAGAGATGATTCACAAAGTAGT 615
Qy 241 CTCTATCTGCAAACTTGAACACTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 300
Db 616 GTCTACCTGCAATGAACACTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 668
Qy 301 CGGGGGCTTCAGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 360
Db 669 -----TAGGGTTCTTACTATGGTATGGACTTGGGTCAGGAGTGAAGAGTGAAGAGT 720
Qy 361 GTCTCCTCA 369
Db 721 GTCTCCTAA 729

RESULT 13
US-09-166-750-22
; Sequence 22, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
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	Query Match	55.3%	Score 204.2	DB 3	Length 738
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Qy	61	TCATGTGCAGCCTCTGGATTCACCTTCCAATAACTACGCATGAATTGGGTCCGCCAGGCT	120		
Db	436	TCCTGTGTCGCTCGATTCACATTTTAGTGACCTACTGGGATGAAGTGGGTCCGCCAGTCT	495		
Qy	121	CCAGGAAAGGGTTTGGAAATGGGTTGCTCGCATATAAGAAAGTAAAGTAATTAATTGCAACA	180		
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QY	181	TTTATGCCGATTCAGTGAAGACAGGTTCACCATCTCAGAGATGATTCACAAAGCATG	241
Db	556	TATTATTCAGATTCTGTGAAGGCGATTCACCATCTCAAGAGATGATTCCAAAGTAGT	615
QY	241	CTCTATCTGCAATGAACACTTTGAAACTGAGGACACACGCCCATGTATTACTGTGTGAGA	300
Db	616	GTCTACCTGCAATGAACAACTTTAAGAGTTGAAGACATGGGTATCTATTACTG-----	668
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QY	361	GTCTCCTCA	369
Db	721	GTCTCCTAA	729
RESULT 15			
RS-09-172-019-22			

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; Sequence 22, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,019
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both )
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
;
US-09-172-019-22

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Query Match	55.3%	Score	204.2	DB	3	Length	738
Best Local Similarity	74.8%	Pred. No.	1.5e-57				
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Db	376	GAAGTTAACTGGATGAGACTGGAGGAGCTTGGTGGCACTGGGAGCCCATGAAACTC	435				
Qy	61	TCATGTCGAGCCTCTGGATTACCTTCAATAACTACGCCATGAATTTGGTCCGCCAGGCT	120				
Db	436	TCCTGTGTGGCTCTGGATTCACTTTTAGTGACCTACTGGATGAATCGGTCCGCCAGTCT	495				
Qy	121	CCAGGAAAGGTTTGGAAATGGTTGCTCGCATAGAAGTAAACGCTAATAATTATTCGCAACA	180				
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
3349.042 Million cell updates/sec

Title: US-09-893-615-86
Perfect score: 369
Sequence: 1 GAAGTGATGCTGGTGAGTC.....CCTCACTCACCGTCTCCCTCA 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues
Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	201.4	54.6	420	10	US-09-286-240-3
8	198.2	53.7	1446	10	US-09-910-059-130
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15	192.4	52.1	357	12	US-10-044-534-4
16	191.4	51.9	424	10	US-09-730-857-62
17	190.4	51.6	1437	9	US-10-124-905-7
18	190	51.5	856	10	US-09-883-758-3
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20	189.8	51.4	424	10	US-09-730-857-50	Sequence 50, Appl
21	189.8	51.4	424	10	US-09-730-857-64	Sequence 64, Appl
22	188.2	51.0	424	10	US-09-730-857-14	Sequence 44, Appl
23	188.2	51.0	424	10	US-09-730-857-48	Sequence 48, Appl
24	188.2	51.0	424	10	US-09-730-857-54	Sequence 54, Appl
25	188.2	51.0	424	10	US-09-730-857-58	Sequence 58, Appl
26	187	50.7	466	10	US-09-881-823-11	Sequence 11, Appl
27	186.6	50.6	424	10	US-09-730-857-28	Sequence 28, Appl
28	186.6	50.6	424	10	US-09-730-857-40	Sequence 40, Appl
29	184	49.9	530	10	US-09-844-684-14	Sequence 14, Appl
30	183.6	49.8	363	10	US-09-822-698A-4	Sequence 4, Appl
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38	183.6	49.8	1143	10	US-09-822-698A-6	Sequence 6, Appl
39	183.6	49.8	1356	10	US-09-822-698A-27	Sequence 27, Appl
40	182.4	49.4	580	10	US-09-844-684-12	Sequence 12, Appl
41	182	49.3	406	9	US-10-046-935-2168	Sequence 2168, Ap
42	179	48.5	504	12	US-10-006-773-3	Sequence 3, Appl
43	178.6	48.4	423	7	US-08-779-784-3	Sequence 3, Appl
44	176.8	47.9	364	7	US-08-779-784-14	Sequence 14, Appl
45	176.4	47.8	532	9	US-09-187-693-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-893-615-86
; Sequence 86, Application US/09893615
; Patent No. US20020082395A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
; Schuman, Richard F.
; Wong, Hing
; Stinson, Jeffrey L.
; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
; POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; Zip: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Elnaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 04995.0041-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..369
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-893-615-86

Query Match      100.0%; Score 369; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.9e-103;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGAGGCTTAAAGGGTCATTGAAACTC 60
DB 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGAGGCTTAAAGGGTCATTGAAACTC 60
QY 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
DB 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
QY 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
DB 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
QY 121 CCAGGAAAGGGTTTGGAAATGGTTCGCGATAAGAAAGTAAAGTAATAATTATGCAACA 180
DB 121 CCAGGAAAGGGTTTGGAAATGGTTCGCGATAAGAAAGTAAAGTAATAATTATGCAACA 180
QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTTCCACTCTCCAGAGATGATTCACAAAGCATG 240
DB 181 TTTTATGCCGATTCAGTGAAGACAGGTTTCCACTCTCCAGAGATGATTCACAAAGCATG 240
QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTTCCACTCTCCAGAGATGATTCACAAAGCATG 240
DB 181 TTTTATGCCGATTCAGTGAAGACAGGTTTCCACTCTCCAGAGATGATTCACAAAGCATG 240
QY 241 CTCTATCTGCAAAATGAACAACCTTCAAACTGAGGACAGCCATGTATTTACTGTGTGAGA 300
DB 241 CTCTATCTGCAAAATGAACAACCTTCAAACTGAGGACAGCCATGTATTTACTGTGTGAGA 300
QY 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
DB 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
QY 361 GTCCTCTCA 369
DB 361 GTCCTCTCA 369

RESULT 2
US-09-881-823-15
; Sequence 15, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(442)
US-09-881-823-15

Query Match      75.7%; Score 279.4; DB 10; Length 466;
Best Local Similarity 86.7%; Pred. No. 6.8e-76;
Matches 320; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGAGGCTTAAAGGGTCATTGAAACTC 60
DB 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGAGGCTTAAAGGGTCATTGAAACTC 60
QY 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
DB 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
QY 121 CCAGGAAAGGGTTTGGAAATGGTTCGCGATAAGAAAGTAAAGTAATAATTATGCAACA 180
DB 121 CCAGGAAAGGGTTTGGAAATGGTTCGCGATAAGAAAGTAAAGTAATAATTATGCAACA 180
QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTTCCACTCTCCAGAGATGATTCACAAAGCATG 240
DB 181 TTTTATGCCGATTCAGTGAAGACAGGTTTCCACTCTCCAGAGATGATTCACAAAGCATG 240
QY 241 CTCTATCTGCAAAATGAACAACCTTCAAACTGAGGACAGCCATGTATTTACTGTGTGAGA 300
DB 241 CTCTATCTGCAAAATGAACAACCTTCAAACTGAGGACAGCCATGTATTTACTGTGTGAGA 300
QY 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
DB 301 CGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
QY 361 GTCCTCTCA 369
DB 361 GTCCTCTCA 369

RESULT 3
US-09-840-459-96
; Sequence 96, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 96
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-840-459-96

Query Match      73.0%; Score 269.2; DB 10; Length 443;
Best Local Similarity 94.0%; Pred. No. 8.5e-73;
Matches 280; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGAGGCTTAAAGGGTCATTGAAACTC 60
DB 58 GAGGTGAGCTTGTGTAGTCTGGAGGAGGATTGGTGAGGCTTAAAGGGTCATTGAAACTC 117
QY 61 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 120
DB 118 TCATGTCGAGCCTCTGGATTACCTTCAATAACTTACGCCATGAATTTGGTCCGCCAGGCT 177
QY 121 CCAGGAAAGGGTTTGGAAATGGTTCGCGATAAGAAAGTAAAGTAATAATTATGCAACA 180
DB 121 CCAGGAAAGGGTTTGGAAATGGTTCGCGATAAGAAAGTAAAGTAATAATTATGCAACA 180
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; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
US-09-840-459-103

Query Match 67.5%; Score 249.2; DB 10; Length 357;
Best Local Similarity 90.5%; Pred. No. 9.8e-67;
Matches 266; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Db 357 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTTCATTGAGACTC 298
Qy 61 TCATGTGAGCCTCTGGATTTCACCTTCAATACTACGCGCATGAATGGTCCGCCAGGCT 120
Db 297 TCATGTGAGCCTCTGGATTTCACCTTCAATACTACGCGCATGAATGGTCCGCCAGGCT 238
Qy 121 CCAGAAAGGGTTTGGATGGTCTCGCATAGAAAGTAAAGTAATAATTATGCAACA 180
Db 237 CCAGAAAGGGTTTGGATGGTCTCGCATAGAAAGTAAAGTAATAATTATGCAACA 178
Qy 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCTCTCCAGAGATGATTCACAAAGCATG 240
Db 177 TATTATGCCGATTCAGTGAAGACAGATTCACCTCTCCAGAGATGATTCACAAAGCATG 118
Qy 241 CTCATCTGCAATGCAACACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 294
Db 117 CTCATCTGCAATGCAACACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 64

RESULT 7
US-09-286-240-3
; Sequence 3, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Felt, James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 10498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(420)
US-09-286-240-3

Query Match 54.68; Score 201.4; DB 10; Length 420;
Best Local Similarity 73.7%; Pred. No. 3.9e-52;
Matches 272; Conservative 0; Mismatches 91; Indels 6; Gaps 1;
Qy 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Db 58 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 117
Qy 61 TCATGTGAGCCTCTGGATTTCACCTTCAATACTACGCGCATGAATGGTCCGCCAGGCT 120
Db 118 TCCGTGAGCCTCTGGATTTCACCTTCAATACTACGCGCATGAATGGTCCGCCAGGCT 177

Qy 121 CCAGAAAGGGTTTGGATGGTCTCGCATAGAAAGTAAAGTAATAATTATGCAACA 180
Db 178 CCGGAGAAGAGGCTGGAGTGGGTCCGCAACCATAGTAGTGGTGGTAA-----CACC 231
Qy 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCTCTCCAGAGATGATTCACAAAGCATG 240
Db 232 TACTATCCAGACAGTGTGAAGGGTCTGATTCACCATCTCCAGAGACATTCGCAAGAACACC 291
Qy 241 CTCATCTGCAATGCAACACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
Db 292 CTGTACCTGCAATGAGCAGTCTGAGGTCTGAGGACACAGGCCCTTGTATTACTGTACAAGA 351
Qy 301 CGGGGGGCTTCAGGATTGACTATGCTATGGACTACTTGGGGTCAAGGAACCTCACTCACC 360
Db 352 TTAGGAGACTACGGCTACGCCCTATATGACTACTTGGGGTCAAGGAACCTCACTCACC 411
Qy 361 GTCTCCTCA 369
Db 412 GTCTCCTCA 420

RESULT 8

US-09-910-059-130
; Sequence 130, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
; NAME/KEY: CDS
; LOCATION: (16)..(1434)
; OTHER INFORMATION:
US-09-910-059-130

Query Match 53.7%; Score 198.2; DB 10; Length 1446;
Best Local Similarity 73.2%; Pred. No. 6.2e-51;
Matches 270; Conservative 0; Mismatches 93; Indels 6; Gaps 1;
Qy 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
Db 742 GAGGTGAAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGTTCCTCGAGACTC 801
Qy 61 TCATGTGAGCCTCTGGATTTCACCTTCAATACTACGCGCATGAATGGTCCGCCAGGCT 120
Db 802 TCCTGTGCAACTTCTGGGTTCACCTTCACTACTACTACTACTACTACTACTACTACTACT 861
Qy 121 CCAGAAAGGGTTTGGATGGTTCCTCGCATAGAAAGTAAAGTAATAATTATGCAACA 180
Db 862 CCAGAAAGGACACTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 921
Qy 181 TTTTATGCCGATTCAGTGAAGACAGGTTCACTCACCCTCCAGAGATGATTCACAAAGCATG 240

Db 922 GAGTACAGTGCATCTGTGAAGGCTCGGTTCACCATCTCCAGAGACAAAATCCCAAGCATC 981
Oy 241 CTCATCTGCAATCAACAACCTTGAAGAGTGGAGACAGCCATCTATTACTGTGTGAGA 300
Db 982 CTCATCTTCAATGAACACCTTGAGAGCTGAGGACAGTCCACATATTACTGTACAAGA 1041
Oy 301 CGGGGGCTTCAGGAGTTCAGTATGCTATGGACTACTGGGGTCAAGGAACCTTCACCTCACC 360
Db 1042 GATAGGGGCTACGCTTCTACT-----TTGACTACTGGGGCAAGGCACCACTCTCACA 1095
Oy 361 GTCCTCTCA 369
Db 1096 GTCCTCTCA 1104

RESULT 9

US-09-756-301A-4
; Sequence 4, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Jumming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09756.301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)

US-09-756-301A-4

Query Match 52.1%; Score 192.4; DB 10; Length 357;
Best Local Similarity 72.7%; Pred. No. 2e-49;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;
Oy 1 GAAGTGATCGTGGAGTCTGGTGGAGATTGGTGCAGCCTAAAGGGTCAATTGAACTC 60
Db 1 GAAGTGAAGCTTGAGGAGTCTGGAGGAGCTGGTGCACCACTGGAGGATCCATGAAGTCTC 60

Oy 61 TCATGTGCGAGCCTCGGATTTCACCTTCAATAACTACGCCATGAATGGGTCCGCCAGGCT 120
Db 61 TCCTGTGTGCTCTCGGATTTCATTTTCAGTAACCACTGGATGAACCTGGGTCCGCCAGTCT 120
Oy 121 CCAGGAAGAGGTTTGGATGGTTCGCTCCCATGAAGAAGTAAAGTAATTAATTATGCAACA 180
Db 121 CCAGAGAAGGGCTTTCAGTGGTTCGCTGAATTAGATCAAAATCTATTAAATTTGCAACA 180
Oy 181 TTTTATGCGGATTTCAGTGAACACAGAGTTTCACCATCTCCAGAGATGATTTCCAAAGCATG 240
Db 181 CATTATGCGGAGTCTGTGAAGGAGGTTTCACCATCTCAAGAGATGATTTCCAAAGTGT 240
Oy 241 CTCATCTGCAAAATGAACAACCTTGAAGAGTGGAGACACAGCCATCTATTACTGTGTGAGA 300
Db 241 GTCACCTGCAAAATGACCGACTTAAAGAACTGAAGACACTGGCGCTTATTACTGTTCAGG 300
Oy 301 CGGGGGCTTCAGGAGTTCAGTATGCTATGGACTACTGGGGTCAAGGAACCTTCACCTCACC 360
Db 301 AATTACTACGGTAGTACCTAC-----GACTACTGGGGCAAGGCACCACTCTCACA 351
Oy 361 GTCCTCC 366
Db 352 GTCCTCC 357

RESULT 10

US-09-927-703-4
; Sequence 4, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Jumming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: (1)...(357)
US-09-927-703--4

Query Match
Best Local Similarity 52.1%; Score 192.4; DB 10; Length 357;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

QY 1 GAAGTGTGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCAATTGAAACTC 60
Db 1 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCAGCCTAAAGGGTCAATTGAAACTC 60
QY 61 TCATGTGCAGCCTCTGGATTCACCTTCAATACTACCCCATGAATTGGGTCCGCCAGGCT 120
Db 61 TCCTGTGTGCTGCTGGATTCATTTTCAGTAACCACTGGATGAAGTGGGTCCGCCAGGCT 120
QY 121 CCAGGAAGGGTGTGGAAATGGTTCGCATGAAGAGTAAAGTAATAATTATGCAACA 180
Db 121 CCAGGAAGGGGCTTGAGTGGTTCGTAATAGATCAAAATCTAATTTCTGCAACA 180
QY 181 TTTATGCCAGCTTCAGTGAAGACAGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 CATTATCGGAGTCTGTGAAGGAGGTTTCCACCATCTCAAGAGATGATTCACAAAGCATG 240
QY 241 CTCTATCTGCAAAATGAACACTTTGAAACTGAGGACACAGCCATGTATTACTGTGAGA 300
Db 241 GTCTACTGCAAAATGACCGACTTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCAGG 300
QY 301 CGGGGGCTTCAGGAGTGTGACTATGTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
Db 301 AATTACTACGGTAGTACCTAC-----GACTACTGGGGCCCAAGGCACCACTCTCACA 351
QY 361 GTCTCC 366
Db 352 GTCTCC 357

RESULT 11
US-09-766-535A-4
; Sequence 4, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Wilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
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; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-09-766-535A-4

Query Match
Best Local Similarity 52.1%; Score 192.4; DB 10; Length 357;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

QY 1 GAAGTGTGCTGGTGGAGTCTGGTGGAGGATTTGGTGCAGCCTAAAGGGTCAATTGAAACTC 60
Db 1 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCAGCCTAAAGGGTCAATTGAAACTC 60
QY 61 TCATGTGCAGCCTCTGGATTCACCTTCAATACTACCCCATGAATTGGGTCCGCCAGGCT 120
Db 61 TCCTGTGTGCTGCTGGATTCATTTTCAGTAACCACTGGATGAAGTGGGTCCGCCAGGCT 120
QY 121 CCAGGAAGGGTGTGGAAATGGTTCGCATGAAGAGTAAAGTAATAATTATGCAACA 180
Db 121 CCAGGAAGGGGCTTGAGTGGTTCGTAATAGATCAAAATCTAATTTCTGCAACA 180
QY 181 TTTATGCCAGCTTCAGTGAAGACAGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
Db 181 CATTATCGGAGTCTGTGAAGGAGGTTTCCACCATCTCAAGAGATGATTCACAAAGCATG 240
QY 241 CTCTATCTGCAAAATGAACACTTTGAAACTGAGGACACAGCCATGTATTACTGTGAGA 300
Db 241 GTCTACTGCAAAATGACCGACTTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCAGG 300
QY 301 CGGGGGCTTCAGGAGTGTGACTATGTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
Db 301 AATTACTACGGTAGTACCTAC-----GACTACTGGGGCCCAAGGCACCACTCTCACA 351
QY 361 GTCTCC 366
Db 352 GTCTCC 357

RESULT 12
US-09-756-161A-4
; Sequence 4, Application US/09756161A
; Patent No. US2002013207A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Wilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
```


; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-09-756-161A-4

Query Match 52.1%; Score 192.4; DB 10; Length 357;
Best Local Similarity 72.7%; Pred. No. 2e-49;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

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Qy 1 GAAGTGAGCTGGTGGAGCTCTGGTGGAGGATTGGTGCAGCCTAAAGGCTCATTTGAAACTC 60
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAAACTC 60

Qy 61 TCATGTGCAGCCTCTGGATTACCTTCAATAACTACGCATGAATTTGGTCCGCCAGGCT 120
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCCTGTGTGCTCTGGATTCAATTTTCAGTAACCACTGGATGGTCCGCCAGTCT 120

Qy 121 CCAGAAAGGCTTGGATGGTTCGCTCGCATAGAACTAAAGTAAATTAATTCGAACA 180
    ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CCAGAAAGGCTTGGATGGTTCGCTCGCATAGAACTAAAGTAAATTAATTCGAACA 180

Qy 181 TTTATGCCGATTCAGTGAAGACAGGTTCCACCTCTCCAGAGATGATTCACAAAGCATG 240
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CATTATGGGAGTCTGTGAAAGGGAGGTTCCACCTCTCAAGAGATGATTTCCAAAAGTCT 240

Qy 241 CTCATCTGCAAACTGAACAACCTTGAAAACCTGAGGACACAGCCATGATTTACTGTGTGAGA 300
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GTCACCTGCAAACTGACCGACTTAGAACTAGAACACTGGGCTTTTACTGTTCCAGG 300

Qy 301 CGGGGGCTTCAGGAGTTGACTATGCTATGACTACTGGGTCAAGAACCTCACTCACC 360
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AATTACTAGGTAGTACCTAC-----GACTACTGGGGCCAAAGGCCACTCTCACA 351

Qy 361 GTCCTCC 366
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Db 352 GTCCTCC 357
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RESULT 13

US-10-010-229-4
; Sequence 4, Application US/10010229
; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-10-010-229-4

Query Match 52.1%; Score 192.4; DB 12; Length 357;
Best Local Similarity 72.7%; Pred. No. 2e-49;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

```
Qy 1 GAAGTGAGCTGGTGGAGCTCTGGTGGAGGATTGGTGCAGCCTAAAGGCTCATTTGAAACTC 60
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAAACTC 60

Qy 61 TCATGTGCAGCCTCTGGATTACCTTCAATAACTACGCATGAATTTGGTCCGCCAGGCT 120
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCCTGTGTGCTCTGGATTCAATTTTCAGTAACCACTGGATGGTCCGCCAGTCT 120

Qy 121 CCAGAAAGGCTTGGATGGTTCGCTCGCATAGAACTAAAGTAAATTAATTCGAACA 180
    ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CCAGAAAGGCTTGGATGGTTCGCTCGCATAGAACTAAAGTAAATTAATTCGAACA 180

Qy 181 TTTATGCCGATTCAGTGAAGACAGGTTCCACCTCTCCAGAGATGATTCACAAAGCATG 240
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CATTATGGGAGTCTGTGAAAGGGAGGTTCCACCTCTCAAGAGATGATTTCCAAAAGTCT 240

Qy 241 CTCATCTGCAAACTGAACAACCTTGAAAACCTGAGGACACAGCCATGATTTACTGTGTGAGA 300
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GTCACCTGCAAACTGACCGACTTAGAACTAGAACACTGGGCTTTTACTGTTCCAGG 300

Qy 301 CGGGGGCTTCAGGAGTTGACTATGCTATGACTACTGGGTCAAGAACCTCACTCACC 360
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AATTACTAGGTAGTACCTAC-----GACTACTGGGGCCAAAGGCCACTCTCACA 351

Qy 361 GTCCTCC 366
    |||||
Db 352 GTCCTCC 357
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RESULT 14

US-10-043-450-4
; Sequence 4, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04

;; PRIOR APPLICATION NUMBER: U.S. 08/192,093
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/010,406
;; PRIOR FILING DATE: 1993-01-29
;; PRIOR APPLICATION NUMBER: U.S. 08/013,413
;; PRIOR FILING DATE: 1993-02-02
;; PRIOR APPLICATION NUMBER: U.S. 07/943,852
;; PRIOR FILING DATE: 1992-09-11
;; PRIOR APPLICATION NUMBER: U.S. 07/853,606
;; PRIOR FILING DATE: 1992-03-18
;; PRIOR APPLICATION NUMBER: U.S. 07/670,827
;; PRIOR FILING DATE: 1991-03-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 357
;; TYPE: DNA
;; ORGANISM: Mus Balb/c
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(357)
US-10-043-450-4

Query Match 52.1%; Score 192.4; DB 12; Length 357;
Best Local Similarity 72.7%; Pred. No. 2e-49;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

QY 1 GAAGTGATCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
DB 1 GAAGTGAACCTTGAGGAGTCTGGAGGAGGCTGGTGCACCTGGAGGATCCATGAAACTC 60

QY 61 TCATGTGACGCTCTGGATTCACCTTCAATAACTAGCCCATGAATGGGTCCGCCAGGCT 120
DB 61 TCCTGTGTTGCCCTCTGGATTCATTTTCAGTACCACCTGGATGAACCTGGGTCCGCCAGGCT 120

QY 121 CCAGGAAGGGTTTGAATGGGTTGCTCCGATGAAGTAAAGTAAATTAATATGCAACA 180
DB 121 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAATAGATCAAAATCTATTAAATCTGCAACA 180

QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
DB 181 CATTATGCCGAGTCTGTGAAGGAGGTTCCACCATCTCAAGAGATGATTCACAAAGCATG 240

QY 241 CTCATCTGCAATGAACAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
DB 241 GTCTACCTGCAATGACCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300

QY 301 CGGGGGCTTCAGGATTCAGTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
DB 301 AATTACTACGGTAGTACCTAC-----GACTACTGGGGCCAGGCACCTCTCTACA 351

QY 361 GTCTCC 366
DB 352 GTCTCC 357

RESULT 15
US-10-044-534-4
;; Sequence 4, Application US/10044534
;; Patent No. US20020146419A1
;; GENERAL INFORMATION:
;; APPLICANT: Le, Junming
;; APPLICANT: Vilcek, Jan
;; APPLICANT: Daddona, Peter
;; APPLICANT: Ghayeb, John
;; APPLICANT: Knight, David M.
;; APPLICANT: Siegel, Scott
;; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;; FILE OF INVENTION: Human Tumor Necrosis Factor
;; FILE REFERENCE: 0975.1005-013
;; CURRENT APPLICATION NUMBER: US/10044,534
;; CURRENT FILING DATE: 2002-01-10
;; PRIOR APPLICATION NUMBER: 09/927,703

;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: U.S. 09/756,398
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: U.S. 09/133,119
;; PRIOR FILING DATE: 1998-08-12
;; PRIOR APPLICATION NUMBER: U.S. 08/570,674
;; PRIOR FILING DATE: 1995-12-11
;; PRIOR APPLICATION NUMBER: U.S. 08/324,799
;; PRIOR FILING DATE: 1994-10-18
;; PRIOR APPLICATION NUMBER: U.S. 08/192,102
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,861
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/192,093
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: U.S. 08/010,406
;; PRIOR FILING DATE: 1993-01-29
;; PRIOR APPLICATION NUMBER: U.S. 08/013,413
;; PRIOR FILING DATE: 1993-02-02
;; PRIOR APPLICATION NUMBER: U.S. 07/943,852
;; PRIOR FILING DATE: 1992-09-11
;; PRIOR APPLICATION NUMBER: U.S. 07/853,606
;; PRIOR FILING DATE: 1992-03-18
;; PRIOR APPLICATION NUMBER: U.S. 07/670,827
;; PRIOR FILING DATE: 1991-03-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 357
;; TYPE: DNA
;; ORGANISM: Mus Balb/c
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(357)
US-10-044-534-4

Query Match 52.1%; Score 192.4; DB 12; Length 357;
Best Local Similarity 72.7%; Pred. No. 2e-49;
Matches 266; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

QY 1 GAAGTGATCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
DB 1 GAAGTGAACCTTGAGGAGTCTGGAGGAGGCTGGTGCACCTGGAGGATCCATGAAACTC 60

QY 61 TCATGTGACGCTCTGGATTCACCTTCAATAACTAGCCCATGAATGGGTCCGCCAGGCT 120
DB 61 TCCTGTGTTGCCCTCTGGATTCATTTTCAGTACCACCTGGATGAACCTGGGTCCGCCAGGCT 120

QY 121 CCAGGAAGGGTTTGAATGGGTTGCTCCGATGAAGTAAAGTAAATTAATATGCAACA 180
DB 121 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAATAGATCAAAATCTATTAAATCTGCAACA 180

QY 181 TTTTATGCCGATTCAGTGAAGACAGGTTCCACCATCTCCAGAGATGATTCACAAAGCATG 240
DB 181 CATTATGCCGAGTCTGTGAAGGAGGTTCCACCATCTCAAGAGATGATTCACAAAGCATG 240

QY 241 CTCATCTGCAATGAACAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
DB 241 GTCTACCTGCAATGACCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300

QY 301 CGGGGGCTTCAGGATTCAGTATGCTATGGACTACTGGGTCAAGGAACCTCACTCACC 360
DB 301 AATTACTACGGTAGTACCTAC-----GACTACTGGGGCCAGGCACCTCTCTACA 351

QY 361 GTCTCC 366
DB 352 GTCTCC 357

Search completed: November 27, 2002, 05:31:00
Job time : 53.4323 secs